

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 4, 2005, 03:31:33 ; Search time 5843 Seconds  
(without alignments)  
11162.198 Million cell updates/sec

Title: US-09-989-724-386  
Perfect score: 1346  
Sequence: 1 gaaagaatgttggtgct.....aaaaaaaaaaaaaaaaaaaa 1346

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1346	100.0	1346	6	AR52633
2	1346	100.0	1346	6	AR528692
3	1346	100.0	1346	6	AX403499
4	1346	100.0	1346	6	AX464348
5	1346	100.0	1346	9	AY359060
6	1328.6	98.7	1605	9	BC014317
7	1325.4	98.5	1377	9	BC050606
8	1325.4	98.5	1440	9	BC015099
9	1324.6	98.4	1447	6	BD205644
10	1321.8	98.2	1401	6	BD083420
11	1309.4	97.3	1347	6	AX083392
12	1307.8	97.2	1345	9	AF229179
13	1305	97.0	1356	6	BD135300
14	845.2	62.8	862	6	BD270445
15	799.4	59.4	848	6	AR177334
16	799.4	59.4	848	6	BD139270
17	799.4	59.4	848	6	BD203799
18	799.4	59.4	848	6	BD247957
19	799.4	59.4	848	6	CQ771919

93	119.8	8.9	3732	6	AR528488	AR528488 Sequence	C 166	64	4.8	138964	2	BX950176	BX950176 Danio rer
94	119.8	8.9	3732	6	AX463938	AX463938 Sequence	C 167	64	4.8	250029	3	AE014830	AE014830 Plasmodi
95	119.8	8.9	3732	5	AY358714	AY358714 Homo sapi	C 168	64	4.8	250029	3	AE014830	AE014830 Plasmodi
96	118	8.8	1879	5	BC053284	BC053284 Danio rer	C 169	63.8	4.7	110000	2	PFMAL13_11	Continuation (12 o
97	117.4	8.7	2920	6	AR353103	AR353103 Sequence	C 170	63.8	4.7	173234	2	CR550306	CR550306 Danio rer
98	111.4	8.3	435	6	CO458859	CO458859 Sequence	C 171	63.8	4.7	180660	2	BX255894	BX255894 Danio rer
99	111.4	8.3	2638	6	AX047762	AX047762 Sequence	C 172	63.8	4.7	202533	2	CR392031	CR392031 Danio rer
100	109.6	8.1	2760	10	AB053181	AB053181 Mus muscu	C 173	63.8	4.7	245072	2	CR381551	CR381551 Danio rer
101	108.6	8.1	1993	10	AB053182	AB053182 Mus muscu	C 174	63.8	4.7	330050	3	PFA929355	AL929355 Plasmodi
102	108.2	8.0	2638	6	AX047765	AX047765 Sequence	C 175	63.6	4.7	164755	2	CR527094	CR527094 Danio rer
103	108.2	8.0	2739	6	CO754224	CO754224 Sequence	C 176	63.6	4.7	183844	2	CR753873	CR753873 Danio rer
104	108.2	8.0	2739	10	BC026801	BC026801 Mus muscu	C 177	63.6	4.7	186005	2	CR927412	CR927412 Danio rer
105	96.8	7.2	2134	6	CO7114933	CO7114933 Sequence	C 178	63.6	4.7	202533	2	CR392031	CR392031 Danio rer
106	96.8	7.2	2262	6	E39034	E39034 MPROT15 pol	C 179	63.6	4.7	226108	2	CR759967	CR759967 Danio rer
107	94.8	7.0	1013	9	AK026461	AK026461 Homo sapi	C 180	63.6	4.7	250029	3	AE014820	AE014820 Plasmodi
108	77.4	5.8	41572	9	AY217547	AY217547 Homo sapi	C 181	63.4	4.7	67970	3	PFMAL1P3	AL031746 Plasmodi
109	77.4	5.8	194492	9	AC097625	AC097625 Homo sapi	C 182	63.4	4.7	110000	2	PFMAL13_05	Continuation (6 of
110	73.4	5.5	84550	3	PFMAL1P2_3	Continuation (4 of	C 183	63.4	4.7	110000	3	AC116305_0	AC116305 Dictyoste
111	69.4	5.2	2350	6	AR263862	AR263862 Sequence	C 184	63.4	4.7	170276	9	AL353143	AL353143 Human DNA
112	69.4	5.2	216259	2	CR749761	CR749761 Danio rer	C 185	63.2	4.7	200260	2	CR753814	CR753814 Danio rer
113	69.2	5.1	202661	2	CR556715	CR556715 Danio rer	C 186	63.2	4.7	206042	2	CR753794	CR753794 Danio rer
114	69.2	5.1	250039	3	AE014830	AE014830 Plasmodi	C 187	63	4.7	3030	3	PFAMRNA	LI2043 Plasmodi
115	69	5.1	287510	2	CR753823	CR753823 Danio rer	C 188	63	4.7	3474	6	AX576256	AX576256 Sequence
116	68.6	5.1	348034	5	CR382400	CR382400 Plasmodi	C 189	63	4.7	164668	9	AC091925	AC091925 Homo sapi
117	68.4	5.1	1119	5	BX935959	BX935959 Gallus ga	C 190	63	4.7	175016	2	CR759867	CR759867 Danio rer
118	68.2	5.1	164979	2	CR847573	CR847573 Danio rer	C 191	63	4.7	188663	2	CR457449	CR457449 Danio rer
119	68	5.1	110000	3	PFMAL1P2_2	Continuation (3 of	C 192	63	4.7	250663	3	AE014826	AE014826 Plasmodi
120	67.8	5.0	167245	2	CR626882	CR626882 Danio rer	C 193	63	4.7	327236	2	CR385026	CR385026 Danio rer
121	67.6	5.0	209719	2	CR847825	CR847825 Danio rer	C 194	62.8	4.7	5286	6	CO806844	CO806844 Sequence
122	67.2	5.0	110000	2	PFMAL7P1_12	Continuation (13 o	C 195	62.8	4.7	5286	6	CO807118	CO807118 Sequence
123	67.2	5.0	172464	2	CR792425	CR792425 Danio rer	C 196	62.8	4.7	5286	6	AX795782	AX795782 Sequence
124	67	5.0	8056	6	AX599046	AX599046 Sequence	C 197	62.8	4.7	5286	6	AX795898	AX795898 Sequence
125	67	5.0	55372	2	CR759965	CR759965 Danio rer	C 198	62.8	4.7	100925	9	AC012627	AC012627 Homo sapi
126	67	5.0	348034	3	CR382400	CR382400 Plasmodi	C 199	62.8	4.7	142514	2	CR790361	CR790361 Danio rer
127	66.8	5.0	348600	1	AB063521	AB063521 Miggleswo	C 200	62.8	4.7	154901	2	CR751231	CR751231 Danio rer
128	66.6	4.9	55372	2	CR759965	CR759965 Danio rer	C 201	62.8	4.7	181557	2	CR847945	CR847945 Danio rer
129	66.6	4.9	251448	3	AE014819	AE014819 Plasmodi	C 202	62.8	4.7	192187	3	AC117072	AC117072 Dictyoste
130	66.2	4.9	58697	2	AC144975	AC144975 Xenopus t	C 203	62.8	4.7	208116	2	CR555302	CR555302 Danio rer
131	66.2	4.9	110000	3	PFMAL1P2_0	AL031745 Plasmodi	C 204	62.8	4.7	214709	2	CR749183	CR749183 Danio rer
132	66.2	4.9	165988	2	CR626888	CR626888 Danio rer	C 205	62.8	4.7	235532	9	AC008739	AC008739 Homo sapi
133	66.2	4.9	171427	9	AC021590	AC021590 Homo sapi	C 206	62.6	4.7	153947	2	CR788315	CR788315 Danio rer
134	66.2	4.9	198627	5	AL845168	AL845168 Zebrafish	C 207	62.6	4.7	168389	9	AC110015	AC110015 Homo sapi
135	66	4.9	93133	9	AC022140	AC022140 Homo sapi	C 208	62.6	4.7	196859	9	AC087277	AC087277 Homo sapi
136	66	4.9	109975	9	AC112497	AC112497 Homo sapi	C 209	62.6	4.7	209852	2	AC151363	AC151363 Gasterost
137	66	4.9	148878	2	CR759816	CR759816 Danio rer	C 210	62.4	4.6	5413	6	AX251450	AX251450 Sequence
138	66	4.9	174402	9	AC016991	AC016991 Homo sapi	C 211	62.4	4.6	9810	6	AX345328	AX345328 Sequence
139	65.8	4.9	60604	2	AC023466	AC023466 Homo sapi	C 212	62.4	4.6	149831	2	CR847943	CR847943 Danio rer
140	65.8	4.9	172578	2	CR812468	CR812468 Danio rer	C 213	62.4	4.6	174001	3	BX927081	BX927081 Plasmodi
141	65.6	4.9	186147	2	CR626891	CR626891 Danio rer	C 214	62.4	4.6	250029	2	AE014816	AE014816 Plasmodi
142	65.4	4.9	116197	2	AC135614	AC135614 Pan trogl	C 215	62.4	4.6	253151	3	AE014842	AE014842 Plasmodi
143	65.4	4.9	158085	2	CR388149	CR388149 Danio rer	C 216	62.4	4.6	335050	3	PFA929356	AL929356 Plasmodi
144	65.2	4.8	170920	9	AC138627	AC138627 Homo sapi	C 217	62.2	4.6	8056	6	AX598900	AX598900 Sequence
145	65.2	4.8	181515	2	CR759824	CR759824 Danio rer	C 218	62.2	4.6	72243	9	AL731858	AL731858 Human DNA
146	65.2	4.8	227073	2	CR846086	CR846086 Danio rer	C 219	62.2	4.6	124114	9	HSJ858M22	AL118510 Human DNA
147	65	4.8	7448	3	AF465305	AF465305 Dictyoste	C 220	62.2	4.6	165797	2	CR847851	CR847851 Danio rer
148	65	4.8	192581	2	PFMAL13P1	AL049180 Plasmodi	C 221	62.2	4.6	186857	2	CR735109	CR735109 Danio rer
149	65	4.8	222825	2	CR628387	CR628387 Danio rer	C 222	62.2	4.6	195319	2	CR388410	CR388410 Danio rer
150	65	4.8	228609	2	CR759885	CR759885 Danio rer	C 223	62.2	4.6	196420	2	BX908771	BX908771 Danio rer
151	64.8	4.8	167124	2	CR812482	CR812482 Danio rer	C 224	62	4.6	121958	2	CR759861	CR759861 Danio rer
152	64.8	4.8	171382	2	CR392331	CR392331 Danio rer	C 225	62	4.6	134799	2	CR352285	CR352285 Danio rer
153	64.8	4.8	172399	2	CR762388	CR762388 Danio rer	C 226	62	4.6	182223	2	CR790384	CR790384 Danio rer
154	64.8	4.8	192676	10	AL671706	AL671706 Mouse DNA	C 227	62	4.6	210718	2	CR589941	CR589941 Danio rer
155	64.8	4.8	204662	2	CR753838	CR753838 Danio rer	C 228	61.8	4.6	110000	2	PFMAL13_22	Continuation (23 o
156	64.8	4.8	234796	2	CR318626	CR318626 Danio rer	C 229	61.8	4.6	133877	2	AC120883	AC120883 Homo sapi
157	64.8	4.8	245165	2	CR383660	CR383660 Danio rer	C 230	61.8	4.6	159448	2	CR627500	CR627500 Danio rer
158	64.8	4.8	76568	3	MBREV	AF538053 Monogiga	C 231	61.8	4.6	166820	2	CR388213	CR388213 Danio rer
159	64.4	4.8	174012	2	CR847512	CR847512 Danio rer	C 232	61.8	4.6	168103	2	CR751601	CR751601 Danio rer
160	64.4	4.8	174198	2	CR762438	CR762438 Danio rer	C 233	61.8	4.6	172285	2	CR381538	CR381538 Danio rer
161	64.4	4.8	250733	2	CR388030	CR388030 Danio rer	C 234	61.8	4.6	230976	2	BX927201	BX927201 Danio rer
162	64.2	4.8	5477	3	PFAATPAS	X71765 P. falcipar	C 235	61.8	4.6	261134	2	CR318600	CR318600 Danio rer
163	64.2	4.8	167872	2	CR792455	CR792455 Danio rer	C 236	61.8	4.6	335050	3	PFA929356	AL929356 Plasmodi
164	64.2	4.8	187144	2	BX957353	BX957353 Danio rer	C 237	61.6	4.6	2706	1	AF268053	AF268053 Candidatu
165	64	4.8	110000	2	PFMAL7P1_07	Continuation (8 of	C 238	61.6	4.6	129240	9	AC084128	AC084128 Homo sapi

239	61.6	4.6	156395	2	CR387986	Danio rer	CR387986	Danio rer	c 312	60	4.5	110000	2	PFMAL7P1_08	Continuation (9 of
240	61.6	4.6	163735	9	AC027277	Homo sapi	AC027277	Homo sapi	c 313	60	4.5	143903	5	BX247887	Zebratfish
241	61.6	4.6	182518	9	AC131649	Homo sapi	AC131649	Homo sapi	c 314	60	4.5	158548	3	PFMAL3P2	AL034558 Plasmid
242	61.6	4.6	185240	2	CR762404	Danio rer	CR762404	Danio rer	c 315	60	4.5	170627	2	AC125567	Rattus no
243	61.6	4.6	196762	2	CR759796	Danio rer	CR759796	Danio rer	316	60	4.5	172556	2	CR762400	Danio rer
244	61.6	4.6	218909	2	CR626875	Danio rer	CR626875	Danio rer	317	60	4.5	183318	2	CR376728	Danio rer
245	61.4	4.6	961	3	AY351412	Continuation (5 of	AY351412	Arcthusan	c 318	60	4.5	187277	9	AC022968	Homo sapi
246	61.4	4.6	110000	2	PFMAL8P1_04	Continuation (8 of	PFMAL8P1_04	Continuation (5 of	c 319	60	4.5	205013	2	AY269187	Homo sapi
247	61.4	4.6	110000	2	PFMAL8P1_07	Continuation (8 of	PFMAL8P1_07	Continuation (5 of	c 320	60	4.5	221924	2	CR388047	Danio rer
248	61.4	4.6	135121	9	AC069525	Homo sapi	AC069525	Homo sapi	c 321	60	4.5	233769	2	CR631124	Danio rer
249	61.4	4.6	163443	2	AC006280	Plasmid	AC006280	Plasmid	c 322	60	4.5	234796	2	CR318626	Danio rer
250	61.4	4.6	165959	2	CR792429	Danio rer	CR792429	Danio rer	323	60	4.5	250621	2	CR792433	Danio rer
251	61.4	4.6	195863	2	CR847978	Danio rer	CR847978	Danio rer	324	59.8	4.4	137594	2	CR812464	Danio rer
252	61.4	4.6	243513	2	CR753817	Danio rer	CR753817	Danio rer	c 325	59.8	4.4	159610	5	BX088559	Zebratfish
253	61.4	4.6	252650	2	AE014847	Plasmid	AE014847	Plasmid	c 326	59.8	4.4	162075	9	HS127D3	Human DNA
254	61.2	4.5	935	3	AY351413	Arcthusan	AY351413	Arcthusan	c 327	59.8	4.4	167518	9	CNS05TEK	Human chr
255	61.2	4.5	173288	2	AC138859	Homo sapi	AC138859	Homo sapi	c 328	59.8	4.4	174832	2	CR293499	Danio rer
256	61.2	4.5	175605	2	CR450746	Danio rer	CR450746	Danio rer	c 329	59.8	4.4	194559	2	CR628365	Danio rer
257	61.2	4.5	188638	2	CR759889	Danio rer	CR759889	Danio rer	c 330	59.8	4.4	196149	2	AC004709	Plasmid
258	61.2	4.5	264232	2	CR626890	Danio rer	CR626890	Danio rer	c 331	59.8	4.4	251797	2	BX890543	Danio rer
259	61	4.5	162977	2	CR631122	Danio rer	CR631122	Danio rer	c 332	59.8	4.4	252632	3	AE014818	Plasmid
260	61	4.5	174001	2	BX927081	Danio rer	BX927081	Danio rer	c 333	59.8	4.4	256879	3	AC116982	Dictyoste
261	61	4.5	192187	2	AC117072	Dictyoste	AC117072	Dictyoste	c 334	59.6	4.4	148385	2	CR749764	Danio rer
262	61	4.5	196759	2	CR788226	Danio rer	CR788226	Danio rer	c 335	59.6	4.4	155758	2	CR792441	Danio rer
263	61	4.5	246611	2	AC111404	Rattus no	AC111404	Rattus no	c 336	59.6	4.4	163724	2	CR788299	Danio rer
264	61	4.5	254449	3	AE014817	Plasmid	AE014817	Plasmid	c 337	59.6	4.4	164443	2	CR751221	Danio rer
265	61	4.5	333321	3	AC116986	Dictyoste	AC116986	Dictyoste	c 338	59.6	4.4	167229	9	AC006269	Homo sapi
266	60.8	4.5	165048	2	CR790371	Danio rer	CR790371	Danio rer	c 339	59.6	4.4	172285	2	CR381538	Danio rer
267	60.8	4.5	175235	2	CR790380	Danio rer	CR790380	Danio rer	c 340	59.6	4.4	182748	2	CR388066	Danio rer
268	60.8	4.5	180540	2	CR847859	Danio rer	CR847859	Danio rer	341	59.6	4.4	194513	2	CR524482	Danio rer
269	60.8	4.5	186040	2	CR391974	Danio rer	CR391974	Danio rer	c 342	59.6	4.4	210343	2	CR753890	Danio rer
270	60.8	4.5	210050	2	CR376844	Danio rer	CR376844	Danio rer	c 343	59.6	4.4	210548	2	CR755168	Danio rer
271	60.6	4.5	57941	9	BX323827	Human DNA	BX323827	Human DNA	c 344	59.6	4.4	225861	2	CR628381	Danio rer
272	60.6	4.5	72143	9	AC131094	Homo sapi	AC131094	Homo sapi	c 345	59.6	4.4	239941	2	CR749176	Danio rer
273	60.6	4.5	81147	9	AL606504	Human DNA	AL606504	Human DNA	346	59.4	4.4	47573	3	AF030694	Plasmid
274	60.6	4.5	83391	6	AX458577	Sequence	AX458577	Sequence	347	59.4	4.4	167548	2	CR759878	Danio rer
275	60.6	4.5	146613	2	CR786569	Danio rer	CR786569	Danio rer	c 348	59.4	4.4	169448	2	CR385039	Danio rer
276	60.6	4.5	146850	2	CR394559	Danio rer	CR394559	Danio rer	349	59.4	4.4	170929	2	CR759865	Danio rer
277	60.6	4.5	156141	2	CR749777	Danio rer	CR749777	Danio rer	350	59.4	4.4	171441	2	BX950202	Danio rer
278	60.6	4.5	169894	2	CR762466	Danio rer	CR762466	Danio rer	c 351	59.4	4.4	181515	9	CR759824	Danio rer
279	60.6	4.5	186175	2	CR318664	Danio rer	CR318664	Danio rer	c 352	59.4	4.4	186165	9	AC112187	Homo sapi
280	60.6	4.5	194561	2	CR450706	Danio rer	CR450706	Danio rer	c 353	59.4	4.4	198349	2	CR788292	Danio rer
281	60.6	4.5	205475	2	CR762392	Danio rer	CR762392	Danio rer	354	59.4	4.4	199145	2	CR759742	Danio rer
282	60.6	4.5	205544	2	CR847834	Danio rer	CR847834	Danio rer	c 355	59.4	4.4	204430	2	CR792453	Danio rer
283	60.6	4.5	210218	8	CR555304	Danio rer	CR555304	Danio rer	c 356	59.4	4.4	243513	2	CR753817	Danio rer
284	60.6	4.5	349751	3	PFMAL4P3	Plasmid	AL035476	Plasmid	c 357	59.2	4.4	110000	2	PFMAL13_25	Continuation (26 o
285	60.4	4.5	113955	9	AC068291	Homo sapi	AC068291	Homo sapi	c 358	59.2	4.4	115952	9	AL772267	Human DNA
286	60.4	4.5	142402	2	CR847574	Danio rer	CR847574	Danio rer	c 359	59.2	4.4	148394	2	CR753884	Danio rer
287	60.4	4.5	144202	2	CR628391	Danio rer	CR628391	Danio rer	360	59.2	4.4	158835	2	CR387984	Danio rer
288	60.4	4.5	185162	9	AC140132	Homo sapi	AC140132	Homo sapi	c 361	59.2	4.4	165574	2	CR847571	Danio rer
289	60.4	4.5	190163	2	CR354398	Danio rer	CR354398	Danio rer	c 362	59.2	4.4	170534	2	CR391918	Danio rer
290	60.4	4.5	199128	9	AC091946	Homo sapi	AC091946	Homo sapi	c 363	59.2	4.4	172816	9	AC093899	Homo sapi
291	60.4	4.5	224175	2	CR812957	Danio rer	CR812957	Danio rer	364	59.2	4.4	180109	2	AC093899	Homo sapi
292	60.4	4.5	346940	2	AC107420	Homo sapi	AC107420	Homo sapi	c 365	59.2	4.4	189149	2	AC046171	Homo sapi
293	60.4	4.5	349418	3	CR382398	Plasmid	AL035476	Plasmid	c 366	59.2	4.4	251448	3	AE014819	Plasmid
294	60.4	4.5	349751	3	PFMAL4P3	Plasmid	AL035476	Plasmid	c 367	59.2	4.4	266335	2	CR762497	Danio rer
295	60.2	4.5	39575	3	AC116925	Dictyoste	AC116925	Dictyoste	c 368	59	4.4	128338	2	CR774177	Danio rer
296	60.2	4.5	93288	9	AC020926	Homo sapi	AC020926	Homo sapi	c 369	59	4.4	153947	2	CR788315	Danio rer
297	60.2	4.5	110000	2	PFMAL13_23	Continuation (24 o	Continuation (24 o	Continuation (24 o	c 370	59	4.4	154044	2	CR786570	Danio rer
298	60.2	4.5	110000	2	PFMAL13P2_0	Continuation (24 o	Continuation (24 o	Continuation (24 o	c 371	59	4.4	156603	2	CR762422	Danio rer
299	60.2	4.5	155609	2	BX927284	Danio rer	BX927284	Danio rer	c 372	59	4.4	168389	9	AC110015	Homo sapi
300	60.2	4.5	162445	9	AL158151	Human DNA	AL158151	Human DNA	c 373	59	4.4	169562	2	CR394565	Danio rer
301	60.2	4.5	168069	2	CR812470	Danio rer	CR812470	Danio rer	c 374	59	4.4	169794	2	AC004688	Plasmid
302	60.2	4.5	181213	2	AC141431	Homo sapi	AC141431	Homo sapi	c 375	59	4.4	173927	2	CR812798	Danio rer
303	60.2	4.5	190482	2	CR450828	Danio rer	CR450828	Danio rer	c 376	59	4.4	176704	2	CR628364	Danio rer
304	60.2	4.5	210548	2	CR751608	Danio rer	CR751608	Danio rer	377	59	4.4	199230	2	CR762470	Danio rer
305	60.2	4.5	213541	9	HUAC004381	Homo sapi	AC004381	Homo sapi	c 378	59	4.4	211748	2	CR392346	Danio rer
306	60.2	4.5	217838	2	BX901955	Danio rer	BX901955	Danio rer	c 379	59	4.4	217621	2	BX901924	Danio rer
307	60.2	4.5	239166	2	BX950179	Danio rer	BX950179	Danio rer	c 380	59	4.4	221953	2	BX928743	Danio rer
308	60.2	4.5	250743	3	AE014836	Plasmid	AE014836	Plasmid	381	59	4.4	246940	2	CR628329	Danio rer
309	60.2	4.5	251762	3	AE014851	Plasmid	AE014851	Plasmid	c 382	58.8	4.4	2503	6	AX033851	Sequence
310	60	4.5	60	6	C0539130	Sequence	C0539130	Sequence	c 383	58.8	4.4	9997	6	AX281374	Sequence
311	60	4.5	82453	9	AC004558	Homo sapi	AC004558	Homo sapi	c 384	58.8	4.4	9997	6	AX345271	Sequence

C 385	58.8	4.4	29993	6	AX825169	AX825169 Sequence	C 458	58.2	4.3	228285	2	CR391925	CR391925 Danio rer
C 386	58.8	4.4	29993	6	AX825171	AX825171 Sequence	C 459	58.2	4.3	24097	2	CR354394	CR354394 Danio rer
C 387	58.8	4.4	38342	6	AX251504	AX251504 Sequence	C 460	58.2	4.3	24943	3	AE014823	AE014823 Plasmodiu
C 388	58.8	4.4	38342	6	AX344503	AX344503 Sequence	C 461	58	4.3	65644	9	AL590364	AL590364 Human DNA
C 389	58.8	4.4	125632	2	CR753868	CR753868 Danio rer	C 462	58	4.3	110000	2	PFMAL7P1_03	Continuation (4 of
C 390	58.8	4.4	135803	2	CR762395	CR762395 Danio rer	C 463	58	4.3	153702	9	AL645730	AL645730 Human DNA
C 391	58.8	4.4	149189	5	AL845366	AL845366 Zebrafish	C 464	58	4.3	156849	2	CR405684	CR405684 Danio rer
C 392	58.8	4.4	162554	2	CR626901	CR626901 Danio rer	C 465	58	4.3	170536	9	AC093914	AC093914 Homo sapi
C 393	58.8	4.4	168936	2	CR735127	CR735127 Danio rer	C 466	58	4.3	172036	9	AC046181	AC046181 Homo sapi
C 394	58.8	4.4	169494	9	AL450083	AL450083 Human DNA	C 467	58	4.3	178687	2	AC148722	AC148722 Ictalur
C 395	58.8	4.4	177623	2	CR394571	CR394571 Danio rer	C 468	58	4.3	181792	2	CR388184	CR388184 Danio rer
C 396	58.8	4.4	179399	2	AX890603	AX890603 Danio rer	C 469	58	4.3	197061	2	CR759830	CR759830 Danio rer
C 397	58.8	4.4	185989	2	CR407587	CR407587 Danio rer	C 470	58	4.3	202169	2	AC149549	AC149549 Gorilla g
C 398	58.8	4.4	190058	2	CR628384	CR628384 Danio rer	C 471	58	4.3	205907	2	CR388065	CR388065 Danio rer
C 399	58.8	4.4	191131	2	CR847965	CR847965 Danio rer	C 472	58	4.3	236119	2	CR788254	CR788254 Danio rer
C 400	58.8	4.4	209866	2	BX546466	BX546466 Danio rer	C 473	58	4.3	236119	2	CR788254	CR788254 Danio rer
C 401	58.8	4.4	213636	2	CR559931	CR559931 Homo sapi	C 474	58	4.3	239323	2	CR788304	CR788304 Danio rer
C 402	58.8	4.4	213636	2	CR559931	CR559931 Homo sapi	C 475	58	4.3	253001	3	AE014834	AE014834 Plasmodiu
C 403	58.8	4.4	237931	9	AC022098	AC022098 Homo sapi	C 476	58	4.3	254436	3	AE014837	AE014837 Plasmodiu
C 404	58.8	4.4	239613	2	CR790367	CR790367 Danio rer	C 477	58	4.3	273394	2	CR792438	CR792438 Danio rer
C 405	58.8	4.4	250022	3	AE014824	AE014824 Plasmodiu	C 478	57.8	4.3	273394	9	AL160031	AL160031 Human DNA
C 406	58.8	4.4	253764	2	BX855620	BX855620 Danio rer	C 479	57.8	4.3	109391	2	CR762428	CR762428 Danio rer
C 407	58.8	4.4	257757	3	AE014837	AE014837 Plasmodiu	C 480	57.8	4.3	142555	2	BX842571	BX842571 Zebrafish
C 408	58.6	4.4	9810	6	AX345329	AX345329 Sequence	C 481	57.8	4.3	145925	5	AC006280	AC006280 Plasmodiu
C 409	58.6	4.4	110000	2	PFMAL13_01	Continuation (2 of	C 482	57.8	4.3	163443	2	AP004174	AP004174 Mycoplas
C 410	58.6	4.4	110000	2	PFMAL13_01	Continuation (13 o	C 483	57.8	4.3	165933	1	BX547933	BX547933 Zebrafish
C 411	58.6	4.4	113515	6	AX347076_12	AX347076 Sequence	C 484	57.8	4.3	177199	5	CR759818	CR759818 Danio rer
C 412	58.6	4.4	126999	9	AL513328	AL513328 Human DNA	C 485	57.8	4.3	180164	2	CR753867	CR753867 Danio rer
C 413	58.6	4.4	137564	2	CR762439	CR762439 Danio rer	C 486	57.8	4.3	189144	2	CR559945	CR559945 Danio rer
C 414	58.6	4.4	149223	2	CR382382	CR382382 Danio rer	C 487	57.8	4.3	204509	2	CR792449	CR792449 Danio rer
C 415	58.6	4.4	153459	2	CR847994	CR847994 Danio rer	C 488	57.8	4.3	205429	2	AC005506	AC005506 Plasmodiu
C 416	58.6	4.4	163651	2	CR790381	CR790381 Danio rer	C 489	57.6	4.3	253132	3	AE014846	AE014846 Plasmodiu
C 417	58.6	4.4	165012	5	BX005274	BX005274 Zebrafish	C 490	57.6	4.3	14591	3	AE001406	AE001406 Plasmodiu
C 418	58.6	4.4	175544	2	AC117342	AC117342 Rattus no	C 491	57.6	4.3	105940	9	AC010606	AC010606 Homo sapi
C 419	58.6	4.4	176122	2	CR628401	CR628401 Danio rer	C 492	57.6	4.3	110000	3	AC116984_2	Continuation (3 of
C 420	58.6	4.4	180096	2	CR626872	CR626872 Danio rer	C 493	57.6	4.3	150962	2	CR847546	CR847546 Danio rer
C 421	58.6	4.4	205479	2	CR847506	CR847506 Danio rer	C 494	57.6	4.3	167068	2	BX323866	BX323866 Danio rer
C 422	58.6	4.4	209561	2	CR383669	CR383669 Danio rer	C 495	57.6	4.3	169357	2	CR847871	CR847871 Danio rer
C 423	58.6	4.4	210954	2	CR545461	CR545461 Danio rer	C 496	57.6	4.3	171295	2	CR388131	CR388131 Danio rer
C 424	58.6	4.4	212683	2	CR388029	CR388029 Danio rer	C 497	57.6	4.3	171867	2	CR628361	CR628361 Danio rer
C 425	58.6	4.4	213402	2	BX901895	BX901895 Danio rer	C 498	57.6	4.3	175014	2	BX942825	BX942825 Danio rer
C 426	58.6	4.4	215231	2	CR385085	CR385085 Danio rer	C 499	57.6	4.3	180450	3	AE014835	AE014835 Plasmodiu
C 427	58.6	4.4	234347	2	CR847960	CR847960 Danio rer	C 500	57.6	4.3	186979	2	CR631129	CR631129 Danio rer
C 428	58.6	4.4	242324	2	CR759863	CR759863 Danio rer	C 501	57.6	4.3	195602	2	CR388375	CR388375 Danio rer
C 429	58.6	4.4	310779	2	AC005140	AC005140 Plasmodiu	C 502	57.6	4.3	198970	2	BX470255	BX470255 Danio rer
C 430	58.6	4.4	340552	3	PFA929354	AL929354 Plasmodiu	C 503	57.6	4.3	204478	2	CR450778	CR450778 Danio rer
C 431	58.4	4.3	99003	2	AL390756	AL390756 Homo sapi	C 504	57.6	4.3	210343	2	CR553890	CR553890 Mus muscu
C 432	58.4	4.3	110000	2	PFMAL8P1_09	Continuation (10 o	C 505	57.6	4.3	227896	2	BX545909	BX545909 Danio rer
C 433	58.4	4.3	122168	9	AC127383	AC127383 Homo sapi	C 506	57.6	4.3	228285	3	CR391925	CR391925 Danio rer
C 434	58.4	4.3	124871	2	CR735110	CR735110 Danio rer	C 507	57.6	4.3	234081	3	PFMAL4P2	PFMAL4P2 Plasmodiu
C 435	58.4	4.3	130349	9	AC011593	AC011593 Homo sapi	C 508	57.6	4.3	250029	3	AE014820	AE014820 Plasmodiu
C 436	58.4	4.3	135203	9	AC025278	AC025278 Homo sapi	C 509	57.6	4.3	251376	2	CR628341	CR628341 Danio rer
C 437	58.4	4.3	148486	2	CR753871	CR753871 Danio rer	C 510	57.6	4.3	251382	2	CR626924	CR626924 Danio rer
C 438	58.4	4.3	166565	2	CR589947	CR589947 Danio rer	C 511	57.4	4.3	254733	3	AC117075	AC117075 Dictyoste
C 439	58.4	4.3	171887	2	CR788232	CR788232 Danio rer	C 512	57.4	4.3	12029	3	AE001401	AE001401 Plasmodiu
C 440	58.4	4.3	183614	2	CR847995	CR847995 Danio rer	C 513	57.4	4.3	17839	3	AE001384	AE001384 Plasmodiu
C 441	58.4	4.3	196567	2	CR318605	CR318605 Danio rer	C 514	57.4	4.3	32704	2	AC151519	AC151519 Danio rer
C 442	58.4	4.3	209515	2	BX571687	BX571687 Danio rer	C 515	57.4	4.3	103344	9	HS1100E15	AL035551 Human DNA
C 443	58.2	4.3	229331	2	CR759914	CR759914 Danio rer	C 516	57.4	4.3	105238	9	AC011458	AC011458 Homo sapi
C 444	58.2	4.3	64394	9	AL928596	AL928596 Human DNA	C 517	57.4	4.3	110000	2	PFMAL13_08	Continuation (9 of
C 445	58.2	4.3	86826	3	PFMAL3P5	AL034556 Plasmodiu	C 518	57.4	4.3	111861	9	AC069435	AC069435 Homo sapi
C 446	58.2	4.3	90550	9	AL592166	AL592166 Human DNA	C 519	57.4	4.3	144784	9	AC009224	AC009224 Homo sapi
C 447	58.2	4.3	110000	2	PFMAL13_02	Continuation (3 of	C 520	57.4	4.3	154071	3	CR115598	CR115598 Dictyoste
C 448	58.2	4.3	110000	3	PFMAL13P2_1	Continuation (2 of	C 521	57.4	4.3	155954	2	CR752653	CR752653 Danio rer
C 449	58.2	4.3	143037	2	AC116305_1	Continuation (2 of	C 522	57.4	4.3	169520	2	CR753882	CR753882 Danio rer
C 450	58.2	4.3	159635	9	AC142351	CR735143 Danio rer	C 523	57.4	4.3	169800	2	CR847821	CR847821 Danio rer
C 451	58.2	4.3	160534	2	CR5450837	AC142351 Pan trogl	C 524	57.4	4.3	174311	2	CR678065	CR678065 Danio rer
C 452	58.2	4.3	176034	2	CR524826	CR5450837 Danio rer	C 525	57.4	4.3	175287	3	AE014835	AE014835 Plasmodiu
C 453	58.2	4.3	194513	2	CR524482	CR524826 Danio rer	C 526	57.4	4.3	180450	3	CR450738	CR450738 Danio rer
C 454	58.2	4.3	196490	2	AC005507	CR524482 Danio rer	C 527	57.4	4.3	182871	9	AC117176	AC117176 Dictyoste
C 455	58.2	4.3	198666	2	CR847504	AC005507 Plasmodiu	C 528	57.4	4.3	185640	5	AL772314	AL772314 Zebrafish
C 456	58.2	4.3	210050	2	CR376844	CR847504 Danio rer	C 529	57.4	4.3	191707	2	CR847971	CR847971 Danio rer
C 457	58.2	4.3	213792	2	BX927177	BX927177 Danio rer	C 530	57.4	4.3	227073	2	CR846086	CR846086 Danio rer



531	57.4	4.3	250078	3	AE014829	AE014829 Plasmodium	c 604	56.8	4.2	110000	2	PFMAL13_18	Continuation (19 o
532	57.4	4.3	252420	3	AE014841	AE014841 Plasmodium	605	56.8	4.2	151143	2	AC141740	AC141740 Apis mell
533	57.4	4.3	253151	3	AE014842	AE014842 Plasmodium	606	56.8	4.2	151544	9	AC1413509	AC1413509 Homo sapi
534	57.4	4.3	259474	9	HUAC004605	AC004605 Homo sapi	c 607	56.8	4.2	152661	3	AC010577	AC010577 Drosophila
535	57.4	4.3	259474	9	HUAC004605	AC004605 Homo sapi	c 608	56.8	4.2	152661	3	CR352289	CR352289 Homo sapi
536	57.2	4.2	5000	3	AF482337	AF482337 Dictyostea	c 609	56.8	4.2	157630	9	AC135012	AC135012 Homo sapi
537	57.2	4.2	8056	6	AX599046	AX599046 Sequence	c 610	56.8	4.2	158249	5	EX470154	EX470154 Zebrafish
538	57.2	4.2	39984	3	AC114258	AC114258 Dictyostea	c 611	56.8	4.2	159910	9	AC009235	AC009235 Homo sapi
539	57.2	4.2	110000	3	PFMALBP1_03	Continuation (4 of	612	56.8	4.2	163448	2	CR846088	CR846088 Danio rer
540	57.2	4.2	110000	3	AC116984_4	Continuation (5 of	613	56.8	4.2	163499	3	PFMAL3P6	PFMAL3P6 Plasmodium
541	57.2	4.2	142514	2	CR790361	CR790361 Danio rer	614	56.8	4.2	164772	2	CR382291	CR382291 Danio rer
542	57.2	4.2	149106	2	CR762407	CR762407 Danio rer	615	56.8	4.2	173395	2	CR762393	CR762393 Danio rer
543	57.2	4.2	157042	2	CR759826	CR759826 Danio rer	c 616	56.8	4.2	174397	9	AC067773	AC067773 Homo sapi
544	57.2	4.2	157194	5	EX005475	EX005475 Zebrafish	c 617	56.8	4.2	180279	2	EX901957	EX901957 Danio rer
545	57.2	4.2	160982	2	CR786564	CR786564 Danio rer	c 618	56.8	4.2	181468	2	CR762391	CR762391 Danio rer
546	57.2	4.2	162954	2	EX548252	EX548252 Danio rer	c 619	56.8	4.2	185048	2	CR392021	CR392021 Danio rer
547	57.2	4.2	165979	2	CR376741	CR376741 Danio rer	c 620	56.8	4.2	185048	2	CR759968	CR759968 Danio rer
548	57.2	4.2	168054	2	EX936460	EX936460 Danio rer	c 621	56.8	4.2	187415	2	CR759968	CR759968 Danio rer
549	57.2	4.2	170823	2	AC133549	AC133549 Homo sapi	c 622	56.8	4.2	187708	2	CR788293	CR788293 Danio rer
550	57.2	4.2	170974	2	CR751545	CR751545 Homo sapi	c 623	56.8	4.2	192389	2	CR751229	CR751229 Danio rer
551	57.2	4.2	172464	2	CR792425	CR792425 Danio rer	c 624	56.8	4.2	201556	2	CR847570	CR847570 Danio rer
552	57.2	4.2	173637	2	CR376735	CR376735 Danio rer	c 625	56.8	4.2	213948	2	CR792432	CR792432 Danio rer
553	57.2	4.2	180004	2	CR352247	CR352247 Danio rer	c 626	56.8	4.2	227211	2	CR847561	CR847561 Danio rer
554	57.2	4.2	180346	9	AC092615	AC092615 Homo sapi	c 627	56.8	4.2	238266	2	CR392026	CR392026 Danio rer
555	57.2	4.2	181792	9	AC098822	AC098822 Homo sapi	c 628	56.8	4.2	250029	3	AE014838	AE014838 Plasmodium
556	57.2	4.2	186369	2	CR388151	CR388151 Danio rer	c 629	56.8	4.2	281723	3	PFAL293359	PFAL293359 Plasmodium
557	57.2	4.2	188777	2	CR774179	CR774179 Danio rer	630	56.6	4.2	104853	9	AC117444	AC117444 Homo sapi
558	57.2	4.2	189598	2	EX957347	EX957347 Danio rer	c 631	56.6	4.2	120192	2	AC093320	AC093320 Homo sapi
559	57.2	4.2	200953	2	CR762483	CR762483 Danio rer	c 632	56.6	4.2	132254	3	AC116330	AC116330 Dictyostea
560	57.2	4.2	202863	2	EX927344	EX927344 Danio rer	c 633	56.6	4.2	135848	2	CR394521	CR394521 Danio rer
561	57.2	4.2	210077	2	CR450750	CR450750 Danio rer	c 634	56.6	4.2	140231	2	EX901943	EX901943 Danio rer
562	57.2	4.2	211376	2	CR762437	CR762437 Danio rer	c 635	56.6	4.2	142275	2	CR788316	CR788316 Danio rer
563	57.2	4.2	223198	2	CR762426	CR762426 Danio rer	c 636	56.6	4.2	154995	9	AC011979	AC011979 Homo sapi
564	57.2	4.2	224514	2	CR376802	CR376802 Danio rer	c 637	56.6	4.2	156395	2	CR387986	CR387986 Danio rer
565	57.2	4.2	226108	2	CR759967	CR759967 Danio rer	c 638	56.6	4.2	161641	9	AC109464	AC109464 Homo sapi
566	57.2	4.2	241048	2	CR753832	CR753832 Danio rer	c 639	56.6	4.2	163475	2	CR628390	CR628390 Danio rer
567	57.2	4.2	250029	3	AE014839	AE014839 Plasmodium	c 640	56.6	4.2	166014	2	CR762396	CR762396 Danio rer
568	57.2	4.2	250195	3	AE014831	AE014831 Plasmodium	641	56.6	4.2	169194	2	CR788297	CR788297 Danio rer
569	57.2	4.2	254050	3	PFAL293358	PFAL293358 Plasmodium	642	56.6	4.2	170276	9	AL353143	AL353143 Human DNA
570	57.2	4.2	293431	2	PFMAL13P4	AL049181 Plasmodium	c 643	56.6	4.2	171302	2	CR762414	CR762414 Danio rer
571	57.2	4.2	297798	2	CR396591	CR396591 Danio rer	c 644	56.6	4.2	173570	2	CR457484	CR457484 Danio rer
572	57.2	4.2	347050	3	PFAL293351	AL293351 Plasmodium	c 645	56.6	4.2	177462	2	CR749767	CR749767 Danio rer
573	57.2	4.2	349980	6	AX344555	AX344555 Sequence	646	56.6	4.2	178025	2	CR752654	CR752654 Danio rer
574	57.2	4.2	349980	6	AX344555	AX344555 Sequence	c 647	56.6	4.2	179213	2	CR792414	CR792414 Danio rer
575	57	4.2	14001	3	PFPCMP1B	X95276 P. falciparum	c 648	56.6	4.2	179571	2	CR361569	CR361569 Danio rer
576	57	4.2	110000	2	EX539337_2	Continuation (3 of	c 649	56.6	4.2	188797	9	AC150210	AC150210 Pan trogl
577	57	4.2	114276	9	AC011355	AC011355 Homo sapi	c 650	56.6	4.2	199874	2	CR626878	CR626878 Danio rer
578	57	4.2	145496	2	CR545470	CR545470 Danio rer	c 651	56.6	4.2	202825	2	EX927088	EX927088 Danio rer
579	57	4.2	155106	9	AC104069	AC104069 Homo sapi	c 652	56.6	4.2	206042	2	CR753794	CR753794 Danio rer
580	57	4.2	156657	2	CR769763	CR769763 Danio rer	c 653	56.6	4.2	209903	2	CR376757	CR376757 Danio rer
581	57	4.2	157467	2	CR792423	CR792423 Danio rer	c 654	56.6	4.2	212365	2	CR589876	CR589876 Danio rer
582	57	4.2	166486	2	CR812469	CR812469 Danio rer	c 655	56.6	4.2	225861	2	CR628381	CR628381 Danio rer
583	57	4.2	169546	2	AC004157	AC004157 Plasmodium	c 656	56.6	4.2	235760	2	CR556713	CR556713 Danio rer
584	57	4.2	176704	2	CR628364	CR628364 Danio rer	c 657	56.6	4.2	237005	2	CR749168	CR749168 Danio rer
585	57	4.2	180861	2	CR393970	CR393970 Danio rer	c 658	56.6	4.2	243096	2	CR388362	CR388362 Danio rer
586	57	4.2	181430	2	CR407555	CR407555 Danio rer	c 659	56.6	4.2	257570	2	CR354431	CR354431 Danio rer
587	57	4.2	187294	2	CR735107	CR735107 Danio rer	c 660	56.6	4.2	273275	3	AE014828	AE014828 Plasmodium
588	57	4.2	199138	2	CR450798	CR450798 Danio rer	c 661	56.6	4.2	285490	2	CR391920	CR391920 Danio rer
589	57	4.2	199296	2	CR753895	CR753895 Danio rer	c 662	56.6	4.2	319520	2	EX936378	EX936378 Danio rer
590	57	4.2	204486	2	CR752655	CR752655 Danio rer	c 663	56.6	4.2	5286	6	AX795682	AX795682 Sequence
591	57	4.2	219074	2	CR769779	CR769779 Danio rer	c 664	56.4	4.2	8633	3	PFPCMP1B	PFPCMP1B P. falciparum
592	57	4.2	228327	2	CR536612	CR536612 Danio rer	c 665	56.4	4.2	40611	3	AC116987	AC116987 Dictyostea
593	57	4.2	233878	2	AC098146	AC098146 Rattus no	c 666	56.4	4.2	99263	2	CNS01DX9	CNS01DX9 Homo sapi
594	57	4.2	250707	3	AE014848	AE014848 Plasmodium	c 667	56.4	4.2	119483	5	EX470158	EX470158 Zebrafish
595	57	4.2	251376	2	CR628341	CR628341 Danio rer	c 668	56.4	4.2	125632	2	CR753868	CR753868 Danio rer
596	57	4.2	255459	2	CR382321	CR382321 Danio rer	c 669	56.4	4.2	156404	2	CR626908	CR626908 Danio rer
597	57	4.2	266335	2	CR762497	CR762497 Danio rer	c 670	56.4	4.2	159726	2	CR356246	CR356246 Danio rer
598	57	4.2	287510	2	CR753823	CR753823 Danio rer	c 671	56.4	4.2	163795	9	AP000356	AP000356 Homo sapi
599	57	4.2	326441	2	CR812467	CR812467 Danio rer	c 672	56.4	4.2	166281	2	CR790386	CR790386 Danio rer
600	57	4.2	347582	3	PFMAL4P1	AL034557 Plasmodium	c 673	56.4	4.2	169215	2	CR318593	CR318593 Danio rer
601	56.8	4.2	16166	2	AC008576_3	AL293364 Plasmodium	c 674	56.4	4.2	169979	2	EX901942	EX901942 Danio rer
602	56.8	4.2	60582	2	AC008576_3	Continuation (4 of	c 675	56.4	4.2	171424	2	CR749743	CR749743 Danio rer
603	56.8	4.2	86826	3	PFMAL3P5	AL034556 Plasmodium	c 676	56.4	4.2	171424	2	CR749743	CR749743 Danio rer

677	56.4	4.2	175058	2	CR753843	Danio rer	750	56	4.2	175919	2	CR786574	Danio rer
678	56.4	4.2	175223	9	AC004617	Homo sapi	751	56	4.2	178388	9	AC079630	Homo sapi
679	56.4	4.2	181002	2	EX957288	Danio rer	C 752	56	4.2	185596	2	AC021553	Homo sapi
680	56.4	4.2	183373	2	CR381594	Danio rer	C 753	56	4.2	187415	2	CR759968	Danio rer
681	56.4	4.2	187010	2	CR627498	Danio rer	754	56	4.2	187962	2	CR759825	Danio rer
682	56.4	4.2	187155	2	CR388186	Danio rer	C 755	56	4.2	196613	2	CR735105	Danio rer
683	56.4	4.2	188406	2	CR381547	Danio rer	C 756	56	4.2	198342	2	CR788292	Danio rer
684	56.4	4.2	196722	2	CR352307	Danio rer	757	56	4.2	206832	2	CR759927	Danio rer
685	56.4	4.2	199236	2	CR753895	Danio rer	C 758	56	4.2	213184	2	CR749750	Danio rer
686	56.4	4.2	210579	2	CR792427	Danio rer	759	56	4.2	222081	2	CR759875	Danio rer
687	56.4	4.2	211723	2	CR749164	Danio rer	760	56	4.2	239323	2	CR788304	Danio rer
688	56.4	4.2	218311	2	CR749741	Danio rer	C 761	56	4.2	239941	2	CR749176	Danio rer
689	56.4	4.2	227211	2	CR847561	Danio rer	762	56	4.2	245802	2	AC006279	Plasmodiu
690	56.4	4.2	228431	2	CR798237	Danio rer	C 763	56	4.2	250621	3	CR792433	Danio rer
691	56.4	4.2	243006	2	EX927082	Danio rer	C 764	56	4.2	260929	3	AE014852	Plasmodiu
692	56.4	4.2	245802	2	AC006279	Plasmodiu	765	56	4.2	320170	2	CR792440	Danio rer
693	56.4	4.2	248167	2	CR627491	Danio rer	C 766	56	4.2	338224	2	CR749766	Danio rer
694	56.4	4.2	252394	3	AE014833	Plasmodiu	C 767	56	4.2	340000	9	HS21C083	Homo sapi
695	56.4	4.2	252450	3	CR753861	Danio rer	768	56	4.2	349174	1	AB063522	Wiggleswo
696	56.4	4.2	260929	3	AE014852	Plasmodiu	769	55.8	4.1	67970	3	PFMAL1P3	Human DNA
697	56.2	4.2	2009	6	AX457067	Sequence	C 770	55.8	4.1	103344	9	HS1100E15	Human DNA
698	56.2	4.2	57304	9	AC004802	Homo sapi	771	55.8	4.1	108908	3	PFMAL3P8	Plasmodiu
699	56.2	4.2	100925	9	AC012627	Homo sapi	C 772	55.8	4.1	110000	2	PFMAL13_04	Continuation (5 of
700	56.2	4.2	110000	2	CR318630	Danio rer	773	55.8	4.1	110000	2	PFMAL8P1_08	Continuation (9 of
701	56.2	4.2	110000	2	CR555291_1	Continuation (2 of	C 774	55.8	4.1	111861	9	AC069435	Homo sapi
702	56.2	4.2	110000	2	CR555291_2	Continuation (3 of	C 775	55.8	4.1	120346	5	BX548060	Zebrafish
703	56.2	4.2	110000	3	AC116305_1	Continuation (2 of	C 776	55.8	4.1	127820	9	HS3612B15	Human DNA
704	56.2	4.2	110000	3	AC116305_2	Continuation (3 of	C 777	55.8	4.1	139760	2	CR388023	Danio rer
705	56.2	4.2	134972	2	CR388177	Danio rer	778	55.8	4.1	141986	2	CR792459	Danio rer
706	56.2	4.2	153701	2	AC147533	Macropus	C 779	55.8	4.1	149238	2	CR847833	Danio rer
707	56.2	4.2	157467	9	CR792423	Danio rer	780	55.8	4.1	151482	9	AC068765	Homo sapi
708	56.2	4.2	158950	9	AL391425	Human DNA	781	55.8	4.1	152359	9	AC093790	Homo sapi
709	56.2	4.2	159300	2	CR759813	Danio rer	C 782	55.8	4.1	154680	2	CR788243	Danio rer
710	56.2	4.2	159603	2	CR762422	Danio rer	783	55.8	4.1	161474	2	AC144356	Danio rer
711	56.2	4.2	160276	2	CR376832	Danio rer	C 784	55.8	4.1	172777	2	CR847809	Danio rer
712	56.2	4.2	166281	2	CR790386	Danio rer	C 785	55.8	4.1	173234	2	CR550306	Danio rer
713	56.2	4.2	167320	2	CR450810	Danio rer	C 786	55.8	4.1	175235	2	CR790380	Danio rer
714	56.2	4.2	169098	2	CR678488	Danio rer	787	55.8	4.1	175260	2	CR786568	Danio rer
715	56.2	4.2	169257	2	CR626961	Danio rer	C 788	55.8	4.1	176196	2	CR762444	Danio rer
716	56.2	4.2	185618	2	CR847796	Danio rer	789	55.8	4.1	179607	2	CR388084	Danio rer
717	56.2	4.2	187478	2	EX927379	Danio rer	C 790	55.8	4.1	185272	2	CR751602	Danio rer
718	56.2	4.2	192772	2	CR735144	Danio rer	C 791	55.8	4.1	187636	2	CR376762	Danio rer
719	56.2	4.2	193505	2	CR628366	Danio rer	C 792	55.8	4.1	189476	2	AC009893	Homo sapi
720	56.2	4.2	208710	2	CR798244	Danio rer	793	55.8	4.1	190890	9	AC087385	Homo sapi
721	56.2	4.2	215231	2	CR385085	Danio rer	C 794	55.8	4.1	195319	2	CR388410	Danio rer
722	56.2	4.2	235532	9	AC008739	Homo sapi	C 795	55.8	4.1	195942	2	CR394542	Danio rer
723	56.2	4.2	236582	2	CR388102	Danio rer	796	55.8	4.1	209215	2	CR751543	Danio rer
724	56.2	4.2	252394	3	AE014833	Plasmodiu	797	55.8	4.1	210338	2	CR753862	Danio rer
725	56.2	4.2	260850	2	CR628328	Danio rer	798	55.8	4.1	213184	2	CR749750	Danio rer
726	56.2	4.2	310003	1	AE014016	Buchnera	799	55.8	4.1	223166	2	CR790362	Danio rer
727	56.2	4.2	349980	6	AX344572	Sequence	C 800	55.8	4.1	228732	2	CR391929	Danio rer
728	56	4.2	2724	1	AF268055	Candidatu	C 801	55.8	4.1	251956	2	CR626889	Danio rer
729	56	4.2	28150	9	AC137733	Homo sapi	C 802	55.6	4.1	5500	3	PFAMDF	M29154 P.falcipar
730	56	4.2	40611	3	AC116987	Dictyoste	C 803	55.6	4.1	14867	3	AE001398	Plasmodiu
731	56	4.2	72487	5	BX294109	Zebrafish	C 804	55.6	4.1	28150	9	AC137733	Homo sapi
732	56	4.2	76354	9	AC048340	Homo sapi	C 805	55.6	4.1	34956	5	AC547122	Zebrafish
733	56	4.2	89665	9	AC063976	Homo sapi	C 806	55.6	4.1	47601	9	AC078802	Danio rer
734	56	4.2	120007	9	AF064864	Homo sapi	C 807	55.6	4.1	58891	2	AC021479	Homo sapi
735	56	4.2	120609	9	AF165176	Homo sapi	C 808	55.6	4.1	103457	2	CR762416	Danio rer
736	56	4.2	127277	9	AC010175	Homo sapi	809	55.6	4.1	110000	2	PFMAL13_11	Continuation (12 o
737	56	4.2	135203	9	AC025278	Homo sapi	810	55.6	4.1	110000	2	PFMAL13_12	Continuation (13 o
738	56	4.2	144314	2	CR751232	Danio rer	C 811	55.6	4.1	110000	3	PFMAL1P2_1	Continuation (2 of
739	56	4.2	148856	2	EX942828	Danio rer	812	55.6	4.1	131149	2	CR626939	Danio rer
740	56	4.2	149603	9	AC022100	Homo sapi	813	55.6	4.1	146667	2	CR555294	Danio rer
741	56	4.2	151951	2	CR762429	Danio rer	814	55.6	4.1	151032	9	AC105201	Homo sapi
742	56	4.2	152356	2	CR762406	Danio rer	815	55.6	4.1	151802	3	AC114263	Dictyoste
743	56	4.2	157605	2	CR450752	Danio rer	C 816	55.6	4.1	157405	3	CR790377	Danio rer
744	56	4.2	162666	9	AC125796	Homo sapi	817	55.6	4.1	158548	2	PFMAL3P2	Plasmodiu
745	56	4.2	163660	2	AC046165	Homo sapi	818	55.6	4.1	161449	2	CR752652	Danio rer
746	56	4.2	163930	2	CR847885	Danio rer	819	55.6	4.1	162325	2	CR774195	Danio rer
747	56	4.2	167396	2	CR352259	Danio rer	820	55.6	4.1	162892	5	BX004873	Zebrafish
748	56	4.2	167592	2	CR847845	Danio rer	C 821	55.6	4.1	167245	2	CR626882	Danio rer
749	56	4.2	170606	2	BX957335	Danio rer	C 822	55.6	4.1	172706	2	AL391135	Homo sapi



969	54.8	4.1	161056	2	CR388093	CR388093	Danio rer	ci1042	54.6	4.1	260850	2	CR628328	CR628328	Danio rer
970	54.8	4.1	165140	2	CR759821	CR759821	Danio rer	ci1043	54.6	4.1	340552	3	PFA929354	AL929354	Plasmodium
971	54.8	4.1	167953	2	AC010948	AC010948	Homo sapi	1044	54.6	4.1	341050	3	PFA929357	AL929357	Plasmodium
C 972	54.8	4.1	170141	2	AL611928	AL611928	Homo sapi	ci1045	54.4	4.0	500	6	CQ398760	Sequence	Sequence
C 973	54.8	4.1	170325	2	CR788305	CR788305	Danio rer	ci1046	54.4	4.0	500	6	CQ405041	Sequence	Sequence
974	54.8	4.1	170703	2	CR789768	CR789768	Danio rer	1047	54.4	4.0	700	6	AX183285	AX183285	Sequence
C 975	54.8	4.1	172206	2	CR788323	CR788323	Danio rer	1048	54.4	4.0	2710	1	AF250388	AF250388	Carsonell
C 976	54.8	4.1	180279	2	CR788333	CR788333	Danio rer	1049	54.4	4.0	6109	6	AX346632	AX346632	Sequence
977	54.8	4.1	182681	2	CR627485	CR627485	Danio rer	ci1050	54.4	4.0	6631	6	AX323725	AX323725	Sequence
C 978	54.8	4.1	185085	2	CR762404	CR762404	Danio rer	ci1051	54.4	4.0	7490	6	AX345185	AX345185	Sequence
C 979	54.8	4.1	186431	2	AC022281	AC022281	Homo sapi	1052	54.4	4.0	57203	3	AC115581	AC115581	Dictyoste
C 980	54.8	4.1	188414	2	CR388091	CR388091	Danio rer	ci1053	54.4	4.0	75523	9	AL627233	AL627233	Human DNA
C 981	54.8	4.1	190165	2	AC012344	AC012344	Homo sapi	ci1054	54.4	4.0	80150	9	AC134620	AC134620	Homo sapi
982	54.8	4.1	191689	2	CR788323	CR788323	Danio rer	ci1055	54.4	4.0	105686	9	AC012072	AC012072	Homo sapi
C 983	54.8	4.1	194392	2	CR788323	CR788323	Danio rer	ci1056	54.4	4.0	110000	9	PFMAL8P1_05	Continuation (6 of	Continuation (6 of
C 984	54.8	4.1	200260	2	CR753814	CR753814	Danio rer	1057	54.4	4.0	110000	3	AC116984_3	Continuation (4 of	Continuation (4 of
C 985	54.8	4.1	205339	2	CR388181	CR388181	Danio rer	1058	54.4	4.0	125685	9	AC073310	AC073310	Homo sapi
986	54.8	4.1	208039	2	CR318659	CR318659	Danio rer	1059	54.4	4.0	132254	3	AC116330	AC116330	Dictyoste
C 987	54.8	4.1	210310	2	CR749177	CR749177	Danio rer	ci1060	54.4	4.0	139409	9	AC069181	AC069181	Homo sapi
988	54.8	4.1	212499	2	CR626887	CR626887	Danio rer	1061	54.4	4.0	148937	2	CR361568	CR361568	Danio rer
C 989	54.8	4.1	215966	2	CR558305	CR558305	Danio rer	1062	54.4	4.0	152724	2	CR769778	CR769778	Danio rer
990	54.8	4.1	218659	2	CR942812	CR942812	Danio rer	1063	54.4	4.0	153702	9	AL645730	AL645730	Human DNA
991	54.8	4.1	222133	2	CR762487	CR762487	Danio rer	ci1064	54.4	4.0	154850	2	CR376747	CR376747	Danio rer
992	54.8	4.1	243066	2	AC120999	AC120999	Rattus no	1065	54.4	4.0	159621	9	AC083801	AC083801	Homo sapi
C 993	54.8	4.1	249995	3	AE014840	AE014840	Plasmodium	ci1066	54.4	4.0	159862	2	CR788253	CR788253	Danio rer
994	54.8	4.1	253924	3	AE014822	AE014822	Plasmodium	1067	54.4	4.0	161444	2	CR9897740	CR9897740	Danio rer
C 995	54.8	4.1	281723	3	PFA929359	AL929359	Plasmodium	ci1068	54.4	4.0	162098	2	CR847881	CR847881	Danio rer
996	54.8	4.1	312724	3	AE003846	AE003846	Drosophil	1069	54.4	4.0	163814	5	AL953863	AL953863	Zebrafish
C 997	54.8	4.1	322588	2	CR385047	CR385047	Danio rer	ci1070	54.4	4.0	164117	2	CR792430	CR792430	Danio rer
998	54.8	4.1	347050	3	PFA929351	AL929351	Plasmodium	ci1071	54.4	4.0	164300	2	CR450717	CR450717	Danio rer
999	54.6	4.1	8622	8	YSCMTCVTOC	M97514	Saccharomyc	1072	54.4	4.0	164376	2	AC135317	AC135317	Medicago
ci1000	54.6	4.1	78578	2	PFMAL13P9	AL096783	Plasmodium	1073	54.4	4.0	167124	2	CR812482	CR812482	Danio rer
1001	54.6	4.1	79018	9	AL627107	AL627107	Human DNA	1074	54.4	4.0	170569	2	CR792421	CR792421	Danio rer
ci1002	54.6	4.1	79018	9	AL627107	AL627107	Human DNA	1075	54.4	4.0	170796	2	AC069416	AC069416	Homo sapi
ci1003	54.6	4.1	86258	5	AX842699	AX842699	Zebrafish	1076	54.4	4.0	171233	2	CR626886	CR626886	Danio rer
1004	54.6	4.1	90373	3	AC115680	AC115680	Dictyoste	ci1077	54.4	4.0	171255	9	AL691447	AL691447	Human DNA
ci1005	54.6	4.1	105320	3	AC116920	AC116920	Dictyoste	ci1078	54.4	4.0	171317	9	AC020941	AC020941	Homo sapi
ci1006	54.6	4.1	110000	2	PFMAL13_15	Continuation (16 o	1079	54.4	4.0	172828	2	CR790379	CR790379	Danio rer	
ci1007	54.6	4.1	120025	9	AC146384	AC146384	Pan trogl	ci1080	54.4	4.0	177462	2	CR749767	CR749767	Danio rer
1008	54.6	4.1	133218	9	AC008410	AC008410	Homo sapi	ci1081	54.4	4.0	178363	2	AC148615	AC148615	Ictalurus
ci1009	54.6	4.1	152971	2	CR769777	CR769777	Danio rer	ci1082	54.4	4.0	178733	9	AC026003	AC026003	Homo sapi
ci1010	54.6	4.1	156657	2	CR769763	CR769763	Danio rer	ci1083	54.4	4.0	181069	2	CR762471	CR762471	Danio rer
ci1011	54.6	4.1	165284	2	CR759767	CR759767	Danio rer	ci1084	54.4	4.0	185142	2	CR678384	CR678384	Danio rer
ci1012	54.6	4.1	167396	2	CR352259	CR352259	Danio rer	ci1085	54.4	4.0	188777	2	CR774179	CR774179	Danio rer
ci1013	54.6	4.1	169794	2	AC004688	AC004688	Plasmodium	ci1086	54.4	4.0	195742	2	AC151362	AC151362	Ictalurus
1014	54.6	4.1	173671	9	AC100778	AC100778	Homo sapi	1087	54.4	4.0	196613	2	CR735105	CR735105	Danio rer
1015	54.6	4.1	175471	2	CR678388	CR678388	Danio rer	ci1088	54.4	4.0	208848	2	AC139608	AC139608	Rattus no
ci1016	54.6	4.1	177301	9	AC103949	CR762472	Danio rer	1089	54.4	4.0	211855	2	CR753866	CR753866	Danio rer
ci1017	54.6	4.1	178045	2	CR762472	CR762472	Danio rer	1090	54.4	4.0	214310	2	CR847982	CR847982	Danio rer
1018	54.6	4.1	183137	2	CR759797	CR759797	Danio rer	1091	54.4	4.0	216831	2	CR627490	CR627490	Danio rer
ci1019	54.6	4.1	183158	2	CR759872	CR759872	Danio rer	ci1092	54.4	4.0	222489	2	CR847953	CR847953	Danio rer
ci1020	54.6	4.1	183293	2	CR769781	CR769781	Danio rer	1093	54.4	4.0	226728	2	CR318596	CR318596	Danio rer
ci1021	54.6	4.1	183580	2	CR552299	CR552299	Danio rer	1094	54.4	4.0	239613	2	CR790367	CR790367	Danio rer
1022	54.6	4.1	186007	2	CR847530	CR847530	Danio rer	1095	54.4	4.0	273275	3	AE014828	AE014828	Plasmodium
1023	54.6	4.1	186723	2	AC027752	CR927370	Homo sapi	ci1096	54.4	4.0	291781	2	CR792436	CR792436	Danio rer
ci1024	54.6	4.1	188529	2	CR927370	CR927370	Danio rer	ci1097	54.2	4.0	859	9	AF385609	AF385609	Homo sapi
ci1025	54.6	4.1	188963	2	CR762411	CR762411	Danio rer	ci1098	54.2	4.0	1987	3	DDIRAP1A	DDIRAP1A	Sequence
ci1026	54.6	4.1	192139	9	AC021955	AC021955	Homo sapi	ci1099	54.2	4.0	9180	6	AX346866	AX346866	Sequence
1027	54.6	4.1	195585	2	CR735129	CR735129	Danio rer	ci1100	54.2	4.0	15980	3	CCA242872	CCA242872	Ceratitidis
1028	54.6	4.1	196149	2	AC004709	AC004709	Plasmodium	ci1101	54.2	4.0	17443	3	AC024806	AC024806	Caenorhab
1029	54.6	4.1	196888	2	CR456627	CR456627	Danio rer	ci1102	54.2	4.0	33651	3	AC114261	AC114261	Dictyoste
ci1030	54.6	4.1	197455	9	AC005701	AC005701	Homo sapi	ci1103	54.2	4.0	59051	9	AC144547	AC144547	Homo sapi
ci1031	54.6	4.1	198572	2	CR792413	CR792413	Danio rer	ci1104	54.2	4.0	110000	2	PFMAL13_23	Continuation (24 o	Continuation (24 o
ci1032	54.6	4.1	199931	2	CR598877	CR598877	Danio rer	ci1105	54.2	4.0	110000	2	PFMAL7P1_02	Continuation (3 of	Continuation (3 of
1033	54.6	4.1	203320	2	AC136933	AC136933	Homo sapi	ci1106	54.2	4.0	110000	2	PFMAL7P1_03	Continuation (4 of	Continuation (4 of
1034	54.6	4.1	219461	2	AX842685	AX842685	Danio rer	ci1107	54.2	4.0	110000	2	PFMAL8P1_06	Continuation (7 of	Continuation (7 of
ci1035	54.6	4.1	223166	2	CR790362	CR790362	Danio rer	ci1108	54.2	4.0	115933	9	AC015842	AC015842	Homo sapi
ci1036	54.6	4.1	224393	2	CR749751	CR749751	Danio rer	ci1109	54.2	4.0	125685	9	AC073310	AC073310	Homo sapi
ci1037	54.6	4.1	232824	2	CR759946	CR759946	Danio rer	ci1110	54.2	4.0	131734	2	CR792420	CR792420	Danio rer
ci1038	54.6	4.1	234009	2	CR383672	CR383672	Danio rer	ci1111	54.2	4.0	136713	9	AC112355	AC112355	Homo sapi
1039	54.6	4.1	247684	2	EX901883	EX901883	Danio rer	ci1112	54.2						

c1115	54.2	4.0	152878	3	CR718D10A	AL034393	Caenorhab	c1188	54	4.0	170536	9	AC093914	Homo sapi
c1116	54.2	4.0	150600	2	AC004153	AC004153	Plasmodiu	c1189	54	4.0	172243	9	AC016730	Homo sapi
c1117	54.2	4.0	165878	2	CR786577	CR786577	Danio rer	c1190	54	4.0	174162	2	CR759781	Danio rer
c1118	54.2	4.0	160654	2	CR788241	CR788241	Danio rer	c1191	54	4.0	174198	2	CR762438	Danio rer
c1119	54.2	4.0	162810	2	CR392028	CR392028	Danio rer	c1192	54	4.0	174574	2	CR759746	Danio rer
c1120	54.2	4.0	163280	2	AC141308	AC141308	Homo sapi	c1193	54	4.0	175722	2	CR762417	Danio rer
c1121	54.2	4.0	163437	9	AC092606	AC092606	Homo sapi	c1194	54	4.0	175959	2	AL450429	Homo sapi
c1122	54.2	4.0	163475	2	CR628390	CR628390	Danio rer	c1195	54	4.0	177164	9	AL365202	Human DNA
c1123	54.2	4.0	164402	2	CR407571	CR407571	Danio rer	c1196	54	4.0	178207	9	AC140172	Homo sapi
c1124	54.2	4.0	164910	2	CR792457	CR792457	Danio rer	c1197	54	4.0	179026	2	CR352332	Danio rer
c1125	54.2	4.0	167376	5	BX004803	BX004803	Zebrafish	c1198	54	4.0	179483	9	AC019230	Homo sapi
c1126	54.2	4.0	174041	9	AL356423	AL356423	Human DNA	c1199	54	4.0	180652	2	CR762436	Danio rer
c1127	54.2	4.0	174070	9	AC146092	AC146092	Pan trogl	c1200	54	4.0	183984	2	CR361550	Danio rer
c1128	54.2	4.0	178095	2	CR753874	CR753874	Danio rer	c1201	54	4.0	187054	2	CR762421	Danio rer
c1129	54.2	4.0	179603	6	CQ870485	CQ870485	Sequence	c1202	54	4.0	187054	2	CR762421	Danio rer
c1130	54.2	4.0	185596	9	AC021553	AC021553	Homo sapi	c1203	54	4.0	194745	2	BX936315	Danio rer
c1131	54.2	4.0	191745	5	AL929309	AL929309	Zebrafish	c1204	54	4.0	196420	2	BX908771	Danio rer
c1132	54.2	4.0	193626	2	CR391971	CR391971	Danio rer	c1205	54	4.0	200557	9	AC090952	Homo sapi
c1133	54.2	4.0	194354	2	CR3908786	CR3908786	Danio rer	c1206	54	4.0	201838	2	CR752642	Danio rer
c1134	54.2	4.0	194392	2	CR788233	CR788233	Danio rer	c1207	54	4.0	202169	2	AC149549	Gorilla g
c1135	54.2	4.0	196049	2	CR388037	CR388037	Danio rer	c1208	54	4.0	202676	2	CR788311	Danio rer
c1136	54.2	4.0	196088	2	CR752642	CR752642	Danio rer	c1209	54	4.0	207281	2	CR847891	Danio rer
c1137	54.2	4.0	201838	2	CR752642	CR752642	Danio rer	c1210	54	4.0	214339	2	CR762403	Danio rer
c1138	54.2	4.0	203320	2	AC136933	AC136933	Homo sapi	c1211	54	4.0	218311	2	CR749741	Danio rer
c1139	54.2	4.0	204272	2	CR762441	CR762441	Danio rer	c1212	54	4.0	218311	2	CR678095	Danio rer
c1140	54.2	4.0	205048	2	CR589944	CR589944	Danio rer	c1213	54	4.0	220158	2	CR376848	Danio rer
c1141	54.2	4.0	205954	2	CR470257	CR470257	Danio rer	c1214	54	4.0	220874	2	CR376848	Danio rer
c1142	54.2	4.0	205980	2	CR788301	CR788301	Danio rer	c1215	54	4.0	223966	2	CR318666	Danio rer
c1143	54.2	4.0	207592	2	CR847888	CR847888	Danio rer	c1216	54	4.0	244683	2	CR392363	Danio rer
c1144	54.2	4.0	216899	2	CR759846	CR759846	Danio rer	c1217	54	4.0	250022	3	AE014824	Plasmodiu
c1145	54.2	4.0	222859	3	AC119799	AC119799	Pan trogl	c1218	54	4.0	251762	3	AE014851	Plasmodiu
c1146	54.2	4.0	237109	3	AC116963	AC116963	Dictyoste	c1219	54	4.0	254436	3	AE014827	Plasmodiu
c1147	54	4.0	245030	3	PF929353	PF929353	Plasmodiu	c1220	54	4.0	266544	3	AC116956	Dictyoste
c1148	54	4.0	5513	9	AC098796	AC098796	Homo sapi	c1221	54	4.0	286544	3	AC005140	Plasmodiu
c1149	54	4.0	6106	6	AX251184	AX251184	Sequence	c1222	54	4.0	310779	9	PF929353	Plasmodiu
c1150	54	4.0	6106	6	AX346375	AX346375	Sequence	c1223	53.8	4.0	343050	3	PFA929353	Plasmodiu
c1151	54	4.0	6106	6	AX348419	AX348419	Sequence	c1224	53.8	4.0	349418	3	CR382398	Plasmodiu
c1152	54	4.0	9424	8	SD044228	SD044228	Saccharom	c1225	53.8	4.0	83728	2	AX592166	Human DNA
c1153	54	4.0	11288	6	AX134885	AX134885	Sequence	c1226	53.8	4.0	90550	9	AL592166	Human DNA
c1154	54	4.0	11288	6	AR182304	AR182304	Sequence	c1227	53.8	4.0	101955	9	AC099759	Homo sapi
c1155	54	4.0	11288	6	AR370519	AR370519	Sequence	c1228	53.8	4.0	110621	2	CR762468	Danio rer
c1156	54	4.0	11288	6	AR479027	AR479027	Sequence	c1229	53.8	4.0	130117	9	AC004907	Homo sapi
c1157	54	4.0	11288	6	AX269130	AX269130	Sequence	c1230	53.8	4.0	137564	2	CR762439	Danio rer
c1158	54	4.0	15056	6	BD195539	BD195539	Adenoviru	c1231	53.8	4.0	141861	2	CR318612	Danio rer
c1159	54	4.0	15056	6	BD224258	BD224258	Adenoviru	c1232	53.8	4.0	148337	2	AC021509	Homo sapi
c1160	54	4.0	15056	6	AR266427	AR266427	Sequence	c1233	53.8	4.0	148348	2	AC104074	Homo sapi
c1161	54	4.0	15056	6	AR474484	AR474484	Sequence	c1234	53.8	4.0	148484	2	CR450693	Danio rer
c1162	54	4.0	15056	6	AX259954	AX259954	Sequence	c1235	53.8	4.0	152956	2	CR762485	Danio rer
c1163	54	4.0	15056	6	AX262359	AX262359	Sequence	c1236	53.8	4.0	152956	2	CR751547	Danio rer
c1164	54	4.0	43337	5	BX511016	BX511016	Sequence	c1237	53.8	4.0	159763	2	CR626888	Danio rer
c1165	54	4.0	105570	9	HS4983	HS4983	Sequence	c1238	53.8	4.0	165988	2	CR626888	Danio rer
c1166	54	4.0	106763	9	AP002091	AP002091	Homo sapi	c1239	53.8	4.0	166949	2	CR352321	Danio rer
c1167	54	4.0	110000	2	PF555291	PF555291	Continuation (3 of	c1240	53.8	4.0	170237	9	AL137070	Human DNA
c1168	54	4.0	110000	2	PF555291	PF555291	Continuation (27 o	c1241	53.8	4.0	170534	2	CR788232	Danio rer
c1169	54	4.0	120026	2	CR388420	CR388420	Danio rer	c1242	53.8	4.0	171887	2	CR788232	Danio rer
c1170	54	4.0	124871	2	CR735110	CR735110	Danio rer	c1243	53.8	4.0	172880	9	AC027419	Homo sapi
c1171	54	4.0	131550	2	CR548629	CR548629	Danio rer	c1244	53.8	4.0	174363	9	AC009133	Homo sapi
c1172	54	4.0	132943	9	AC011287	AC011287	Homo sapi	c1245	53.8	4.0	178025	9	CR752654	Danio rer
c1173	54	4.0	142025	2	CR792461	CR792461	Danio rer	c1246	53.8	4.0	180430	9	AC096768	Homo sapi
c1174	54	4.0	143117	2	CR762399	CR762399	Danio rer	c1247	53.8	4.0	180941	9	AC092373	Homo sapi
c1175	54	4.0	145992	9	AC134919	AC134919	Homo sapi	c1248	53.8	4.0	181165	2	BX908767	Danio rer
c1176	54	4.0	148491	2	CR626866	CR626866	Danio rer	c1249	53.8	4.0	183951	2	CR318651	Danio rer
c1177	54	4.0	153943	2	AC027417	AC027417	Homo sapi	c1250	53.8	4.0	184039	9	AC099327	Homo sapi
c1178	54	4.0	157544	9	AC098590	AC098590	Homo sapi	c1251	53.8	4.0	184431	9	CR628331	Danio rer
c1179	54	4.0	161699	9	AC107300	AC107300	Homo sapi	c1252	53.8	4.0	185411	9	AL845331	Human DNA
c1180	54	4.0	163835	9	AC136488	AC136488	Homo sapi	c1253	53.8	4.0	185111	9	CR376762	Danio rer
c1181	54	4.0	164468	9	AC136489	AC136489	Homo sapi	c1254	53.8	4.0	187636	2	CR376762	Danio rer
c1182	54	4.0	164481	2	CR759908	CR759908	Danio rer	c1255	53.8	4.0	189598	2	CR376762	Danio rer
c1183	54	4.0	164515	2	BX000040	BX000040	Danio rer	c1256	53.8	4.0	189598	2	CR376762	Danio rer
c1184	54	4.0	165574	2	CR847571	CR847571	Danio rer	c1257	53.8	4.0	189662	2	CR376762	Danio rer
c1185	54	4.0	166014	2	CR762396	CR762396	Danio rer	c1258	53.8	4.0	189662	2	CR376762	Danio rer
c1186	54	4.0	166284	2	AC108485	AC108485	Homo sapi	c1259	53.8	4.0	198143	2	CR759948	Danio rer
c1187	54	4.0	170189	2	BX957358	BX957358	Danio rer	c1260	53.8	4.0	199240	2	CR759948	Danio rer

1261	53.8	4.0	202324	2	AC144712	AC144712	Danio rer	1334	53.4	4.0	163382	6	CQ869778	CQ869778	Sequence
1262	53.8	4.0	204223	2	CR759958	CR759958	Danio rer	1335	53.4	4.0	165979	9	CR376741	CR376741	Danio rer
1263	53.8	4.0	204509	2	CR792449	CR792449	Danio rer	1336	53.4	4.0	165995	9	AC103776	AC103776	Homo sapi
1264	53.8	4.0	210718	2	CR589941	CR589941	Danio rer	C1337	53.4	4.0	168202	2	CR759804	CR759804	Danio rer
1265	53.8	4.0	213056	9	AC103590	AC103590	Homo sapi	1338	53.4	4.0	169562	2	CR394565	CR394565	Danio rer
1266	53.8	4.0	214147	2	CR769774	CR769774	Danio rer	C1339	53.4	4.0	170703	2	EX897681	EX897681	Danio rer
1267	53.8	4.0	221501	2	CR762440	CR762440	Danio rer	C1340	53.4	4.0	170920	9	AC138627	AC138627	Homo sapi
1268	53.8	4.0	227440	2	CR626904	CR626904	Danio rer	1341	53.4	4.0	171403	9	AC092701	AC092701	Homo sapi
1269	53.8	4.0	229435	2	CR457452	CR457452	Danio rer	C1342	53.4	4.0	177796	2	CR751235	CR751235	Danio rer
1270	53.8	4.0	240437	2	CR391961	CR391961	Danio rer	1343	53.4	4.0	178723	2	CR450794	CR450794	Danio rer
1271	53.8	4.0	246785	2	CR790385	CR790385	Danio rer	C1344	53.4	4.0	180290	9	AC005081	AC005081	Homo sapi
1272	53.8	4.0	248167	2	CR627491	CR627491	Danio rer	1345	53.4	4.0	184954	2	CR376796	CR376796	Danio rer
1273	53.8	4.0	250663	3	AE014826	AE014826	Plasmodiu	1346	53.4	4.0	190535	2	CR735130	CR735130	Danio rer
1274	53.8	4.0	258645	2	CR555295	CR555295	Danio rer	1347	53.4	4.0	192994	2	CR318588	CR318588	Danio rer
1275	53.8	4.0	348174	3	CR382399	CR382399	Plasmodiu	C1348	53.4	4.0	195488	2	CR753885	CR753885	Danio rer
1276	53.6	4.0	3586	5	BC070012	BC070012	Danio rer	C1349	53.4	4.0	195602	2	CR388375	CR388375	Danio rer
1277	53.6	4.0	30157	9	AC073242	AC073242	Homo sapi	1350	53.4	4.0	197225	9	AC093835	AC093835	Homo sapi
1278	53.6	4.0	32036	9	AL645638	AL645638	Human DNA	C1351	53.4	4.0	199533	2	CR450834	CR450834	Danio rer
1279	53.6	4.0	67885	2	CR339061 <sup>4</sup>	Continuation (5 of	1352	53.4	4.0	201656	2	CR786582	CR786582	Danio rer	
1280	53.6	4.0	116256	9	AL139101	Human DNA	1353	53.4	4.0	203216	2	AC097328	AC097328	Pan trogl	
1281	53.6	4.0	134798	5	AL954697	AL954697	Zebrafish	C1354	53.4	4.0	204662	2	CR753838	CR753838	Danio rer
1282	53.6	4.0	142275	2	CR788316	CR788316	Danio rer	C1355	53.4	4.0	205181	2	CR759842	CR759842	Danio rer
1283	53.6	4.0	144563	2	EX28742	EX28742	Danio rer	1356	53.4	4.0	221924	2	CR388047	CR388047	Danio rer
1284	53.6	4.0	145856	2	CR759812	CR759812	Danio rer	1357	53.4	4.0	223509	2	CR388007	CR388007	Danio rer
1285	53.6	4.0	148385	2	CR749764	CR749764	Danio rer	C1358	53.4	4.0	227441	2	CR589875	CR589875	Danio rer
1286	53.6	4.0	148878	2	CR759816	CR759816	Danio rer	1359	53.4	4.0	233769	2	CR631124	CR631124	Danio rer
1287	53.6	4.0	149122	2	EX927105	EX927105	Danio rer	C1360	53.4	4.0	248925	2	CR749745	CR749745	Plasmodiu
1288	53.6	4.0	152358	2	CR628402	CR628402	Danio rer	1361	53.4	4.0	250823	3	AE014825	AE014825	Plasmodiu
1289	53.6	4.0	152594	2	CR759923	CR759923	Danio rer	C1362	53.4	4.0	250823	3	AE014821	AE014821	Plasmodiu
1290	53.6	4.0	156360	9	BS000087	BS000087	Pan trogl	C1363	53.4	4.0	301450	1	AP003185	AP003185	Clostridi
1291	53.6	4.0	156849	2	CR405684	CR405684	Danio rer	1364	53.4	4.0	331039	3	AC116979	AC116979	Dictyoste
1292	53.6	4.0	163651	2	CR790381	CR790381	Danio rer	C1365	53.4	4.0	341153	2	EX914212	EX914212	Danio rer
1293	53.6	4.0	168103	2	CR751601	CR751601	Danio rer	1366	53.2	4.0	434	8	AY021974	AY021974	Oryza sat
1294	53.6	4.0	169397	2	CR774191	CR774191	Danio rer	1367	53.2	4.0	1509	3	LFAJ5426	LFAJ5426	Lysopt
1295	53.6	4.0	170179	2	CR555290	CR555290	Danio rer	1368	53.2	4.0	2710	1	AF250387	AF250387	Carsonell
1296	53.6	4.0	170832	2	CR376769	CR376769	Danio rer	C1369	53.2	4.0	11469	3	AE001411	AE001411	Plasmodiu
1297	53.6	4.0	171514	2	CR759903	CR759903	Danio rer	1370	53.2	4.0	12029	3	AE001373	AE001373	Plasmodiu
1298	53.6	4.0	179354	2	CR354588	CR354588	Danio rer	C1371	53.2	4.0	53932	2	AC023371	AC023371	Homo sapi
1299	53.6	4.0	179798	2	EX927244	EX927244	Danio rer	C1372	53.2	4.0	76568	3	MBREV	MBREV	Monosiga
1300	53.6	4.0	180629	2	CR388025	CR388025	Danio rer	1373	53.2	4.0	86020	5	CR556723	CR556723	Zebrafish
1301	53.6	4.0	182390	2	EX927075	EX927075	Danio rer	1374	53.2	4.0	104992	2	AC005504	AC005504	Plasmodiu
1302	53.6	4.0	184470	9	AL589823	AL589823	Human DNA	C1375	53.2	4.0	110000	2	CR339061 <sup>2</sup>	Continuation (3 of	
1303	53.6	4.0	184630	2	CR548632	CR548632	Danio rer	1376	53.2	4.0	110000	2	AC024562 <sup>2</sup>	Continuation (3 of	
1304	53.6	4.0	185162	9	AC140132	AC140132	Homo sapi	1377	53.2	4.0	110000	2	CR753903 <sup>0</sup>	CR753903	Danio rer
1305	53.6	4.0	185748	2	AC137308	AC137308	Rattus no	C1378	53.2	4.0	110000	2	PFMAL1 <sup>04</sup>	Continuation (5 of	
1306	53.6	4.0	199128	9	AC091946	AC091946	Homo sapi	C1379	53.2	4.0	110000	3	PFMAL1 <sup>2</sup>	Continuation (3 of	
1307	53.6	4.0	206964	5	EX664610	EX664610	Zebrafish	C1380	53.2	4.0	120058	2	CR759961	CR759961	Rattus no
1308	53.6	4.0	207325	2	CR376835	CR376835	Danio rer	1381	53.2	4.0	123589	9	AC104790	AC104790	Homo sapi
1309	53.6	4.0	210873	2	CR753899	CR753899	Danio rer	C1382	53.2	4.0	132112	2	CR626862	CR626862	Danio rer
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1311	53.6	4.0	232822	2	AC130204	AC130204	Pan trogl	1384	53.2	4.0	138278	2	CR790373	CR790373	Danio rer
1312	53.6	4.0	233659	2	CR545476	CR545476	Danio rer	C1385	53.2	4.0	140288	2	CR631128	CR631128	Danio rer
1313	53.6	4.0	236120	14	AF063866	AF063866	Melanoplu	C1386	53.2	4.0	145650	2	CR762412	CR762412	Danio rer
1314	53.6	4.0	249995	3	AE014840	AE014840	Plasmodiu	1387	53.2	4.0	145856	2	CR759812	CR759812	Danio rer
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1316	53.6	4.0	253755	2	CR812465	CR812465	Danio rer	1389	53.2	4.0	150671	2	CR847829	CR847829	Danio rer
1317	53.6	4.0	254050	3	PF829358	PF829358	Plasmodiu	C1390	53.2	4.0	151475	2	CR759945	CR759945	Danio rer
1318	53.6	4.0	258658	3	AE014832	AE014832	Plasmodiu	C1391	53.2	4.0	158095	2	EX936345	EX936345	Danio rer
1319	53.4	4.0	6641	6	AX281294	AX281294	Sequence	C1392	53.2	4.0	158951	2	CR318594	CR318594	Danio rer
1320	53.4	4.0	9642	6	AX345217	AX345217	Sequence	1393	53.2	4.0	159925	2	CR354424	CR354424	Danio rer
1321	53.4	4.0	14001	3	PF00MP18	PF00MP18	Sequence	C1394	53.2	4.0	159994	2	AC073471	AC073471	Homo sapi
1322	53.4	4.0	27491	9	AC010284	AC010284	Homo sapi	1395	53.2	4.0	161802	2	CR628383	CR628383	Danio rer
1323	53.4	4.0	110000	2	PFMAL13 <sup>09</sup>	Continuation (10 of	C1396	53.2	4.0	163809	2	CR392044	CR392044	Danio rer	
1324	53.4	4.0	111998	9	AC011509	AC011509	Homo sapi	1397	53.2	4.0	164300	2	CR450717	CR450717	Danio rer
1325	53.4	4.0	114576	9	AC074397	AC074397	Homo sapi	C1398	53.2	4.0	168069	2	CR812470	CR812470	Danio rer
1326	53.4	4.0	116061	9	AL732324	AL732324	Human DNA	1399	53.2	4.0	169227	2	CR788248	CR788248	Danio rer
1327	53.4	4.0	136240	3	AC117070	AC117070	Dictyoste	C1400	53.2	4.0	169546	2	AC004157	AC004157	Plasmodiu
1328	53.4	4.0	137889	9	AC073269	AC073269	Homo sapi	1401	53.2	4.0	171424	2	CR749743	CR749743	Danio rer
1329	53.4	4.0	147792	2	CR457463	CR457463	Danio rer	C1402	53.2	4.0	171867	2	CR628361	CR628361	Danio rer
1330	53.4	4.0	150209	2	CR759744	CR759744	Danio rer	1403	53.2	4.0	172036	9	AC046181	AC046181	Homo sapi
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1332	53.4	4.0	157904	2	AC025150	AC025150	Homo								

1407	53.2	4.0	181468	2	CR762391	Danio rer	CR762391	Danio rer	53	3.9	198627	5	AL845168	AL845168 Zebrafish	
1408	53.2	4.0	183844	2	CR753873	Danio rer	CR753873	Danio rer	53	3.9	200131	9	CR786565	CR786565 Danio rer	
1409	53.2	4.0	184060	2	CR759845	Danio rer	CR759845	Danio rer	53	3.9	204939	9	AP001835	AP001835 Homo sapi	
1410	53.2	4.0	184435	2	CR626906	Danio rer	CR626906	Danio rer	53	3.9	208478	2	CR626905	CR626905 Danio rer	
1411	53.2	4.0	186780	2	CR626943	Danio rer	CR626943	Danio rer	53	3.9	212499	2	CR626887	CR626887 Danio rer	
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1413	53.2	4.0	191887	2	CR407563	Danio rer	CR407563	Danio rer	53	3.9	213528	2	CR762381	CR762381 Danio rer	
1414	53.2	4.0	192337	2	CR762383	Danio rer	CR762383	Danio rer	53	3.9	214098	9	AC097381	AC097381 Homo sapi	
1415	53.2	4.0	196523	2	CR628409	Danio rer	CR628409	Danio rer	53	3.9	215967	2	CR759785	CR759785 Danio rer	
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1417	53.2	4.0	198899	9	AC090192	Homo sapi	AC090192	Homo sapi	53	3.9	252997	2	EX927091	EX927091 Danio rer	
1418	53.2	4.0	202324	2	AC144712	Danio rer	AC144712	Danio rer	53	3.9	258658	3	AE014832	AE014832 Plasmodiu	
1419	53.2	4.0	205907	2	CR388065	Danio rer	CR388065	Danio rer	53	3.9	267861	2	CR628327	CR628327 Danio rer	
1420	53.2	4.0	210207	2	CR457459	Danio rer	CR457459	Danio rer	52.8	3.9	840	8	CNS0180K	AL110675 Botrytis	
1421	53.2	4.0	210218	2	CR555304	Danio rer	CR555304	Danio rer	52.8	3.9	12469	3	AE001377	AE001377 Plasmodiu	
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1423	53.2	4.0	216259	2	CR749761	Danio rer	CR749761	Danio rer	52.8	3.9	34003	9	AV594694	AV594694 Homo sapi	
1424	53.2	4.0	221143	2	CR759874	Danio rer	CR759874	Danio rer	52.8	3.9	37957	8	U17009	U17009 Phycophthor	
1425	53.2	4.0	221953	2	EX928743	Danio rer	EX928743	Danio rer	52.8	3.9	64707	3	AC115607	AC115607 Dictyoste	
1426	53.2	4.0	225990	2	CR936371	Danio rer	CR936371	Danio rer	52.8	3.9	72143	9	AC131094	AC131094 Homo sapi	
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1428	53.2	4.0	233658	2	CR354421	Danio rer	CR354421	Danio rer							
1429	53.2	4.0	237023	2	CR751568	Danio rer	CR751568	Danio rer							
1430	53.2	4.0	250421	3	AE014849	Plasmodiu	AE014849	Plasmodiu							
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1433	53.2	4.0	263169	2	EX927111	Danio rer	EX927111	Danio rer							
1434	53.2	4.0	313050	3	PPA929352	Plasmodiu	PPA929352	Plasmodiu							
1435	53.2	4.0	327236	2	CR385026	Danio rer	CR385026	Danio rer							
1436	53	3.9	530	6	CQ398223	Sequence	CQ398223	Sequence							
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1438	53	3.9	4601	3	DMU11584	U11584 Drosophila	DMU11584	U11584 Drosophila							
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1442	53	3.9	37330	9	AC133133	Homo sapi	AC133133	Homo sapi							
1443	53	3.9	54345	3	AC084152	Caenorhab	AC084152	Caenorhab							
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1449	53	3.9	111864	9	AP003042	Homo sapi	AP003042	Homo sapi							
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1451	53	3.9	119288	9	CR354589	Danio rer	CR354589	Danio rer							
1452	53	3.9	122556	9	AL391863	Human DNA	AL391863	Human DNA							
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1458	53	3.9	144784	9	AC009224	Homo sapi	AC009224	Homo sapi							
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1460	53	3.9	155667	2	AC018619	Homo sapi	AC018619	Homo sapi							
1461	53	3.9	156441	9	AC091869	Homo sapi	AC091869	Homo sapi							
1462	53	3.9	157865	2	CR450836	Danio rer	CR450836	Danio rer							
1463	53	3.9	158183	2	CR847496	Danio rer	CR847496	Danio rer							
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1465	53	3.9	164399	3	PFMAL3P6	Plasmodium	PFMAL3P6	Plasmodium							
1466	53	3.9	164481	2	CR759908	Danio rer	CR759908	Danio rer							
1467	53	3.9	166486	2	CR812469	Danio rer	CR812469	Danio rer							
1468	53	3.9	174311	2	CR678065	Danio rer	CR678065	Danio rer							
1469	53	3.9	174718	2	CR788318	Danio rer	CR788318	Danio rer							
1470	53	3.9	175757	2	CR522883	Danio rer	CR522883	Danio rer							
1471	53	3.9	177045	2	EX957238	Danio rer	EX957238	Danio rer							
1472	53	3.9	177320	9	AC104441	Homo sapi	AC104441	Homo sapi							
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1478	53	3.9	189962	2	CR753887	Danio rer	CR753887	Danio rer							
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1480	53	3.9	198627	5	AL845168	AL845168 Zebrafish
1481	53	3.9	200131	9	CR786565	CR786565 Danio rer
1482	53	3.9	204939	9	AP001835	AP001835 Homo sapi
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1485	53	3.9	212881	2	CR450705	Danio rer
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1487	53	3.9	214098	9	AC097381	Homo sapi
1488	53	3.9	215967	2	CR759785	Danio rer
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1495	52.8	3.9	26000	6	AR336949	AR336949 Sequence
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1497	52.8	3.9	37957	8	U17009	Phytophthor
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1499	52.8	3.9	72143	9	AC131094	Homo sapi
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ALIGNMENTS

RESULT 1

AR252633

Sequence 386 from patent US 6478825.

LOCUS

AR252633

AR252633.1

GI:27300541

ACCESSION

AR252633

VERSION

AR252633.1

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1346)

WINTERBOTTOM,J.M., SHIMP,L., BOYCE,T.M. and KAES,D.

AUTHORS

Implant, method of making same and use of the implant for the

TITLE

treatment of bone defects

JOURNAL

Patent: US 6478825-A 386 12-NOV-2002;

FEATURES

Location/Qualifiers

source

1..1346

/organism="unknown"

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ORIGIN

Query Match 100.0%; Score 1346; DB 6; Length 1346;

Best Local Similarity 100.0%; Pred. No. 7.5e-266;

Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAAAGAAATGTTGGCTGCTCTTTTCTTGGTGAAGTCCCAATTCATGCTGAACCTCTGTCAA 60

Qy 61 CCAGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTAGTACAGACAGCTCTGGGAGATAAA 120

Db 61 CCAGGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTAGTACAGACAGCTCTGGGAGATAAA 120

Qy 121 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTTCCCATG 180

Db 121 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTTCCCATG 180

Qy 181 AGAAAAAGTTCCCAACAGAGAAGCAAGAAATTTCCCATGTCCTACTTTTCCAATGTGAACC 240

Db 181 AGAAAAAGTTCCCAACAGAGAAGCAAGAAATTTCCCATGTCCTACTTTTCCAATGTGAACC 240

Qy 241 CAGAGGGTATCATTTCTGGTTTGGTTTACAGACCCCTTCAAAAAATCACACCCCTTCTGCT 300

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Qy 301 GTTGAGGTGCAATCAGCCATTAAGAATGAACAAAGAACCGGATCAACAAATGCTCTTTCTTA 360

## ALIGNMENTS

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LOCUS	AR252633	Sequence 386 from patent US 6478825.	1346 bp	DNA	linear	PAT 20-DEC-2002
DEFINITION	AR252633	Sequence 386 from patent US 6478825.				
ACCESSION	AR252633	Sequence 386 from patent US 6478825.				
VERSION	AR252633.1	GI:27300541				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 1346)					
AUTHORS	Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.					
TITLE	Implant, method of making same and use of the implant for the					
JOURNAL	treatment of bone defects					
FEATURES	Patent: US 6478825-A 386 12-NOV-2002;					
source	Location/Qualifiers					
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ORIGIN						
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Best Local Similarity	100.0%;	Pred. No. 7.5e-266;				
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Qy	121	GCATATGCTTGGGATACCAATGAAGTAACCTCTTCAAGCGATGGTAGCTTTCTCATG	180			
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LOCUS ARS28692 1346 bp DNA linear PAT 08-OCT-2004  
DEFINITION Sequence 481 from patent US 6725730.  
ACCESSION ARS28692  
VERSION ARS28692.1 GI:53916770  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
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AUTHORS Bollinger,C.L. Jr.  
TITLE Crane test weight assembly and method  
JOURNAL Patent: US 6725730-A 481 27-APR-2004;  
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LOCUS AX403499 1346 bp DNA linear PAT 14-JUN-2002  
DEFINITION Sequence 386 from Patent WO0073454.  
ACCESSION AX403499  
VERSION AX403499.1 GI:21436987  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,  
Ferrara,N., Gerber,H., Gerecht,M., Goddard,A., Godowski,P.,  
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,  
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,  
Williams,P., Wood,W.I. and Zhang,Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
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JOURNAL Patent: WO 0073454-A 386 07-DEC-2000;  
Genentech Inc. (US)  
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Query Match 100.0%; Score 1346; DB 6; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 7.5e-266;  
Matches 1346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4  
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LOCUS AX464348  
DEFINITION Sequence 481 from Patent WO0140466.  
ACCESSION AX464348  
VERSION AX464348.1 GI:21899190  
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SOURCE  
ORGANISM Homo sapiens (human)  
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Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,  
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JOURNAL Patent: WO 0140466-A 481 07-JUN-2001;  
Genentech Inc. (US)  
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Query Match 100.0%; Score 1346; DB 6; Length 1346;  
Best Local Similarity 100.0%; Pred No. 7.5e-266; Mismatches 0; Gaps 0;  
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ACCESSION AY359060  
VERSION AY359060.1 GI:37183237  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
Heidens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
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Xie,M.H., Yaneura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
Goddard,A., Wood,W.I. and Godowski,P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
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2 (bases 1 to 1346)  
Clark,H.F.  
Direct Submission  
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
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Matches 1346; Conservative 0; Mismatches 0;  
Qy 1 GAAAGAGTGTGTGGCTCTCTTTTCTGTGACTGCCATTCATGCTGAACTCTGTCAA 60  
Db 1 GAAAGAGTGTGTGGCTCTCTTTTCTGTGACTGCCATTCATGCTGAACTCTGTCAA 60  
Qy 61 CCAGGTGAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120  
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Qy 121 GCATATGCTGGGATACCAATGAGAAATACCTCTTCAAAGGATGGTAGCTTCTCCATG 180  
Db 121 GCATATGCTGGGATACCAATGAGAAATACCTCTTCAAAGGATGGTAGCTTCTCCATG 180  
Qy 181 AGAAAGTTCCTCAACAGAGAGCAACAGAAATTTCCCATGTCCTACCTTTGCAATGTAACC 240  
Db 181 AGAAAGTTCCTCAACAGAGAGCAACAGAAATTTCCCATGTCCTACCTTTGCAATGTAACC 240  
Qy 241 CAGAGGTATCATCTCTGGTTGTGGTTACAGACCTTTCAAAAATATCACACCTTCTCTGCT 300  
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Db 241 CAGAGGTATCATCTCTGGTTGTGGTTTACAGACCTTTCAAAAATATCACACCTTCTCTGCT 300  
Qy 301 GTTGAGGTGCAATCAGCCATAGAAATGAAACAAGACCGGATCAACATATGCTTCTTTCTA 360  
Db 301 GTTGAGGTGCAATCAGCCATAGAAATGAAACAAGACCGGATCAACATATGCTTCTTTCTA 360  
Qy 361 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGACACCCATGAGACCCA 420  
Db 361 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGACACCCATGAGACCCA 420  
Qy 421 TCTGTGCCCATCTGGATTTATTTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480  
Db 421 TCTGTGCCCATCTGGATTTATTTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480  
Qy 481 GCATCTACTGATTTTATCAGGGATCTGCAACAGTAGAAGAAAGAACAAAGAACCATCTGAA 540  
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Qy 541 GTGATGACGCTGAAAGATAGTGTAACAATGATGATCAATTTGAAATTTGGATCTCTCT 600  
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Qy 601 GATCCCTCTGACATGAGGGGGGCATATTAATGATGCTTCTCATGACAGAGATGAGAGGC 660  
Db 601 GATCCCTCTGACATGAGGGGGGCATATTAATGATGCTTCTCATGACAGAGATGAGAGGC 660  
Qy 661 TCACCCCTCTCTGAGGGCTGTTTGTCTCTCAAGAAATTAACAATTTGTTTCTGT 720  
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Qy 721 GTGACTGCTGAGCATCCTGAAATACCAAGACGAGATCATATATTTTGTGTTTCAACATTTT 780  
Db 721 GTGACTGCTGAGCATCCTGAAATACCAAGACGAGATCATATATTTTGTGTTTCAACATTTT 780  
Qy 781 CTTTTGTAATAATTTTGAATGCTTGAAGTGAAGCAATCAATATATACCCACCAAC 840  
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Db 841 ACCACTGAAATCATAGCTATTCACGACTCAAAATATTTCTAAAATATTTTCTGACAGTA 900  
Qy 901 TAGTGATATAATGCTGCTATGCTGATTTTGTAGTATTTAGTAAAGCAATTTTGAAGTA 960  
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Qy 1081 CTTATATACCTCTGTATATGACTTAAGTAAACAAAAGTGAGAGTAATTTTGTAAATGGA 1140  
Db 1081 CTTATATACCTCTGTATATGACTTAAGTAAACAAAAGTGAGAGTAATTTTGTAAATGGA 1140  
Qy 1141 TGGATAAAAATGGAATTTACTCATATACAGGGTGAATTTTATCTGTTATCACACCAACA 1200  
Db 1141 TGGATAAAAATGGAATTTACTCATATACAGGGTGAATTTTATCTGTTATCACACCAACA 1200  
Qy 1201 GTTGATTTATATATTTTCTGAATATACGCCCTTAATAGGCAATTTCTATTGTTGACCAT 1260  
Db 1201 GTTGATTTATATATTTTCTGAATATACGCCCTTAATAGGCAATTTCTATTGTTGACCAT 1260  
Qy 1261 TCTACAAATTTGTAAGAGTCCAATCTCTGTGTAATTAAGTAATTAATCATCTCTTTT 1320  
Db 1261 TCTACAAATTTGTAAGAGTCCAATCTCTGTGTAATTAAGTAATTAATCATCTCTTTT 1320  
Qy 1321 AAAAAAATTTGTAAGAGTCCAATCTCTGTGTAATTAAGTAATTAATCATCTCTTTT 1346  
Db 1321 AAAAAAATTTGTAAGAGTCCAATCTCTGTGTAATTAAGTAATTAATCATCTCTTTT 1346

RESULT 6	BC014317	1605 bp	mRNA	linear	PRI 29-JUN-2004
LOCUS	Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:22707				
DEFINITION	IMAGE:4048217), complete cds.				
ACCESSION	BC014317				
VERSION	BC014317.1	GI:15680012			
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
AUTHORS	1 (bases 1 to 1605)				
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zdobych,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 1605)				
AUTHORS	Strausberg,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (17-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>				
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA sequencing by: Institute for Systems Biology <a href="http://www.systemsbio.org">http://www.systemsbio.org</a> contact: <a href="mailto:amadn@systemsbiology.org">amadn@systemsbiology.org</a> Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting				
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>				
	Series: IRAL Plate: 31 Row: n Column: 3				
	This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.				
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	/mol_type="mRNA"				
	/db_xref="taxon:9606"				
	/clone="MGC:22707 IMAGE:4048217"				
	/tissue_type="Bone marrow, chronic myelogenous leukemia"				
/clone_lib="NIH_MGC_54"					
/lab_host="DH10B"					
/note="Vector: pDNR-LIB"					
1. .1605					
gene					

CDS																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
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Db	183	AGAAAGTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTCTATTGTCRAATGTAACC	242
QY	241	CAGAGGGTATCATCTCTGGTTGGTTGGTTAGACAGCCCTTCAAAAAATCACACCCTTCTCTGCT	300
Db	243	CAGAGGGTATCATCTCTGGTTGGTTGGTTACAGACCCCTTCAAAAAATCACACCCTTCTCTGCT	302
QY	301	GTGAGGTGCAATCAGCATTAAAGATGAACAAGACCGGATCAACCAATGCGCTTCTTTCTTA	360
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QY	361	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACACCACCCATGGRACCA	420
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QY	421	TCTGTGCCATCTGGATTAATATTTGGTGTGATATTTTGGCATCATCATAGTTGCAAT	480
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QY	481	GCACTACTGATTTTATCAGGATCTGCAACGTAGAGAAAGAACAAAGAACCATCTGAA	540
Db	483	GCACTACTGATTTTATCAGGATCTGCAACGTAGAGAAAGAACAAAGAACCATCTGAA	542
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QY	601	GATCCCTGACATGAAGGG- GGGCATATTAATGATGCGCTTCATGACAGAGATGAGAG	659
Db	603	GATCCCTGACATGAAGGGAGGCGCATATTAATGATGCGCTTCATGACAGAGATGAGAG	662
QY	660	CTCACCCCTCTGMAAGGCTGTCTGCTCTTCCCAAGAAATTAACAAATTGTTTCTTG	719
Db	663	CTCACCCCTCTGMAAGGCTGTCTGCTCTTCCCAAGAAATTAACAAATTGTTTCTTG	722
QY	720	TGTGACTGCTGAGCATCCTGAATAACAGAGCAGATCATATATTTGTTTCCACCATCT	779
Db	723	TGTGACTGCTGAGCATCCTGAATAACAGAGCAGATCATATATTTGTTTCCACCATCT	782
QY	780	TCTTTTGTAATAATTTTGAATGTGCTTGAAGTGAAGCAATCAATATACCCACCA	839
Db	783	TCTTTTGTAATAATTTTGAATGTGCTTGAAGTGAAGCAATCAATATACCCACCA	842
QY	840	CACCACTGAATCATAGCTATTCAGACTCAAAATTTCTAAATATTTTCTGACAGT	899
Db	843	CACCACTGAATCATAGCTATTCAGACTCAAAATTTCTAAATATTTTCTGACAGT	902
QY	900	ATAGTGTATAAATGTGCTCATGTGGTATTTGTAGTTATTCATTTAAGCATTTTAGAAAT	959
Db	903	ATAGTGTATAAATGTGCTCATGTGGTATTTGTAGTTATTCATTTAAGCATTTTAGAAAT	962
QY	960	AAGATCAGGCATATGATATATTTTTCACATTCAGAGCCTAAGGAAAAATAAATTTTCC	1019
Db	963	AAGATCAGGCATATGATATATTTTTCACATTCAGAGCCTAAGGAAAAATAAATTTTCC	1022
QY	1020	AGTGGAGAAATACATATATGTTAGTAAATCATTTGAAATGATCCTTTTGGAGATC	1079
Db	1023	AGTGGAGAAATACATATATGTTAGTAAATCATTTGAAATGATCCTTTTGGAGATC	1082
QY	1080	ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAGTAAATTTGTAATGG	1139
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QY	1140	ATGGATAAAATGGAATATCTCATATACAGGGTGAATTTTATCCCTGTTATACACCAAC	1199
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QY	1200	AGTTGATATATTTTCTGAATATCAGCCCTTAATAGGCAATTTCTATTGTTGACCAT	1259
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QY	1260	TTCTACAAATTTGTAAGAGTCCAATCTGTGCTAACTTAATAAGATTAATATCATCTCTTTT	1319

Db	1263	TTCTACAAATTTGTAAGAGTCCAATCTGTGCTAACTTAATAAGATAATAATCATCTCTTTT	1322
QY	1320	TAAAAAATAAAAAAAAAAAAAAAAAAAAAA	1346
Db	1323	TGATTGTGAAAAAATAAAAAAAAAAAAAA	1349
RESULT 8			
LOCUS	BC015099	1440 bp	mRNA linear PRI 29-JUN-2004
DEFINITION	Homo sapiens transmembrane protein 27, mRNA (CDNA clone MGC:22827 IMAGE:3829035), complete cds.		
ACCESSION	BC015099		
VERSION	BC015099.1 GI:15929328		
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 1440)		
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altshuler, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahay, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Greenchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Shreen, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.		
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)		
PUBMED	12477932		
REFERENCE	2 (bases 1 to 1440)		
AUTHORS	Strausberg, R.		
TITLE	Direct Submission		
JOURNAL	Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>		
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapps-r@mail.nih.gov">cgapps-r@mail.nih.gov</a> Tissue Procurement: ATCC cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology <a href="http://www.systemsbio.org">http://www.systemsbio.org</a> Contact: <a href="mailto:amadan@systemsbiology.org">amadan@systemsbiology.org</a> Anup Madan, Jessica Fahney, Brin Helton, Mark Kettman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting		
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAL Plate: 31 Row: d Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, Similarity but not identity to protein.		
source	Location/Qualifiers 1. .1440 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:22827 IMAGE:3829035"		

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/lab\_host="DH10B"

/note="Vector: pDNR-LIB"

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89. 757

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/db\_xref="GI:15929329"

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SAIRMNKRNINNAFLNDOTLEPLKIPSTLAPMDPSVPIWIIIFGVIFCIILVAIAL

LILSGIQRRRNKKEPSEVDDAEKCNEMITIENGIPSDPLDMKGGHINDAFWTEDEK

LTPL"

## ORIGIN

Query Match 98.5%; Score 1325.4; DB 9; Length 1440;

Best Local Similarity 99.5%; Pred. No. 1.3e-261;

Matches 1340; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy	1	GAAGAAATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTCATGCTGAACCTGTCAA	60
Db	83	GAAGAAATGTTGTGGCTGCTCTTTTCTGGTGACTGCCATTCATGCTGAACCTGTCAA	142
Qy	61	CCAGGTGAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAAAGCTCTGGGAGATAAA	120
Db	143	CCAGGTGAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAAAGCTCTGGGAGATAAA	202
Qy	121	GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATG	180
Db	203	GCATATGCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATG	262
Qy	181	AGAAAGTTCCTCAACAGAGAACACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC	240
Db	263	AGAAAGTTCCTCAACAGAGAACACAGAAATTTCCCATGTCCTACTTTGCAATGTAACC	322
Qy	241	CAGAGGTATCATTTCTGGTTGGTTGACAGCCCTTCAAAAATCAGCCCTTCCTGCT	300
Db	323	CAGAGGTATCATTTCTGGTTGGTTGACAGCCCTTCAAAAATCAGCCCTTCCTGCT	382
Qy	301	GTTGAGTGCATCAGCCATGAAGATGAACAAGAACCGGATCAACATGCTCTTCTTA	360
Db	383	GTTGAGTGCATCAGCCATGAAGATGAACAAGAACCGGATCAACATGCTCTTCTTA	442
Qy	361	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCAACCCATGGACCA	420
Db	443	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCAACCCATGGACCA	502
Qy	421	TCTGTGCCATCTCGATATATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT	480
Db	503	TCTGTGCCATCTCGATATATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT	562
Qy	481	GCATCTATGATTTTATCAGGATCTGGCAAGCTGAGAGAGAGAAACCAAGACCATCTGAA	540
Db	563	GCATCTATGATTTTATCAGGATCTGGCAAGCTGAGAGAGAGAAACCAAGACCATCTGAA	622
Qy	541	GTGATGACGCTGAAGATAAGTGTGAAGAACATGATCAATTTGAAATGGCATCCCTCT	600
Db	623	GTGATGACGCTGAAGATAAGTGTGAAGAACATGATCAATTTGAAATGGCATCCCTCT	682
Qy	601	GATCCCTGGACATGAAGGG-GGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGG	659
Db	683	GATCCCTGGACATGAAGGGAGGGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGG	742
Qy	660	CTACCCCTCTCTGAAGGCTGTGTTCTGCTGCTCTCAAGAAATTAACAATTTGTTCTG	719
Db	743	CTACCCCTCTCTGAAGGCTGTGTTCTGCTGCTCTCAAGAAATTAACAATTTGTTCTG	802

Qy	720	TGTGACTGCTGAGCATCTCTGAAATATCCAGAGAGAGATCATATATTTTGTTCACCATCT	779
Db	803	TGTGACTGCTGAGCATCTCTGAAATATCCAGAGAGAGATCATATATTTTGTTCACCATCT	862
Qy	780	TCCTTTGTGTAATAATTTTGAATGTGCTTGAAGTGAAAAGCAATCAATATACCCACCA	839
Db	863	TCCTTTGTGTAATAATTTTGAATGTGCTTGAAGTGAAAAGCAATCAATATACCCACCA	922
Qy	840	CACCACCTGAAATCATAGCTATTTCACGACTCAAAATATTTCTAAATATTTTCTGACAGT	899
Db	923	CACCACCTGAAATCATAGCTATTTCACGACTCAAAATATTTCTAAATATTTTCTGACAGT	982
Qy	900	ATAGTGTATAAATGTGCTGATGTTGTAGTATTGTTGATTTAAGCATTTTGTAGAAAT	959
Db	983	ATAGTGTATAAATGTGCTGATGTTGTAGTATTGTTGATTTAAGCATTTTGTAGAAAT	1042
Qy	960	AAGATCAGGCTATGTATATATTTTTCACACTTCAAGACCTTAAGGAAATAAATTTTCC	1019
Db	1043	AAGATCAGGCTATGTATATATTTTTCACACTTCAAGACCTTAAGGAAATAAATTTTCC	1102
Qy	1020	AGTGGAGATACATATAATATGTTAGAAATCATTTGAAATGGATCCTTTTGTGACGATC	1079
Db	1103	AGTGGAGATACATATAATATGTTAGAAATCATTTGAAATGGATCCTTTTGTGACGATC	1162
Qy	1080	ACTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAGTAATTTTGTAAATGG	1139
Db	1163	ACTTATATCACTCTGTATATGACTAAGTAAACAAAGTGAGAGTAATTTTGTAAATGG	1222
Qy	1140	ATGGATAAATGGAATTAATCATATACAGGGTGGAAATTTTATCCTGTTATCACCAAC	1199
Db	1223	ATGGATAAATGGAATTAATCATATACAGGGTGGAAATTTTATCCTGTTATCACCAAC	1282
Qy	1200	AGTTGATTATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTTATTTGTTGACAT	1259
Db	1283	AGTTGATTATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTTATTTGTTGACAT	1342
Qy	1260	TTCTACAAATTTTAAAGTCCAATCTGTGCTAACTTAATAAGTAATTAATCATCTTTT	1319
Db	1343	TTCTACAAATTTTAAAGTCCAATCTGTGCTAACTTAATAAGTAATTAATCATCTTTT	1402
Qy	1320	TAAATAAAAAAAAAAAAAAAAAAAAAA	1346
Db	1403	TGATTGTGAAAAAAAAAAAAAAAAAAAA	1429
RESULT 9			
BD205644			
LOCUS	BD205644	1447 bp	linear
DEFINITION	97 human secreted proteins.		
ACCESSION	BD205644		
VERSION	BD205644.1		
KEYWORDS	JP 2002533058-A/21.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1447)		
AUTHORS	Ruben, S.M., Florence, K., Ni, J., Rosen, C.A., Carter, K.C., Moore, P.A., Olsen, H.S., Shi, Y., Young, P.E., Wei, F.F., Brewer, L.A., Soppet, D.R., Lafleur, D.W., Endress, G.A. and Ebner, R.		
TITLE	97 human secreted proteins		
JOURNAL	Patent: JP 2002533058-A 21 08-OCT-2002;		
COMMENT	HUMAN GENOME SCIENCES INC		
OS	Homo sapiens (human)		
PN	JP 2002533058-A/21		
PD	08-OCT-2002		
PF	06-MAY-1999	JP 2000548451	60/085094 PR
PR	12-MAY-1998	US 60/085105, 12-MAY-1998	US 60/085180 PR
12-MAY-1998	US 60/085927, 18-MAY-1998	US 60/085906 PR	
18-MAY-1998	US 60/085924, 18-MAY-1998	US 60/085922 PR	
18-MAY-1998	US 60/085923, 18-MAY-1998	US 60/085921 PR	



18-MAY-1998 US	60/085925,18-MAY-1998 US	60/085928 PR
18-MAY-1998 US	60/085920	
PI STEVEN M RUBEN,KIMBERLY FLORENCE,JIAN NI,CRAIG A ROSEN,KENNETH C CARTER,		
PI PAUL A MOORE,HENRIK S OLSEN,YANGGU SHI,PAUL E YOUNG,FING FEI WEI,		
PI LAURIE A BREWER,DANIEL R SOPPET,DAVID W LAFLEUR,GREGORY A PI ENDRESS,		
PI REINHARD EBNER		
PC C12N15/09,C07K14/00,C07K14/435,C07K16/18,C12N1/15,C12N1/19,PC C12N1/21,		
PC C12N5/10,C12P21/02,C12N15/00,C12N5/00		
CC 97 human secreted proteins.		
FH Key	Location/Qualifiers	
FT source	1..1447	
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Best Local Similarity	99.3%; Pred. No. 1.8e-261;	
Matches 1338; Conservative	2; Mismatches 6; Indels 1; Gaps 1;	
QY 1	GAAGAATGTTGGCTGCTCTTTTAAAGTCAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	60
DB 71	GAAGAATGTTGGCTGCTCTTTTCTGGTGACTGCCAATTCATGCTGAACCTGTGCAA	130
QY 61	CCAGGTCGAGAAATGCTTTTAAAGTCAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	120
DB 131	CCAGGTCGAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	190
QY 121	GCATATGCTGGGATACCAATGAAGAAATCCTCTTCAAAGCGATGGTAGCTTTCTCCATG	180
DB 191	GCATATGCTGGGATACCAATGAAGAAATCCTCTTCAAAGCGATGGTAGCTTTCTCCATG	250
QY 181	AGAAAAGTTCCCAACAGAGAAGCAAGAAATTTCCCATGCTCTACTTTTGCATGTGAACC	240
DB 251	AGAAAAGTTCCCAACAGAGAAGCAAGAAATTTCCCATGCTCTACTTTTGCATGTGAACC	310
QY 241	CAGAGGATATCATTTCTGGTTTGGTTTACAGACCCTTCAAAAATCACACCTTTCCTGCT	300
DB 311	CAGAGGATATCATTTCTGGTTTGGTTTACAGACCCTTCAAAAATCACACCTTTCCTGCT	370
QY 301	GTTGAGGTGCAATCAGCGATGAAGAAATGAACAAAGAACCGGATCAACAATGCTCTTTCTTA	360
DB 371	GTTGAGGTGCAATCAGCGATGAAGAAATGAACAAAGAACCGGATCAACAATGCTCTTTCTTA	430
QY 361	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACACCCCATGGACCCA	420
DB 431	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACACCCCATGGACCCA	490
QY 421	TCTGTGCCCATCTGGATTTATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT	480
DB 491	TCTGTGCCCATCTGGATTTATATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT	550
QY 481	GCATCTGATTTTTATCAGGATCTGGCAACGTAGAGAAAGAAACAAAGAACCATCTGAA	540
DB 551	GCATCTGATTTTTATCAGGATCTGGCAACGTAGAGAAAGAAACAAAGAACCATCTGAA	610
QY 541	GTGATGACGCTGAAGATAAGTGTGAAAAATGATATCAATTTGAAAAATGGCATCCCTCT	600
DB 611	GTGATGACGCTGAAGATAAGTGTGAAAAATGATATCAATTTGAAAAATGGCATCCCTCT	670
QY 601	GATCCCTGACATGAAGGG-GGGCATATTAATGATGCCCTTCATGACAGAGGATGAGAGG	659
DB 671	GATCCCTGACATGAAGGGGGGCGCATTAATTAATGATGCCCTTCATGACAGAGGATGAGAGG	730
QY 660	CTCACCCCTCTCTGAAGGGGCTGTGTTCTGCTTCTCAAGAAATTAACAAATTTGTTTCTG	719



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FH	Key	Location/Qualifiers
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Query Match		
Best Local Similarity		
Matches 1334; Conservative 0; Mismatches 2; Indels 1; Gaps 1;		
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Db	65	GAAGAAGTGTGGCTGCTCTTTTCTGTGACTGCCATTCATGCTGAACCTGTGCAA 124
Qy	61	CCAGGTGAGAAATGCTTTTAAAGTGAGCTTAGTATCAGAACGCTCTGGGAGATAA 120
Db	125	CCAGGTGAGAAATGCTTTTAAAGTGAGCTTAGTATCAGAACGCTCTGGGAGATAA 184
Qy	121	GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTCTCCATG 180
Db	185	GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTCTCCATG 244
Qy	181	AGAAAAGTTCCTCAACAGAGAAGCAAGAAATTTCCCATGTCCTACTTTGCAATGTAAAC 240
Db	245	AGAAAAGTTCCTCAACAGAGAAGCAAGAAATTTCCCATGTCCTACTTTGCAATGTAAAC 304
Qy	241	CAGAGGTATCATTTCTGGTTTGTGGTTACAGACCTTCAAAAATCAGCCCTTCCGTCT 300
Db	305	CAGAGGTATCATTTCTGGTTTGTGGTTACAGACCTTCAAAAATCAGCCCTTCCGTCT 364
Qy	301	GTTGAGGTGCAATCAGCCATGAAGTGAACCAAGAACCGGATCAACAATGCTTCTTCTA 360
Db	365	GTTGAGGTGCAATCAGCCATGAAGTGAACCAAGAACCGGATCAACAATGCTTCTTCTA 424
Qy	361	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCAACCATGGACCA 420
Db	425	AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCAACCATGGACCA 484
Qy	421	TCTGTGCCATCTGGATATATATATTTGGTGTGATATTTGTCATCATATAGTTGCAATT 480
Db	485	TCTGTGCCATCTGGATATATATATTTGGTGTGATATTTGTCATCATATAGTTGCAATT 544
Qy	481	GCATCTGATTTTATCAGGGATCTGCAAGTGAAGAAGCAAGAACCAACCATCTGAA 540
Db	545	GCATCTGATTTTATCAGGGATCTGCAAGTGAAGAAGCAAGAACCAACCATCTGAA 604
Qy	541	GTGGATGACGCTGAAGATAAGTGTGAACAATGATCAATTTGAAAAATGGCATCCCTCT 600
Db	605	GTGGATGACGCTGAAGATAAGTGTGAACAATGATCAATTTGAAAAATGGCATCCCTCT 664
Qy	601	GATCCCTGGACATGAGGG-GGGCATATTAATGATGCTTCATGACAGGATGAGAG 659
Db	665	GATCCCTGGACATGAGGGAGGGCATATTAATGATGCTTCATGACAGGATGAGAGG 724
Qy	660	CTCACCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTG 719
Db	725	CTCACCCTCTCTGAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACATTTGTTCTG 784
Qy	720	TGTGACTGCTGAGCATCTGAAATACCAAGACGAGATCATATATTTTGTTCACCATCT 779
Db	785	TGTGACTGCTGAGCATCTGAAATACCAAGACGAGATCATATATTTTGTTCACCATCT 844
Qy	780	TCTTTGTATATAATTTTGAATGTGCTTGAAGTGAAGCAATTAATACCCACAA 839
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Db	905	CACCACGAAATCATAGCTATTCCAGCTCAAAATATTCTTAATATTTTCTGACAGT 964
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Db	965	ATAGTGATATAAATGTGTGTCATGTGGTATTTGTAGTATTGATTTAAGCAATTTTAGAAAT 1024
Qy	960	AGATCAGGCATATGTATATATTTTTCACACTTCAAGACCTTAAGGAAAAATAAATTTTCC 1019
Db	1025	AGATCAGGCATATGTATATATTTTTCACACTTCAAGACCTTAAGGAAAAATAAATTTTCC 1084
Qy	1020	AGTGGAGATACATATAATATGTGTAGAAATCATTTGAAAAATGGATCCTTTTGGACGATC 1079
Db	1085	AGTGGAGATACATATAATATGTGTAGAAATCATTTGAAAAATGGATCCTTTTGGACGATC 1144
Qy	1080	ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAGTAATATTGTAAATGG 1139
Db	1145	ACTTATATCACTCTGTATATGACTAAGTAAACAAAAGTGAGAGTAATATTGTAAATGG 1204
Qy	1140	ATGATAAAAATGGAATTACTCATATACAGGGTGGAAATTTTATCTGTTATCACACCAAC 1199
Db	1205	ATGATAAAAATGGAATTACTCATATACAGGGTGGAAATTTTATCTGTTATCACACCAAC 1264
Qy	1200	AGTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATTGTTGACCAT 1259
Db	1265	AGTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATTGTTGACCAT 1324
Qy	1260	TTCTACAAATTTGTAAGTCCAAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1319
Db	1325	TTCTACAAATTTGTAAGTCCAAATCTGTGCTAACTTAATAAAGTAATAATCATCTCTTTT 1384
Qy	1320	TAAAAAATAAAAAA 1336
Db	1385	AAAAAATAAAAAA 1401
RESULT 11		
AX083392		
LOCUS		
DEFINITION		
AX083392	Sequence 84 from Patent WO0112660.	
AX083392	Accession	
VERSION	AX083392.1	GI:13185232
KEYWORDS		
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	1	
AUTHORS	Kato, S. and Kimura, T.	
TITLE	Human proteins having hydrophobic domains and dnas encoding these proteins	
JOURNAL	Patent: WO 0112660-A 84 22-FEB-2001;	
FEATURES	SAGAMI CHEMICAL RESEARCH CENTER (JP) ; Protegene Inc. (JP)	
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ORIGIN		
Query Match	97.3%;	Score 1309.4; DB 6; Length 1347;
Best Local Similarity	99.8%;	Pred. No. 2.4e-258;
Matches 1321; Conservative 0; Mismatches 1; Indels 1; Gaps 1;		
Qy	1	GAAGAAGTGTGTGGCTGCTCTTTTCTGGTGACGCCATTCATGCTGAACCTGTGCAA 60

Db	20	GAAAGAAATGTTGGTGCCTCTTTTTTCTGGTGACTGCCATTCATGCTGCAACTCTGTCAA	79
QY	61	CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	120
Db	80	CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA	139
QY	121	GCATATGCTCGGGATCCCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG	180
Db	140	GCATATGCTCGGGATCCCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG	199
QY	181	AGAAAAGTCCCAACAGAGAGCAACAGAAAATTTCCCATGCTCTTGGCAATGTAACC	240
Db	200	AGAAAAGTCCCAACAGAGAGCAACAGAAAATTTCCCATGCTCTTGGCAATGTAACC	259
QY	241	CAGAGGTATCATCTCTGGTTTGGTTTACAGACCTTCAAAGAAATCACACCCCTTCCTGCT	300
Db	260	CAGAGGTATCATCTCTGGTTTGGTTTACAGACCTTCAAAGAAATCACACCCCTTCCTGCT	319
QY	301	GTTGAGGTGCAATCAGCCATAAGAATGAAACAAGAACCGGATCAACAATGCTTCTTTCTA	360
Db	320	GTTGAGGTGCAATCAGCCATAAGAATGAAACAAGAACCGGATCAACAATGCTTCTTTCTA	379
QY	361	AATGACAAACTCTGGAATTTTAAATCCCTTCCACACTTGCAACACCCATGGAACCA	420
Db	380	AATGACAAACTCTGGAATTTTAAATCCCTTCCACACTTGCAACACCCATGGAACCA	439
QY	421	TCGTGCCCATCTGGATTATATATTGGTGTGATATTTTGGCATCATCATAGTTCGAATT	480
Db	440	TCGTGCCCATCTGGATTATATATTGGTGTGATATTTTGGCATCATCATAGTTCGAATT	499
QY	481	GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAAGAAACAAGAACCATCTGAA	540
Db	500	GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAAGAAACAAGAACCATCTGAA	559
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Db	560	GTGGATGACGCTGAAGATAAGTGTGAAAACATGATCACAATGAAATGGCATCCCTCT	619
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Db	620	GATCCCTCGACATGAGGGAGGCATATTAATGATGCCCTTCATGACAGGATGAGAGG	679
QY	660	CTCACCCCTCTGAAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACAATTTGTTCTG	719
Db	680	CTCACCCCTCTGAAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACAATTTGTTCTG	739
QY	720	TGTGACTGTGACATCCTGAAATACCAAGAGCAGATCATATATTTGTTTCAACATCT	779
Db	740	TGTGACTGTGACATCCTGAAATACCAAGAGCAGATCATATATTTGTTTCAACATCT	799
QY	780	TCCTTTGTAATAATTTTGAATGCTTGAAGTGAAGCAATCAATATACCCACCA	839
Db	800	TCCTTTGTAATAATTTTGAATGCTTGAAGTGAAGCAATCAATATACCCACCA	859
QY	840	CACCACTGAAATCATAGCTATTACGACCTCAAAATATTCTAAATATTTTCTGCAGT	899
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QY	960	AGATCAGGCATATGATATATTTTTCACACTTCAAGACCTAAGGAAATAAATTTTCC	1019
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QY	1200	AGTTGAATATATATTTTCTGAATATCAGCCCTAATAGACAAATTCATTTGTTGACCAT	1259			
Db	1220	AGTTGAATATATATTTTCTGAATATCAGCCCTAATAGACAAATTCATTTGTTGACCAT	1279			
QY	1260	TTCTCAAAATTTCTAAAGTCCCAATCTGTGCTAACTTAATAAAGTATAATATCTCTTTT	1319			
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Db	1340	TGA 1342				
RESULT 12						
AF229179						
LOCUS	AF229179	1345 bp	mRNA linear PRI 05-APR-2002			
DEFINITION	Homo sapiens collectrin mRNA, complete cds.					
ACCESSION	AF229179					
VERSION	AF229179.1 GI:9957753					
KEYWORDS	.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						
REFERENCE	1 (bases 1 to 1345)					
AUTHORS	Zhang,H., Wada,J., Hida,K., Tsuchiyama,Y., Hiragushi,K., Shikata,K., Wang,H., Lin,S., Kanwar,Y.S. and Makino,H.					
TITLE	Collectrin, a collecting duct-specific transmembrane glycoprotein, is a novel homolog of ACE2 and is developmentally regulated in embryonic kidneys					
JOURNAL	J. Biol. Chem. 276 (20), 17132-17139 (2001)					
MEDLINE	21264468					
PUBMED	11278314					
REFERENCE	2 (bases 1 to 1345)					
AUTHORS	Zhang,H., Wada,J. and Makino,H.					
TITLE	Human kidney specific membrane protein (NX-17) Unpublished					
JOURNAL	3 (bases 1 to 1345)					
AUTHORS	Zhang,H., Wada,J. and Makino,H.					
TITLE	Direct Submission					
JOURNAL	Submitted (28-JAN-2000) Department of Medicine III, Okayama University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558, Japan					
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ORIGIN						
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Best Local Similarity 99.8%; Pred. No. 5.2e-258;						
Matches 1320; Conservative 0; Mismatches 2; Indels 1; Gaps 1;						

Qy 1 GAAAGAAATGTTGGTGGCTCTTTTCTGGTGAATGCGCATTCATGCTGAACCTCTGTCAA 60  
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18 GAAAGAAATGTTGGTGGCTCTTTTCTGGTGAATGCGCATTCATGCTGAACCTCTGTCAA 77  
Qy |||||  
61 CCAGGTGCAGAAAATGCTTTTAAAGTGGAGCTTAGTATCAGAACAGCTCTGGGAGATAAA 120  
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ACCESSION BD135300  
VERSION BD135300.1 GI:23230245  
KEYWORDS JP 2002508167-A/51.  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Moore, P.A., Ruben, S.M., Carter, K.C., Shi, Y., Rosen, C.A.,  
Soppet, D.R., Cao, H., Wei, Y.P., Florence, K., Duan, R.D.,  
Florence, C., Greene, J.M., Feng, P., Ferrie, A.M., Yu, G.L., Janat, F.  
and Ni, J.  
TITLE 110 human secretory proteins  
JOURNAL Patent: JP 2002508167-A 51 19-MAR-2002;  
HUMAN GENOME SCIENCES INC  
COMMENT OS Homo sapiens (human)  
PN JP 2002508167-A/51  
PD 19-MAR-2002  
PF 17-DEC-1998 JP 2000539040  
PR 18-DEC-1997 US 60/070 923, 18-DEC-1997 US 60/068 007 PR  
18-DEC-1997 US 60/068 057, 18-DEC-1997 US 60/068 006 PR  
18-DEC-1997 US 60/068 008, 18-DEC-1997 US 60/068 054 PR  
18-DEC-1997 US 60/068 064, 18-DEC-1997 US 60/068 053 PR  
19-DEC-1997 US 60/068 169, 19-DEC-1997 US 60/068 368 PR  
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19-DEC-1997 US 60/068 365  
PI PAUL A MOORE, STEVEN M RUBEN, KENNETH C CARTER, YANGGU SHI, CRAIG  
PI A ROSEN,  
PI DANIEL R SOPPET, HARA CAOU, YING FEI WEI, KIMBERLY FLORENCE, PI  
ROSANNE D DUAN,  
PI CHARLES FLORENCE, JOHN M GREENE, PING FENG, ANN M FERRIE, GUO PI  
LIANG YU,  
PI FORD JANAT, JIAN NI  
PC C12N15/09, A61K38/00, A61K48/00, A61P9/00, A61P9/10, A61P15/00, PC  
A61P25/00,  
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PC A61P25/28,  
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10, C12P21/02, C12Q1/68, G01N33/15, G01N33/50, G01N33/53, C12N15/00, PC  
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.
SUMMARIES

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RESULT 1
ID AA65097 standard; cDNA; 1346 BP.
DE Membrane-bound protein PRO1312 encoding cDNA.
FN WO9963088-A2.
PD 09-DEC-1999.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 2
ID AAC58612 standard; cDNA; 1346 BP.
DE Human PRO1312 protein UNQ678 encoding cDNA SEQ ID NO:160.
FN WO200053758-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 3; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 3
ID AAA7680 standard; cDNA; 1346 BP.
DE Human PRO1312 cDNA sequence SEQ ID NO:213.
FN WO200032221-A2.
PD 08-JUN-2000.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 4
ID AAS21484 standard; cDNA; 1346 BP.
DE Human cDNA sequence encoding for PRO1312 polypeptide.
FN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 4; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 5
ID AAF4243 standard; cDNA; 1346 BP.
DE Human PRO1312 (UNQ678) nucleotide sequence SEQ ID NO:386.
FN WO200073454-A1.
PD 07-DEC-2000.
PA (GETH ) GENENTECH INC.

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Query Match 100.0%; Score 1346; DB 5; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
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ID ACA64416 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
FN US2003003531-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 8; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 7
ID ACA03843 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
FN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 8
ID ABX89381 standard; cDNA; 1346 BP.
DE DNA encoding novel secreted and transmembrane protein PRO1312.
FN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 9
ID ABX80875 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein cDNA, #157.
FN US2003027162-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 10
ID ACD4384 standard; cDNA; 1346 BP.
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FN US2002127576-A1.
PD 12-SEP-2002.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 11
ID ACD42035 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #241.
FN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;
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FN US2002142961-A1.
PD 03-OCT-2002.
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PD 30-JAN-2003.
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FN US2003027985-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;
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DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 481.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
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PN US2003017476-A1.  
PD 23-JAN-2003.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
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PN US2002123463-A1.  
PD 05-SEP-2002.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
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PN US2002177164-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
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RESULT 19  
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PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
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DE cDNA encoding human PRO1312 polypeptide.  
PN US2003017981-A1.  
PD 23-JAN-2003.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
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DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
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DE Human PRO polynucleotide #241.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 23  
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DE Human PRO polynucleotide #241.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
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DE Homo sapiens.  
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PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
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PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
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PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
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PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
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DE Human PRO polynucleotide #241.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 29  
ID ADA37897 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US200308297-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
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PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
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Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
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DE Human cDNA encoding secreted/transmembrane polypeptide PRO1312.  
PN US2003054404-A1.  
PD 20-MAR-2003.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 32  
ID ADA10370 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein, PRO1312.  
PN US2003059831-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 33  
ID ADA67654 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;



RESULT 34  
ID ADB30661 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
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PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
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PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
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PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 38  
ID ADA79473 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 39  
ID ADA87612 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 40  
ID ADB16814 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 41  
ID ADA28022 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003054359-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 42  
ID ADA91906 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 43  
ID ADB14969 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.

PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 44  
ID ADB18930 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 45  
ID ADA94145 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 46  
ID ADB20041 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 47  
ID ADB13353 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 48  
ID ACD98664 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 49  
ID ADA94602 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003059832-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 50  
ID ADA74607 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 51  
ID ADB24840 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide SEQ ID NO 481.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 52  
ID ADA82364 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082701-A1.  
PD 01-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 53
ID ADA75327 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 54
ID ADA85405 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 55
ID ADA84853 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 56
ID ADB30109 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 57
ID ADA80637 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 58
ID ADA75879 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 59
ID ADA38827 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059780-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 60
ID ADA47104 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 61
ID ADB25400 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 62
ID ADA93576 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 63
ID ADB26926 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 64
ID ADB31213 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 65
ID ADA92948 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003060407-A1.
PD 27-MAR-2003.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 66
ID ADA61141 standard; cDNA; 1346 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 67
ID ADB24288 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 68
ID ADA96617 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 69
ID ADA81189 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 70
ID ADA96065 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 9; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 71
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ID ADB26374 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 72  
ID ADB21859 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 73  
ID ADA77638 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 74  
ID ADB18378 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 75  
ID ADA87061 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 76  
ID ADA88164 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 77  
ID ADA46552 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 78  
ID ADB28582 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 79  
ID ADB29134 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 80  
ID ACH65530 standard; cDNA; 1346 BP.

DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003044806-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 81  
ID ADA77086 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 82  
ID ADA22509 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1312.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 83  
ID ADA88716 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 84  
ID ADA97721 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 85  
ID ADB27478 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 86  
ID ADB22411 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 87  
ID ACD39520 standard; cDNA; 1346 BP.  
DE Human cDNA encoding PRO1192.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 88  
ID ADA06675 standard; cDNA; 1346 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #121.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 89  
ID ADA39368 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 90  
ID ADA67102 standard; cDNA; 1346 BP.

DE Human PRO polynucleotide #241.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 91  
ID ADB22963 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 92  
ID ADB23736 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide SEQ ID NO 481.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 93  
ID ADA92458 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 94  
ID ADB15521 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 95  
ID ADB38773 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 96  
ID ADB96394 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #121.  
PN US2003054403-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 97  
ID ADB38221 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 9; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 98  
ID ADB66693 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 99  
ID ADB89773 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082698-A1.

PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 100  
ID ADB90505 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 101  
ID ADB39606 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 102  
ID ADB47229 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 103  
ID ADB86836 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 104  
ID ADB77441 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 105  
ID ADB34598 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide SEQ ID NO 481.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 106  
ID ADB35702 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide SEQ ID NO 481.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 107  
ID ADB34046 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide SEQ ID NO 481.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 108  
ID ADB35150 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide SEQ ID NO 481.  
PN US2003077718-A1.  
PD 24-APR-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 109  
ID ADB36254 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide SEQ ID NO 481.  
PN US2003077720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 110  
ID ADB46649 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 111  
ID ADC57866 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #121.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 112  
ID ADC55230 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #121.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 113  
ID ADC12097 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 114  
ID ADC56519 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #121.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 115  
ID ADC07574 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 116  
ID ADC11564 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 117  
ID ADC50522 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 118  
ID ADC72069 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003092107-A1.

PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 119  
ID ADC60048 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 120  
ID ADC53055 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 121  
ID ADC57409 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 122  
ID ADC60600 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 123  
ID ADC51075 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 124  
ID ADC65602 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 125  
ID ADC54700 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 126  
ID ADC53661 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 127  
ID ADC59184 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087359-A1.  
PD 08-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 128  
ID ADC56062 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 129  
ID ADC58632 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 130  
ID ADC14686 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 131  
ID ADC14686 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082546-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 132  
ID ADC90298 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 133  
ID ADC82043 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #121.  
PN US2003083461-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 134  
ID ADC69717 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 135  
ID ADC48606 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 136  
ID ADC48606 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 137

ID ADD10135 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 138  
ID ADD07685 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2002193299-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 139  
ID ADD04710 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 140  
ID ADC82576 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #121.  
PN US2003059833-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 141  
ID ADC80666 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 142  
ID ADD11173 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 143  
ID ADC48054 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 144  
ID ADD08756 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003073090-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 145  
ID ADC80114 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 146  
ID ADD07005 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2002193300-A1.

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PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 147
ID ADD09583 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 148
ID ADC83252 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003059783-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 149
ID ADD41296 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 150
ID ADD52435 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 151
ID ADD53175 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 152
ID ADD53727 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 153
ID ADD55359 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003077593-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 154
ID ADD56317 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003077594-A1.
PD 24-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 155
ID ADD51883 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 156
ID ADE22354 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 157
ID ADD02116 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 158
ID ADD54298 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 159
ID ADD54755 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2002132253-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 160
ID ADD92615 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 161
ID ADD91511 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 162
ID ADE04125 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 163
ID ADE26909 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 164
ID ADE32422 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 10; Length 1346;
RESULT 165
ID ADE22354 standard; cDNA; 1346 BP.
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DE cDNA encoding human PRO polypeptide #241.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 166
ID ADE19035 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 176
ID ADE43231 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 177
ID ADD96020 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 178
ID ADE22906 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 179
ID ADD79024 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 180
ID ADE26376 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 181
ID ADE32974 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 182
ID ADE42666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 183
ID ADD80682 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207418-A1.
PD 06-NOV-2003.

DE cDNA encoding human PRO polypeptide #241.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 166
ID ADE19035 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 176
ID ADE43231 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 177
ID ADD96020 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 178
ID ADE22906 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 179
ID ADD79024 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 180
ID ADE26376 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 181
ID ADE32974 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 182
ID ADE42666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 10; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 183
ID ADD80682 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207418-A1.
PD 06-NOV-2003.
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PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 184  
ID ADG89710 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003199028-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 185  
ID ADE40994 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 186  
ID ADE04793 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 187  
ID ADE29222 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 188  
ID ADF67313 standard; cDNA; 1346 BP.  
DE Human PRO1312 nucleotide sequence SEQ ID NO:386.  
PN US2002198148-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 189  
ID ADG21631 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 190  
ID ADG23272 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 191  
ID ADF97607 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 192  
ID ADG80671 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 193  
ID ADG80119 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 194  
ID ADH55411 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 195  
ID ADH55963 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 196  
ID ADI35567 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #121.  
PN US2003050457-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 197  
ID ADI64182 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 198  
ID ADI65131 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 199  
ID ADI63630 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 200  
ID ADH82044 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 201  
ID ADI00060 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003049682-A1.  
PD 13-MAR-2003.  
Query Match 100.0%; Score 1346; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 202

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ID ADH81492 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 10; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 203
ID ABX77959 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003027163-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 10; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 204
ID ABX80371 standard; DNA; 1346 BP.
DE Novel human secreted or transmembrane protein PRO1192 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 10; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 205
ID ACA69277 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003032023-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 10; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 206
ID ACD24093 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 10; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 207
ID ABX90348 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein cDNA, #157.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 10; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 208
ID ABX64194 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
  Query Match 100.0%; Score 1346; DB 10; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 209
ID ACA67234 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 10; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 210
ID ADM82661 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 11; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 211
ID ADN16060 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087353-A1.
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PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 11; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 212
ID ADN16689 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 11; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 213
ID ADN15508 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 11; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 214
ID ADN14956 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 11; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 215
ID ADC81218 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 12; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 216
ID ADD76666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 12; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 217
ID ADD88030 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 12; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 218
ID ADD86434 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 12; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 219
ID ADE75882 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
  Query Match 100.0%; Score 1346; DB 12; Length 1346;
  Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 220
ID ADE23458 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092108-A1.
PD 15-MAY-2003.
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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 221
ID ADE24010 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 222
ID ADE24653 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 223
ID ADE87478 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 224
ID ADE89344 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 225
ID ADE18483 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 226
ID ADE88792 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 227
ID ADE94812 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 228
ID ADE91223 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 229
ID ADF35512 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003194760-A1.
PD 16-OCT-2003.
Query Match
100.0%; Score 1346; DB 12; Length 1346;

PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 230
ID ADE95364 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 231
ID ADE93474 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 232
ID ADF35055 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 233
ID ADE92370 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 234
ID ADE90671 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 235
ID ADE91818 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 236
ID ADG11762 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003228655-A1.
PD 11-DEC-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 237
ID ADG02397 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
RESULT 238
ID ADG22183 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;
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[illegible]

DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 258  
ID AGS5358 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 259  
ID ADG61022 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 260  
ID ADG62126 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 261  
ID ADG82327 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 262  
ID ADG57566 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 263  
ID ADG57014 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 264  
ID ADG55910 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 265  
ID ADG58670 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 266  
ID ADG71036 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.

PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 267  
ID AGS8118 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 268  
ID ADG53702 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 269  
ID ADG71588 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 270  
ID ADG81775 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 271  
ID ADH19632 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 272  
ID ADH30737 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 273  
ID ADH12104 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 274  
ID ADG52526 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1346; DB 12; Length 1346;  
RESULT 275  
ID ADG54254 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207416-A1.  
PD 06-NOV-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 276
ID ADG81223 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 277
ID ADG56462 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 278
ID ADH12728 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 279
ID ADH21125 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003224358-A1.
PD 04-DEC-2003.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 280
ID ADG61574 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 281
ID ADH20165 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003219856-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 282
ID ADG54806 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 283
ID ADG54806 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 284
ID ADG59846 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 285
ID ADI81270 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 286
ID ADG10013 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 287
ID ADI15484 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 288
ID ADG09361 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 289
ID ADI14816 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 290
ID ADI18411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 291
ID ADJ63692 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 292
ID ADJ77587 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 293
ID ADJ65709 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
RESULT 294
ID ADG59846 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1346; DB 12; Length 1346;
Best Local Similarity 100.0%; Pred. No. 2.3e-262;
```

RESULT 294  
ID ADM27845 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
FN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 12; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 295  
ID ADM42569 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
FN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 12; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 296  
ID ADM28431 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
FN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 12; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 297  
ID ADI95913 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
FN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 13; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 298  
ID ADI96465 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
FN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 13; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 299  
ID ADI94383 standard; cDNA; 1346 BP.  
DE Human PRO1312 cDNA sequence.  
FN AU2003259607-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1346; DB 13; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 2.3e-262;  
RESULT 300  
ID ADA39900 standard; cDNA; 1432 BP.  
DE Human secreted protein encoding cDNA.  
FN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 98.5%; Score 1325.4; DB 8; Length 1432;  
Best Local Similarity 99.5%; Pred. No. 3.3e-258;  
RESULT 301  
ID ADA11489 standard; DNA; 1432 BP.  
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 17.  
FN US2003055236-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 98.5%; Score 1325.4; DB 9; Length 1432;  
Best Local Similarity 99.5%; Pred. No. 3.3e-258;  
RESULT 302  
ID ADD37613 standard; cDNA; 1432 BP.  
DE Human secreted protein encoding sequence #95.  
FN WO2002090526-A2.  
PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 98.5%; Score 1325.4; DB 10; Length 1432;  
Best Local Similarity 99.5%; Pred. No. 3.3e-258;  
RESULT 303

ID ADA56090 standard; DNA; 1432 BP.  
DE Gene encoding human secreted protein #369.  
FN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 98.5%; Score 1325.4; DB 10; Length 1432;  
Best Local Similarity 99.5%; Pred. No. 3.3e-258;  
RESULT 304  
ID AA265261 standard; DNA; 1447 BP.  
DE Human secreted protein gene 12.  
FN WO9958660-A1.  
PD 18-NOV-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 98.4%; Score 1324.6; DB 3; Length 1447;  
Best Local Similarity 99.3%; Pred. No. 4.8e-258;  
RESULT 305  
ID ADE11650 standard; cDNA; 1447 BP.  
DE Human secreted polypeptide cDNA #12.  
FN US2003100051-A1.  
PD 29-MAY-2003.  
PA (RUBE/) RUBEN S M.  
PA (FLOR/) FLORENCE K A.  
PA (NIJJ/) NI J.  
PA (ROSE/) ROSEN C A.  
PA (CART/) CARTER K C.  
PA (MOOR/) MOORE P A.  
PA (OLSE/) OLSEN H S.  
PA (SHIY/) SHI Y.  
PA (YOUN/) YOUNG P E.  
PA (WEIY/) WEI Y.  
PA (BREW/) BREWER L A.  
PA (SOPP/) SOPPET D R.  
PA (LAFL/) LAFLEUR D W.  
PA (ENDR/) ENDRESS G A.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Query Match 98.4%; Score 1324.6; DB 10; Length 1447;  
Best Local Similarity 99.3%; Pred. No. 4.8e-258;  
RESULT 306  
ID AAV40540 standard; cDNA; 1401 BP.  
DE Homo sapiens secreted protein clone AW42\_3.  
FN WO9832853-A2.  
PD 30-JUL-1998.  
PA (GEMY ) GENETICS INST INC.  
Query Match 98.2%; Score 1321.8; DB 2; Length 1401;  
Best Local Similarity 99.8%; Pred. No. 1.8e-257;  
RESULT 307  
ID AAF94470 standard; cDNA; 1347 BP.  
DE Human hydrophobic domain containing protein clone HPI0720 cDNA #84.  
FN WO200112660-A2.  
PD 22-FEB-2001.  
PA (SAGA ) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
Query Match 97.3%; Score 1309.4; DB 4; Length 1347;  
Best Local Similarity 99.8%; Pred. No. 5.6e-255;  
RESULT 308  
ID AB278127 standard; cDNA; 1345 BP.  
DE Human cancer-related coding sequence, 156PID4.  
FN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 97.2%; Score 1307.8; DB 8; Length 1345;  
Best Local Similarity 99.8%; Pred. No. 1.2e-254;  
RESULT 309  
ID AAH98224 standard; cDNA; 1365 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 81.  
FN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 97.1%; Score 1307.4; DB 4; Length 1365;  
Best Local Similarity 99.4%; Pred. No. 1.4e-254;  
RESULT 310  
ID AAX97957 standard; DNA; 1356 BP.

DE Human secreted protein gene 42.  
PN W09931117-A1.  
PD 24-JUN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 97.0%; Score 1305; DB 2; Length 1356;  
Best Local Similarity 99.0%; Pred. No. 4.4e-254;  
RESULT 311  
ID ADA40381 standard; cDNA; 1356 BP.  
DE Human secreted protein encoding cDNA.  
PN W02002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 97.0%; Score 1305; DB 8; Length 1356;  
Best Local Similarity 99.0%; Pred. No. 4.4e-254;  
RESULT 312  
ID ADA11594 standard; DNA; 1356 BP.  
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 122.  
PN US2003055236-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 97.0%; Score 1305; DB 9; Length 1356;  
Best Local Similarity 99.0%; Pred. No. 4.4e-254;  
RESULT 313  
ID ADD37752 standard; cDNA; 1356 BP.  
DE Human secreted protein encoding sequence #234.  
PN W0200290526-A2.  
PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 97.0%; Score 1305; DB 10; Length 1356;  
Best Local Similarity 99.0%; Pred. No. 4.4e-254;  
RESULT 314  
ID ADA5545 standard; DNA; 1356 BP.  
DE Gene encoding human secreted protein #269.  
PN W02002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 97.0%; Score 1305; DB 10; Length 1356;  
Best Local Similarity 99.0%; Pred. No. 4.4e-254;  
RESULT 315  
ID ADI02664 standard; cDNA; 1312 BP.  
DE Human cDNA differentially expressed in the vascular endothelium #205.  
PN US2003166903-A1.  
PD 04-SEP-2003.  
PA (ASTR/) ASTROMOFF A.  
PA (BAND/) BANDMAN O.  
PA (COCK/) COCKS B G.  
Query Match 96.4%; Score 1297; DB 10; Length 1312;  
Best Local Similarity 99.9%; Pred. No. 1.8e-252;  
RESULT 316  
ID RAC66136 standard; DNA; 862 BP.  
DE Human kidney disease associated gene SEQ ID 6.  
PN W0200061622-A2.  
PD 19-OCT-2000.  
PA (INCY-) INCYTE PHARM INC.  
Query Match 62.8%; Score 845.2; DB 3; Length 862;  
Best Local Similarity 99.5%; Pred. No. 3.3e-161;  
RESULT 317  
ID AAX19983 standard; cDNA; 848 BP.  
DE Human secreted protein 5' EST SEQ ID NO:27.  
PN W09906439-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 2; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 318  
ID AAX39430 standard; DNA; 848 BP.  
DE Human secreted protein 5' EST SEQ ID NO: 27.  
PN W09906551-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 2; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 319  
ID ADJ45874 standard; cDNA; 848 BP.

ID AAX41369 standard; cDNA; 848 BP.  
DE Extended cDNA obtained from 5' EST, SEQ ID NO: 27 from WO 9906553.  
PN W09906553-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 2; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 320  
ID AAX97564 standard; DNA; 848 BP.  
DE Extended human secreted protein coding sequence, SEQ ID NO. 27.  
PN W09931236-A2.  
PD 24-JUN-1999.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 2; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 321  
ID AAX40770 standard; DNA; 848 BP.  
DE Secreted protein extended EST coding sequence #6.  
PN W09940189-A2.  
PD 12-AUG-1999.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 2; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 322  
ID AAX26672 standard; RNA; 848 BP.  
DE Extended cDNA derived from a 5' EST encoding a secreted protien.  
PN W09906554-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 2; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 323  
ID AAX51777 standard; cDNA; 848 BP.  
DE Human secreted protein 5' EST clone 58-35-2-F10-FL2.  
PN W09906552-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 2; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 324  
ID AAX51449 standard; DNA; 848 BP.  
DE Human secreted protein 5' EST SEQ ID NO. 27.  
PN W09906549-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 2; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 325  
ID AAX40428 standard; cDNA; 848 BP.  
DE Extended cDNA derived from 5' EST.  
PN W09906550-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 2; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 326  
ID AAX42251 standard; cDNA; 848 BP.  
DE Human full length cDNA 58-35-2-F10-FL2.  
PN W09953051-A2.  
PD 21-OCT-1999.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 3; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 327  
ID AAC00012 standard; cDNA; 848 BP.  
DE Human secreted protein cDNA sequence #3.  
PN BP1033401-A2.  
PD 06-SEP-2000.  
PA (GEST ) GENSET.  
Query Match 59.4%; Score 799.4; DB 3; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 328  
ID ADJ45874 standard; cDNA; 848 BP.



DE Novel human secreted protein-related cDNA sequence SeqID27.  
PN US2003144490-A1.  
PD 31-JUL-2003.  
PA (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLERT A.  
PA (BOUG/) BOUGUERET L.  
Query Match 59.4%; Score 799.4; DB 10; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 329  
ID ADM77746 standard; cDNA; 848 BP.  
DE EST encoding signal sequence #6.  
PN US2003162176-A1.  
PD 28-AUG-2003.  
PA (EDWA/) EDWARDS J D M.  
PA (DUCL/) DUCLERT A.  
PA (BOUG/) BOUGUERET L.  
Query Match 59.4%; Score 799.4; DB 11; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.9e-152;  
RESULT 330  
ID AAX88191 standard; cDNA; 848 BP.  
DE Human secreted protein 6 extended cDNA.  
PN WO925825-A2.  
PD 27-MAY-1999.  
PA (GEST ) GENSET.  
Query Match 59.3%; Score 798.8; DB 2; Length 848;  
Best Local Similarity 98.8%; Pred. No. 7.7e-152;  
RESULT 331  
ID AAX30083 standard; cDNA; 847 BP.  
DE Human secreted protein 5' EST SEQ ID NO:27.  
PN WO9906548-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 59.3%; Score 797.8; DB 2; Length 847;  
Best Local Similarity 98.7%; Pred. No. 1.2e-151;  
RESULT 332  
ID AAF94460 standard; cDNA; 666 BP.  
DE Human hydrophobic domain containing protein clone HPI0720 cDNA #74.  
PN WO200112860-A2.  
PD 22-FEB-2001.  
PA (SAGA ) SAGAMI CHEM RES CENT.  
PA (PROT-) PROTEGENE INC.  
Query Match 48.6%; Score 654; DB 4; Length 666;  
Best Local Similarity 99.8%; Pred. No. 1.3e-122;  
RESULT 333  
ID ADO07092 standard; cDNA; 774 BP.  
DE Human protein modification and maintenance molecule 26 (PMW-26) cDNA.  
PN WO2004033636-A2.  
PD 22-APR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 42.9%; Score 578; DB 12; Length 774;  
Best Local Similarity 88.7%; Pred. No. 3.1e-107;  
RESULT 334  
ID ABP42042 standard; DNA; 1181 BP.  
DE Toxicity modelling related rat gene SEQ ID No 1744.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 40.1%; Score 539.6; DB 10; Length 1181;  
Best Local Similarity 71.5%; Pred. No. 1.9e-99;  
RESULT 335  
ID AAX40832 standard; cDNA; 439 BP.  
DE Human secreted protein 5' EST SEQ ID NO: 44.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GEST ) GENSET.  
Query Match 30.4%; Score 409.4; DB 2; Length 439;  
Best Local Similarity 99.8%; Pred. No. 3.4e-73;  
RESULT 336  
ID AAV86301 standard; cDNA; 462 BP.  
DE EST clone AM42.  
PN WO9845435-A2.  
PD 15-OCT-1998.  
PA (GEMY ) GENETICS INST INC.

Query Match 30.1%; Score 405; DB 2; Length 462;  
Best Local Similarity 98.1%; Pred. No. 2.6e-72;  
RESULT 337  
ID ABS69507 standard; DNA; 532 BP.  
DE Novel murine polynucleotide isolated using gene trap technology #570.  
PN US2002102543-A1.  
PD 01-AUG-2002.  
PA (FRIE/) FRIEDRICH G.  
PA (ZAMB/) ZAMBROWICZ B.  
PA (SAND/) SANDS A T.  
Query Match 23.5%; Score 316.6; DB 6; Length 532;  
Best Local Similarity 84.9%; Pred. No. 1.9e-54;  
RESULT 338  
ID ADO50701 standard; DNA; 609 BP.  
DE Novel canine microarray-related DNA sequence SeqID2003.  
PN WO2004063324-A2.  
PD 29-JUL-2004.  
PA (GENE-) GENE LOGIC INC.  
PA (PFIZ ) PFIZER PROD INC.  
Query Match 19.3%; Score 260.4; DB 13; Length 609;  
Best Local Similarity 72.2%; Pred. No. 4.5e-43;  
RESULT 339  
ID ABL78658 standard; cDNA; 355 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:1636.  
PN WO200192581-A2.  
PD 06-DEC-2001.  
PA (CORI-) CORIXA CORP.  
Query Match 17.3%; Score 232.6; DB 6; Length 355;  
Best Local Similarity 83.9%; Pred. No. 1.7e-37;  
RESULT 340  
ID ABZ78108 standard; cDNA; 212 BP.  
DE Human Suppression subtractive hybridisation cDNA fragment #7.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC.  
Query Match 15.8%; Score 212; DB 8; Length 212;  
Best Local Similarity 100.0%; Pred. No. 2.3e-33;  
RESULT 341  
ID ADN43035 standard; cDNA; 379 BP.  
DE Human secreted protein SECP-21 cDNA.  
PN WO2004037987-A2.  
PD 06-MAY-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 15.2%; Score 204.4; DB 12; Length 379;  
Best Local Similarity 99.5%; Pred. No. 8.7e-32;  
RESULT 342  
ID ABA71751 standard; DNA; 213 BP.  
DE Human foetal liver single exon nucleic acid probe #20056.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.7%; Score 197.4; DB 4; Length 213;  
Best Local Similarity 99.5%; Pred. No. 2.1e-30;  
RESULT 343  
ID AAI52077 standard; DNA; 213 BP.  
DE Probe #20763 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.7%; Score 197.4; DB 4; Length 213;  
Best Local Similarity 99.5%; Pred. No. 2.1e-30;  
RESULT 344  
ID ABA37840 standard; DNA; 213 BP.  
DE Probe #16306 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.7%; Score 197.4; DB 4; Length 213;  
Best Local Similarity 99.5%; Pred. No. 2.1e-30;  
RESULT 345  
ID AAK46169 standard; DNA; 213 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 20726.  
PN WO200157276-A2.

PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.7%; Score 197.4; DB 4; Length 213;  
Best Local Similarity 99.5%; Pred. No. 2.1e-30;  
RESULT 346  
ID AAK20115 standard; DNA; 213 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 20106.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.7%; Score 197.4; DB 4; Length 213;  
Best Local Similarity 99.5%; Pred. No. 2.1e-30;  
RESULT 347  
ID ABA54586 standard; DNA; 213 BP.  
DE Human liver single exon probe, SEQ ID No 20876.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.7%; Score 197.4; DB 4; Length 213;  
Best Local Similarity 99.5%; Pred. No. 2.1e-30;  
RESULT 348  
ID ABA520478 standard; DNA; 213 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID No 20469.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.7%; Score 197.4; DB 6; Length 213;  
Best Local Similarity 99.5%; Pred. No. 2.1e-30;  
RESULT 349  
ID ABA59231 standard; DNA; 464 BP.  
DE Human foetal liver single exon nucleic acid probe #7536.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.0%; Score 188.2; DB 4; Length 464;  
Best Local Similarity 96.0%; Pred. No. 1.7e-28;  
RESULT 350  
ID AAI39012 standard; DNA; 464 BP.  
DE Probe #7698 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.0%; Score 188.2; DB 4; Length 464;  
Best Local Similarity 96.0%; Pred. No. 1.7e-28;  
RESULT 351  
ID ABA27979 standard; DNA; 464 BP.  
DE Probe #6445 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.0%; Score 188.2; DB 4; Length 464;  
Best Local Similarity 96.0%; Pred. No. 1.7e-28;  
RESULT 352  
ID AAK33216 standard; DNA; 464 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 7773.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.0%; Score 188.2; DB 4; Length 464;  
Best Local Similarity 96.0%; Pred. No. 1.7e-28;  
RESULT 353  
ID AAK07438 standard; DNA; 464 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 7429.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.0%; Score 188.2; DB 4; Length 464;  
Best Local Similarity 96.0%; Pred. No. 1.7e-28;  
RESULT 354  
ID ABA32964 standard; DNA; 464 BP.  
DE Human liver single exon probe, SEQ ID No 7954.  
PN WO200157273-A2.  
PD 09-AUG-2001.

PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.0%; Score 188.2; DB 4; Length 464;  
Best Local Similarity 96.0%; Pred. No. 1.7e-28;  
RESULT 355  
ID ABA08046 standard; DNA; 464 BP.  
DE Human genome-derived single exon probe from lung SEQ ID No 8037.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Query Match 14.0%; Score 188.2; DB 6; Length 464;  
Best Local Similarity 96.0%; Pred. No. 1.7e-28;  
RESULT 356  
ID AAC84367 standard; DNA; 2415 BP.  
DE Human Zace2 protein encoding degenerate sequence.  
PN WO200070032-A1.  
PD 23-NOV-2000.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 10.7%; Score 144.2; DB 4; Length 2415;  
Best Local Similarity 39.1%; Pred. No. 1.7e-19;  
RESULT 357  
ID ABX93334 standard; DNA; 2415 BP.  
DE Degenerate DNA sequence encoding human zinc metalloproteinase Zace2.  
PN US2002177211-A1.  
PD 28-NOV-2002.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 10.7%; Score 144.2; DB 10; Length 2415;  
Best Local Similarity 39.1%; Pred. No. 1.7e-19;  
RESULT 358  
ID AAC84369 standard; DNA; 2415 BP.  
DE Mouse Zace2-5 protein encoding degenerate sequence.  
PN WO200070032-A1.  
PD 23-NOV-2000.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 9.3%; Score 125.6; DB 4; Length 2415;  
Best Local Similarity 38.6%; Pred. No. 9.6e-16;  
RESULT 359  
ID ABX93336 standard; DNA; 2415 BP.  
DE Degenerate DNA sequence encoding mouse zinc metalloproteinase mZace-5.  
PN US2002177211-A1.  
PD 28-NOV-2002.  
PA (ZYMO) ZYMOGENETICS INC.  
Query Match 9.3%; Score 125.6; DB 10; Length 2415;  
Best Local Similarity 38.6%; Pred. No. 9.6e-16;  
RESULT 360  
ID ADL95396 standard; cDNA; 2415 BP.  
DE Angiotensin converting enzyme-2 (ACE-2) coding sequence.  
PN US6610497-B1.  
PD 26-AUG-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 9.3%; Score 125; DB 11; Length 2415;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 361  
ID AAZ59465 standard; DNA; 2418 BP.  
DE Human MPROT15 coding sequence #1.  
PN JP11318472-A.  
PD 24-NOV-1999.  
PA (SMIK) SMITHKLINE BEECHAM PLC.  
Query Match 9.3%; Score 125; DB 3; Length 2418;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 362  
ID ACN43792 standard; cDNA; 3064 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2667.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 9.3%; Score 125; DB 13; Length 3064;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 363  
ID ACH03967 standard; cDNA; 3324 BP.  
DE Human cDNA differentially expressed in lung cancer #172.  
PN US2003085157-A1.  
PD 03-APR-2003.  
PA (LASEK) LASEK A W.

Query Match 9.3%; Score 125; DB 9; Length 3324;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 364  
ID ADC38727 standard; cDNA; 3325 BP.  
DE Human cDNA encoding a secreted protein #41.  
PN US2002193567-A1.  
PD 19-DEC-2002.  
PA (GBMY ) GENETICS INST INC.  
Query Match 9.3%; Score 125; DB 10; Length 3325;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 365  
ID AAC84366 standard; cDNA; 3334 BP.  
DE Human Zace2 protein encoding cDNA.  
PN WO200070032-A1.  
PD 23-NOV-2000.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 9.3%; Score 125; DB 4; Length 3334;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 366  
ID ABX93333 standard; cDNA; 3334 BP.  
DE cDNA encoding human zinc metalloproteinase Zace2.  
PN US2002177211-A1.  
PD 28-NOV-2002.  
PA (ZYMO ) ZYMOGENETICS INC.  
Query Match 9.3%; Score 125; DB 10; Length 3334;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 367  
ID AAA12764 standard; cDNA; 3396 BP.  
DE cDNA encoding a human angiotensin converting enzyme-2 (ACE-2).  
PN WO200018899-A2.  
PD 06-APR-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 9.3%; Score 125; DB 3; Length 3396;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 368  
ID AAU02758 standard; cDNA; 3396 BP.  
DE Human angiotensin converting enzyme-2 (ACE-2) cDNA.  
PN US6194556-B1.  
PD 27-FEB-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 9.3%; Score 125; DB 4; Length 3396;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 369  
ID AAD32586 standard; cDNA; 3396 BP.  
DE Human ACE-2 full-length cDNA.  
PN WO200212471-A2.  
PD 14-FEB-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 9.3%; Score 125; DB 6; Length 3396;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 370  
ID ABX87623 standard; cDNA; 3396 BP.  
DE cDNA encoding human angiotensin converting enzyme-2 (ACE-2) protein.  
PN WO200239997-A2.  
PD 23-MAY-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 9.3%; Score 125; DB 6; Length 3396;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 371  
ID ADA03343 standard; DNA; 3396 BP.  
DE Human angiotensin converting enzyme 2-like protein gene.  
PN WO200298448-A1.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.3%; Score 125; DB 8; Length 3396;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 372  
ID ACC79022 standard; cDNA; 3396 BP.  
DE Human ACE-2 protein encoding cDNA SEQ ID NO:141.  
PN WO200298906-A1.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 9.3%; Score 125; DB 8; Length 3396;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 373  
ID ADL95394 standard; cDNA; 3396 BP.  
DE Human angiotensin converting enzyme-2 (ACE-2) cDNA.  
PN US6610497-B1.  
PD 26-AUG-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 9.3%; Score 125; DB 11; Length 3396;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 374  
ID ADH51356 standard; DNA; 3404 BP.  
DE Human angiotensin-converting enzyme homologue ACE2 DNA.  
PN WO2004000367-A1.  
PD 31-DEC-2003.  
PA (UYHE-) UNIV HEALTH NETWORK.  
Query Match 9.3%; Score 125; DB 12; Length 3404;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 375  
ID ABS60632 standard; cDNA; 3405 BP.  
DE Human cDNA encoding angiotensin converting enzyme 2 variant #1.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match 9.3%; Score 125; DB 6; Length 3405;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 376  
ID ABS60371 standard; cDNA; 3405 BP.  
DE Human cDNA encoding angiotensin converting enzyme 2.  
PN WO200261131-A2.  
PD 08-AUG-2002.  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Query Match 9.3%; Score 125; DB 6; Length 3405;  
Best Local Similarity 57.3%; Pred. No. 1.3e-15;  
RESULT 377  
ID AAS21279 standard; cDNA; 3732 BP.  
DE Human cDNA sequence encoding for PRO1885 polypeptide.  
PN WO200140466-A2.  
PD 07-JUN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 4; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 378  
ID ACA03638 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 8; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 379  
ID ABX89176 standard; cDNA; 3732 BP.  
DE DNA encoding novel secreted and transmembrane protein PRO1885.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 8; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 380  
ID ACD41830 standard; cDNA; 3732 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #36.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 8; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 381  
ID ACA04059 standard; cDNA; 3732 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 71.  
PN US2003032155-A1.

PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 8; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 382  
ID ADA45590 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 383  
ID ADA76021 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 384  
ID ADA18671 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 385  
ID ADA61294 standard; cDNA; 3732 BP.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 386  
ID ADB19079 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 387  
ID ADB27620 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 388  
ID ADA86099 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 389  
ID ADB15663 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 390  
ID ADA47449 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003073215-A1.  
PD 17-APR-2003.

PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 391  
ID ADA67244 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 392  
ID ADB30251 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 393  
ID ADA85547 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 394  
ID ADA96759 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 395  
ID ADA79063 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 396  
ID ADA87202 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 397  
ID ADB16404 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 398  
ID ADA91496 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 9; Length 3732;  
Query Match 57.7%; Pred. No. 1.5e-14;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 399  
ID ADB14559 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 400  
ID ADB18520 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 401  
ID ADA93735 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 402  
ID ADB19631 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 403  
ID ADB12943 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 404  
ID AC98459 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US200304945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 405  
ID ADA74197 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003068798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 406  
ID ADB24430 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide SEQ ID NO 71.  
PN US2003077713-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 407  
ID ADA81954 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 408  
ID ADA74917 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;

Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 409  
ID ADA84995 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 410  
ID ADA84443 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 411  
ID ADB29699 standard; cDNA; 3732 BP.  
DE CDNA encoding human PRO polypeptide #36.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 412  
ID ADA80227 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 413  
ID ADA75469 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 414  
ID ADA46694 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 415  
ID ADB24990 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide SEQ ID NO 71.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 416  
ID ADA93166 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003077721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 417  
ID ADB26516 standard; cDNA; 3732 BP.  
DE CDNA encoding human PRO polypeptide #36.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;

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RESULT 418
ID ADB30803 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 419
ID ADA60731 standard; cDNA; 3732 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 420
ID ADB23878 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 421
ID ADA96207 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 422
ID ADA80779 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 423
ID ADA95655 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 424
ID ADB25964 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 425
ID ADB21449 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 426
ID ADA77228 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 427
ID ADB27068 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 428
ID ADA86651 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 429
ID ADA87754 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 430
ID ADA46142 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 431
ID ADB28172 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 432
ID ADB28724 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 433
ID ADA76676 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 434
ID ADA88306 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 435
ID ADA97311 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
  Query Match      8.9%; Score 119.8; DB 9; Length 3732;
  Best Local Similarity 57.7%; Pred. No. 1.5e-14;
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DE cDNA encoding human PRO polypeptide #36.  
FN US2003022339-A1.  
PD 30-JAN-2003.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 437  
ID ADB22001 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003087344-A1.  
PD 08-MAY-2003.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 438  
ID ADA66692 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 439  
ID ADB22553 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 440  
ID ADB23326 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide SEQ ID NO 71.  
FN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 441  
ID ADA92048 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 442  
ID ADB15111 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 443  
ID ADB38363 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 444  
ID ADB37811 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 445  
ID ADB66283 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003082689-A1.  
PD 01-MAY-2003.

PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 9; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 446  
ID ADB89363 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 447  
ID ADB90095 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 448  
ID ADB39196 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 449  
ID ADB46819 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 450  
ID ADB86426 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 451  
ID ADB77031 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 452  
ID ADB34188 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide SEQ ID NO 71.  
FN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 453  
ID ADB35292 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide SEQ ID NO 71.  
FN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 454  
ID ADB33636 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide SEQ ID NO 71.  
FN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.





RESULT 473  
ID ADD69307 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
FN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 474  
ID ADC48196 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 475  
ID ADD09725 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 476  
ID ADD04300 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 477  
ID ADC80256 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 478  
ID ADD10763 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 479  
ID ADC47644 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 480  
ID ADC79704 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 481  
ID ADD09173 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 482

ID ADD40886 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 483  
ID ADD52025 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
FN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 484  
ID ADD52765 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
FN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 485  
ID ADD53317 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 486  
ID ADD51473 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
FN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 487  
ID ADD02272 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 488  
ID ADD01706 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 489  
ID ADD53888 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 490  
ID ADD92205 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 491  
ID ADD91101 standard; cDNA; 3732 BP.

DE Human PRO polynucleotide #36.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 492  
ID ADE03715 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 493  
ID ADE32012 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 494  
ID ADE21944 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 495  
ID ADD79168 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 496  
ID ADE41704 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 497  
ID ADE17521 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 498  
ID ADD91653 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 499  
ID ADE33116 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 500  
ID ADE33668 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.

PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 501  
ID ADD79720 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 502  
ID ADD92757 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 503  
ID ADE19177 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 504  
ID ADE18625 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 505  
ID ADE42821 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 506  
ID ADD95610 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199059-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 507  
ID ADE22496 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003199064-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 508  
ID ADD78614 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003203429-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 509  
ID ADE32564 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003194766-A1.

PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 510  
 ID AD842256 standard; cDNA; 3732 BP.  
 DE Human PRO polynucleotide #36.  
 PN US2003199032-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 511  
 ID AD80272 standard; cDNA; 3732 BP.  
 DE cDNA encoding human PRO polypeptide #36.  
 PN US2003207418-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 512  
 ID AD89300 standard; cDNA; 3732 BP.  
 DE Human PRO polynucleotide #36.  
 PN US2003199028-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 513  
 ID AD840584 standard; cDNA; 3732 BP.  
 DE Human PRO polynucleotide #36.  
 PN US2003199031-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 514  
 ID ADE04383 standard; cDNA; 3732 BP.  
 DE Human PRO polynucleotide #36.  
 PN US2003199034-A1.  
 PD 23-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 515  
 ID ADE92512 standard; cDNA; 3732 BP.  
 DE Human PRO polynucleotide #36.  
 PN US2003194777-A1.  
 PD 16-OCT-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 516  
 ID ADG21221 standard; cDNA; 3732 BP.  
 DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
 PN US2003207355-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 517  
 ID ADG22862 standard; cDNA; 3732 BP.  
 DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
 PN US2003207384-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 518  
 ID ADF97197 standard; cDNA; 3732 BP.  
 DE Human PRO polynucleotide #36.  
 PN US2003207370-A1.  
 PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 519  
 ID ADG80261 standard; cDNA; 3732 BP.  
 DE Human PRO polynucleotide #36.  
 PN US2003207373-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 520  
 ID ADG79709 standard; cDNA; 3732 BP.  
 DE Human PRO polynucleotide #36.  
 PN US2003207372-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 521  
 ID ADH55001 standard; cDNA; 3732 BP.  
 DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
 PN US2003207381-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 522  
 ID ADH55553 standard; cDNA; 3732 BP.  
 DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
 PN US2003207379-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 523  
 ID ADI64721 standard; cDNA; 3732 BP.  
 DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
 PN US2003207386-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 524  
 ID ADH81634 standard; cDNA; 3732 BP.  
 DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
 PN US2003207388-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 525  
 ID ADH81082 standard; cDNA; 3732 BP.  
 DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
 PN US2003207377-A1.  
 PD 06-NOV-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 526  
 ID ACD23888 standard; cDNA; 3732 BP.  
 DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
 PN US2003032156-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 8.9%; Score 119.8; DB 10; Length 3732;  
 Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
 RESULT 527  
 ID ACA67029 standard; cDNA; 3732 BP.  
 DE cDNA encoding human PRO polypeptide #36.  
 PN US2003004311-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC.

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Query Match      8.9%; Score 119.8; DB 10; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 528
ID ADM82251 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 529
ID ADN15650 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 530
ID ADN16279 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 531
ID ADN15098 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 532
ID ADN14546 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 533
ID ADI63772 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 534
ID ADI63220 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 11; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 535
ID ADC80808 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 536
ID ADD76256 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 537
ID ADD87620 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 538
ID ADD86024 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 539
ID ADE75472 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 540
ID ADE23048 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 541
ID ADE23600 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 542
ID ADE24243 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 543
ID ADD87068 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 544
ID ADE88934 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 545
ID ADE18073 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match      8.9%; Score 119.8; DB 12; Length 3732;
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
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RESULT 546  
ID ADE88382 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 547  
ID ADE94402 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 548  
ID ADE90813 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 549  
ID ADE94954 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 550  
ID ADE93064 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 551  
ID ADF34645 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 552  
ID ADE91960 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 553  
ID ADE90261 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 554  
ID ADE91408 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 555  
ID ADG04916 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 556  
ID ADG21773 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 557  
ID ADG19843 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 558  
ID ADF97749 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 559  
ID ADG23966 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 560  
ID ADF98320 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 561  
ID ADG03151 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 562  
ID ADF98872 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 563  
ID ADG16457 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;

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DE Human PRO polynucleotide #36.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 565
ID ADG19183 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 566
ID ADG13020 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 567
ID ADG08077 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 568
ID ADG15247 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 569
ID ADP96645 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 570
ID ADG05830 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 571
ID ADG23414 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 572
ID ADG03703 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 573
ID ADG24604 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 574
ID ADG06901 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 575
ID ADG07453 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 576
ID ADG54948 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 577
ID ADG60612 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 578
ID ADG61716 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 579
ID ADG81917 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 580
ID ADG57156 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 581
ID ADG56604 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC. 8.9%; Score 119.8; DB 12; Length 3732;
Query Match
Best Local Similarity 57.7%; Pred. No. 1.5e-14;
RESULT 582
ID ADG55500 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003207365-A1.
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Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 592  
ID ADG53844 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003207416-A1.  
PN 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 593  
ID ADG80813 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003194793-A1.  
PN 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 594  
ID ADG56052 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003207366-A1.  
PN 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 595  
ID ADH12318 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003207378-A1.  
PN 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 596  
ID ADG61164 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003207429-A1.  
PN 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 597  
ID ADH28251 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
FN US2003022331-A1.  
PN 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 598  
ID ADG54396 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003207367-A1.  
PN 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 599  
ID ADG59436 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
FN US2003207369-A1.  
PN 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 600  
ID ADI80860 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
FN US2003207361-A1.  
PN 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;

Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 601  
ID ADG09603 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2004009548-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 602  
ID ADI15074 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207382-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 603  
ID ADG08951 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2004009547-A1.  
PD 15-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 604  
ID ADI14406 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 605  
ID ADI18001 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 606  
ID ADJ63282 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 607  
ID ADJ77177 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 608  
ID ADJ65299 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 609  
ID ADM27435 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 610  
ID ADM42159 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 611  
ID ADM28021 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 12; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 612  
ID ADI95503 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 13; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 613  
ID ADI96055 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 8.9%; Score 119.8; DB 13; Length 3732;  
Best Local Similarity 57.7%; Pred. No. 1.5e-14;  
RESULT 614  
ID AAS14890 standard; cDNA; 2911 BP.  
DE Human cDNA encoding novel human protein NHP #11.  
PN WO200174896-A1.  
PD 11-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.7%; Score 117; DB 4; Length 2911;  
Best Local Similarity 57.6%; Pred. No. 5.4e-14;  
RESULT 615  
ID AAS14880 standard; cDNA; 2920 BP.  
DE Human cDNA encoding novel human protein NHP #1.  
PN WO200174896-A1.  
PD 11-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.7%; Score 117; DB 4; Length 2920;  
Best Local Similarity 57.6%; Pred. No. 5.4e-14;  
RESULT 616  
ID ADA03339 standard; DNA; 2920 BP.  
DE Human angiotensin converting enzyme 2 gene.  
PN WO200298448-A1.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.7%; Score 117; DB 8; Length 2920;  
Best Local Similarity 57.6%; Pred. No. 5.4e-14;  
RESULT 617  
ID ACC79021 standard; cDNA; 2920 BP.  
DE Human ACE-2 protein encoding cDNA SEQ ID NO:137.  
PN WO200298906-A1.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 8.7%; Score 117; DB 8; Length 2920;  
Best Local Similarity 57.6%; Pred. No. 5.4e-14;  
RESULT 618  
ID ABL78659 standard; cDNA; 435 BP.  
DE Human ovarian cancer related cDNA clone SEQ ID NO:1637.  
PN WO200192581-A2.  
PD 06-DEC-2001.  
PA (CORI-) CORIYA CORP.  
Query Match 8.3%; Score 111.4; DB 6; Length 435;  
Best Local Similarity 63.3%; Pred. No. 5.5e-13;  
RESULT 619



ID AAC84368 standard; cDNA; 2638 BP.  
 DE Mouse Zace2-5 protein encoding cDNA.  
 PN WO200070032-A1.  
 PD 23-NOV-2000.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 Query Match 8.3%; Score 111.4; DB 4; Length 2638;  
 Best Local Similarity 56.9%; Pred. No. 7.2e-13;  
 RESULT 620  
 ID ABX93335 standard; cDNA; 2638 BP.  
 DE cDNA encoding mouse zinc metalloproteinase mZace-5.  
 PN US2002177211-A1.  
 PD 28-NOV-2002.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 Query Match 8.3%; Score 111.4; DB 10; Length 2638;  
 Best Local Similarity 56.9%; Pred. No. 7.2e-13;  
 RESULT 621  
 ID AAC84370 standard; cDNA; 2638 BP.  
 DE Mouse Zace2-10 protein encoding cDNA.  
 PN WO200070032-A1.  
 PD 23-NOV-2000.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 Query Match 8.0%; Score 108.2; DB 4; Length 2638;  
 Best Local Similarity 56.5%; Pred. No. 3.2e-12;  
 RESULT 622  
 ID ABX93337 standard; cDNA; 2638 BP.  
 DE cDNA encoding mouse zinc metalloproteinase mZace-10.  
 PN US2002177211-A1.  
 PD 28-NOV-2002.  
 PA (ZYMO ) ZYMOGENETICS INC.  
 Query Match 8.0%; Score 108.2; DB 10; Length 2638;  
 Best Local Similarity 56.5%; Pred. No. 3.2e-12;  
 RESULT 623  
 ID ADH51358 standard; DNA; 2739 BP.  
 DE Mouse angiotensin-converting enzyme homologue ACE2 DNA.  
 PN WO2004000367-A1.  
 PD 31-DEC-2003.  
 PA (UTHE-) UNIV HEALTH NETWORK.  
 Query Match 8.0%; Score 108.2; DB 12; Length 2739;  
 Best Local Similarity 56.5%; Pred. No. 3.2e-12;  
 RESULT 624  
 ID ABQ57861 standard; cDNA; 561 BP.  
 DE Human colon cancer related nucleotide sequence SEQ ID NO:1556.  
 PN WO200229086-A2.  
 PD 11-APR-2002.  
 PA (FARB ) BAYER CORP.  
 Query Match 7.2%; Score 96.8; DB 6; Length 561;  
 Best Local Similarity 57.8%; Pred. No. 5.1e-10;  
 RESULT 625  
 ID AA259466 standard; DNA; 2262 BP.  
 DE Human MPROT15 coding sequence #2.  
 PN JP11318472-A.  
 PD 24-NOV-1999.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 Query Match 7.2%; Score 96.8; DB 3; Length 2262;  
 Best Local Similarity 57.8%; Pred. No. 6.2e-10;  
 RESULT 626  
 ID ACN43791 standard; cDNA; 3072 BP.  
 DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2666.  
 PN WO2004023973-A2.  
 PD 25-MAR-2004.  
 PA (INCY-) INCYTE CORP.  
 Query Match 7.2%; Score 96.8; DB 13; Length 3072;  
 Best Local Similarity 57.8%; Pred. No. 6.5e-10;  
 RESULT 627  
 ID ABK30270 standard; cDNA; 2350 BP.  
 DE Human G-protein-coupled protease #40.  
 PN US6331427-B1.  
 PD 18-DEC-2001.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 5.2%; Score 69.4; DB 6; Length 2350;  
 Best Local Similarity 55.1%; Pred. No. 0.00022;  
 RESULT 628  
 ID ABZ10246 standard; DNA; 8056 BP.

DE Haematopoietic cell proliferation disorder related DNA sequence #386.  
 PN WO200277272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 5.0%; Score 67; DB 8; Length 8056;  
 Best Local Similarity 48.3%; Pred. No. 0.00079;  
 RESULT 629  
 ID AAS42515 standard; cDNA; 3474 BP.  
 DE Human cDNA encoding an mddt protein, clone LI:347572.1:2000MAY01.  
 PN WO200162922-A2.  
 PD 30-AUG-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 4.7%; Score 63; DB 5; Length 3474;  
 Best Local Similarity 55.8%; Pred. No. 0.0045;  
 RESULT 630  
 ID ADS89278 standard; DNA; 5286 BP.  
 DE Oligonucleotide of the invention SEQ ID NO:294.  
 PN WO2004035803-A2.  
 PD 29-APR-2004.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 62.8; DB 13; Length 5286;  
 Best Local Similarity 48.0%; Pred. No. 0.0053;  
 RESULT 631  
 ID ADS89552 standard; DNA; 5286 BP.  
 DE Oligonucleotide of the invention SEQ ID NO:568.  
 PN WO2004035803-A2.  
 PD 29-APR-2004.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.7%; Score 62.8; DB 13; Length 5286;  
 Best Local Similarity 48.0%; Pred. No. 0.0053;  
 RESULT 632  
 ID AAS46694 standard; DNA; 5413 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #417.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.6%; Score 62.4; DB 4; Length 5413;  
 Best Local Similarity 45.6%; Pred. No. 0.0064;  
 RESULT 633  
 ID ABL32426 standard; DNA; 9810 BP.  
 DE Human immune system associated gene SEQ ID NO: 399.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.6%; Score 62.4; DB 6; Length 9810;  
 Best Local Similarity 45.6%; Pred. No. 0.0069;  
 RESULT 634  
 ID ABZ10100 standard; DNA; 8056 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #240.  
 PN WO200277272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.6%; Score 62.2; DB 8; Length 8056;  
 Best Local Similarity 47.8%; Pred. No. 0.0074;  
 RESULT 635  
 ID ADL17884 standard; cDNA; 158001 BP.  
 DE Human phosphotyrosyl phosphatase activator, PTPA, gene.  
 PN US2004023906-A1.  
 PD 05-FEB-2004.  
 PA (ISIS-) ISIS PHARM INC.  
 Query Match 4.6%; Score 61.8; DB 12; Length 158001;  
 Best Local Similarity 46.1%; Pred. No. 0.014;  
 RESULT 636  
 ID ABQ67093 standard; DNA; 83391 BP.  
 DE Human angiogenesis associated polynucleotide SEQ ID NO 123.  
 PN WO200246454-A2.  
 PD 13-JUN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.5%; Score 60.6; DB 6; Length 83391;  
 Best Local Similarity 44.8%; Pred. No. 0.022;  
 RESULT 637  
 ID AEN36017 standard; DNA; 60 BP.  
 DE Human spliced transcript detection oligonucleotide SEQ ID NO:8765.

PN WO200210449-A2.  
PD 07-FEB-2002.  
PA (COMP-) COMPUGEN INC. 4.5%; Score 60; DB 6; Length 60;  
Query Match 100.0%; Pred. No. 0.0099;  
Best Local Similarity 100.0%; Pred. No. 0.0099;  
RESULT 638  
ID AQAQ53480 standard; CDNA; 2503 BP.  
DE PNXP30 xylanase cDNA.  
PN WO9325671-A1.  
PD 23-DEC-1993.  
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.  
Query Match 4.4%; Score 58.8; DB 2; Length 2503;  
Best Local Similarity 45.6%; Pred. No. 0.03;  
RESULT 639  
ID ABL32369 standard; DNA; 9997 BP.  
DE Human immune system associated gene SEQ ID NO: 342.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 58.8; DB 6; Length 9997;  
Best Local Similarity 47.1%; Pred. No. 0.037;  
RESULT 640  
ID ABL34485 standard; DNA; 9997 BP.  
DE Human metastasis associated gene SEQ ID NO: 38.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 58.8; DB 6; Length 9997;  
Best Local Similarity 47.1%; Pred. No. 0.037;  
RESULT 641  
ID ADS99746 standard; DNA; 9997 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #19.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 4.4%; Score 58.8; DB 7; Length 9997;  
Best Local Similarity 47.1%; Pred. No. 0.037;  
RESULT 642  
ID ADB37663 standard; DNA; 29993 BP.  
DE Human chemically pretreated EYA4 gene SEQ ID NO:5.  
PN WO2003072812-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 58.8; DB 10; Length 29993;  
Best Local Similarity 43.4%; Pred. No. 0.044;  
RESULT 643  
ID ADB37661 standard; DNA; 29993 BP.  
DE Human chemically pretreated EYA4 gene SEQ ID NO:3.  
PN WO2003072812-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 58.8; DB 10; Length 29993;  
Best Local Similarity 43.4%; Pred. No. 0.044;  
RESULT 644  
ID AAS46746 standard; DNA; 38342 BP.  
DE Tumour suppressor gene derived chemically modified sequence #470.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 58.8; DB 4; Length 38342;  
Best Local Similarity 43.4%; Pred. No. 0.046;  
RESULT 645  
ID ABL31507 standard; DNA; 38342 BP.  
DE Signal transduction associated gene modified complementary DNA #175.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 58.8; DB 6; Length 38342;  
Best Local Similarity 43.4%; Pred. No. 0.046;  
RESULT 646  
ID ABL32427 standard; DNA; 9810 BP.

DE Human immune system associated gene SEQ ID NO: 400.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 58.6; DB 6; Length 9810;  
Best Local Similarity 44.8%; Pred. No. 0.041;  
RESULT 647  
ID ABL34174 standard; DNA; 113515 BP.  
DE Human immune system associated gene SEQ ID NO: 2147.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.4%; Score 58.6; DB 6; Length 113515;  
Best Local Similarity 45.7%; Pred. No. 0.059;  
RESULT 648  
ID ABZ10246 standard; DNA; 8056 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #386.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 57.2; DB 8; Length 8056;  
Best Local Similarity 48.8%; Pred. No. 0.076;  
RESULT 649  
ID ADH10017 standard; DNA; 365186 BP.  
DE Human chromosome 2p21-22 fragment containing the DRIP gene.  
PN WO2003093310-A1.  
PD 13-NOV-2003.  
PA (UYER-) UNIV BREMEN.  
Query Match 4.2%; Score 57.2; DB 10; Length 110000;  
Best Local Similarity 44.6%; Pred. No. 0.11;  
RESULT 650  
ID ADQ97960 standard; DNA; 390183 BP.  
DE Human cancer associated sequence HD11-029, SEQ ID 937.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 4.2%; Score 56.8; DB 12; Length 110000;  
Best Local Similarity 45.1%; Pred. No. 0.14;  
RESULT 651  
ID ADS89008 standard; DNA; 5286 BP.  
DE Human GGT1 gene SEQ ID NO:24.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.2%; Score 56.4; DB 13; Length 5286;  
Best Local Similarity 47.2%; Pred. No. 0.1;  
RESULT 652  
ID ADS89278 standard; DNA; 5286 BP.  
DE Oligonucleotide of the invention SEQ ID NO:294.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 55.4; DB 13; Length 5286;  
Best Local Similarity 44.4%; Pred. No. 0.16;  
RESULT 653  
ID ADS89552 standard; DNA; 5286 BP.  
DE Oligonucleotide of the invention SEQ ID NO:568.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 55.4; DB 13; Length 5286;  
Best Local Similarity 44.4%; Pred. No. 0.16;  
RESULT 654  
ID ABL33544 standard; DNA; 10328 BP.  
DE Human immune system associated gene SEQ ID NO: 1517.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.1%; Score 55.4; DB 6; Length 10328;  
Best Local Similarity 47.3%; Pred. No. 0.18;  
RESULT 655  
ID AAK73165 standard; DNA; 20420 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27977.

PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.1%; Score 55.2; DB 4; Length 20420;  
 Best Local Similarity 48.0%; Pred. No. 0.22;  
 RESULT 656  
 ID ABK69933 standard; DNA; 20420 BP.  
 DE Human secreted protein gene 68 genomic DNA fragment #21.  
 PN WO200226931-A2.  
 PD 04-APR-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 4.1%; Score 55.2; DB 6; Length 20420;  
 Best Local Similarity 48.0%; Pred. No. 0.22;  
 RESULT 657  
 ID ADA711938 standard; DNA; 2000 BP.  
 DE Rice gene, SEQ ID 5263.  
 PN WO2003000898-A1.  
 PD 03-JAN-2003.  
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
 Query Match 4.1%; Score 55; DB 8; Length 2000;  
 Best Local Similarity 9.3%; Pred. No. 0.17;  
 RESULT 658  
 ID ADS89551 standard; DNA; 5286 BP.  
 DE Oligonucleotide of the invention SEQ ID NO:567.  
 PN WO2004035803-A2.  
 PD 29-APR-2004.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.1%; Score 55; DB 13; Length 5286;  
 Best Local Similarity 47.0%; Pred. No. 0.2;  
 RESULT 659  
 ID ADS89277 standard; DNA; 5286 BP.  
 DE Oligonucleotide of the invention SEQ ID NO:293.  
 PN WO2004035803-A2.  
 PD 29-APR-2004.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.1%; Score 55; DB 13; Length 5286;  
 Best Local Similarity 47.0%; Pred. No. 0.2;  
 RESULT 660  
 ID ABK31366 standard; DNA; 6181 BP.  
 DE Signal transduction associated gene modified DNA #105.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.1%; Score 55; DB 6; Length 6181;  
 Best Local Similarity 46.1%; Pred. No. 0.2;  
 RESULT 661  
 ID ABL70323 standard; DNA; 6181 BP.  
 DE Chemically treated cell signalling DNA sequence#107.  
 PN WO200202807-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.1%; Score 55; DB 6; Length 6181;  
 Best Local Similarity 46.1%; Pred. No. 0.2;  
 RESULT 662  
 ID AAS61270 standard; DNA; 6181 BP.  
 DE Human gene regulation-associated gene oligonucleotide #225.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.1%; Score 55; DB 6; Length 6181;  
 Best Local Similarity 46.1%; Pred. No. 0.2;  
 RESULT 663  
 ID ABL32625 standard; DNA; 16217 BP.  
 DE Human immune system associated gene SEQ ID NO: 598.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.1%; Score 55; DB 6; Length 16217;  
 Best Local Similarity 46.3%; Pred. No. 0.23;  
 RESULT 664  
 ID ADL13897 standard; DNA; 11631 BP.  
 DE Osteoarthritis-associated polymorphic nucleotide #429.  
 PN WO2003054166-A2.

PD 03-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Query Match 4.1%; Score 54.8; DB 10; Length 11631;  
 Best Local Similarity 46.3%; Pred. No. 0.24;  
 RESULT 665  
 ID ADI73089 standard; DNA; 500 BP.  
 DE Human ovarian cancer DNA marker #5831.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.0%; Score 54.4; DB 5; Length 500;  
 Best Local Similarity 39.1%; Pred. No. 0.18;  
 RESULT 666  
 ID ADL38222 standard; DNA; 500 BP.  
 DE Human ovarian cancer DNA marker #12112.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 4.0%; Score 54.4; DB 5; Length 500;  
 Best Local Similarity 39.1%; Pred. No. 0.18;  
 RESULT 667  
 ID AAH93026 standard; DNA; 700 BP.  
 DE Human inflammatory bowel disease related gene fragment IGR3319a.  
 PN WO200142511-A2.  
 PD 14-JUN-2001.  
 PA (WHED) WHITEHEAD INST BIOMEDICAL RES.  
 Query Match 4.0%; Score 54.4; DB 4; Length 700;  
 Best Local Similarity 46.2%; Pred. No. 0.19;  
 RESULT 668  
 ID ABL33730 standard; DNA; 6109 BP.  
 DE Human immune system associated gene SEQ ID NO: 1703.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.0%; Score 54.4; DB 6; Length 6109;  
 Best Local Similarity 47.5%; Pred. No. 0.27;  
 RESULT 669  
 ID ABK28339 standard; DNA; 6631 BP.  
 DE DNA transcription associated genomic DNA #107.  
 PN WO200192565-A2.  
 PD 06-DEC-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.0%; Score 54.4; DB 6; Length 6631;  
 Best Local Similarity 49.5%; Pred. No. 0.27;  
 RESULT 670  
 ID ABL32283 standard; DNA; 7490 BP.  
 DE Human immune system associated gene SEQ ID NO: 256.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.0%; Score 54.4; DB 6; Length 7490;  
 Best Local Similarity 48.2%; Pred. No. 0.28;  
 RESULT 671  
 ID ABL33964 standard; DNA; 9180 BP.  
 DE Human immune system associated gene SEQ ID NO: 1937.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.0%; Score 54.2; DB 6; Length 9180;  
 Best Local Similarity 46.7%; Pred. No. 0.31;  
 RESULT 672  
 Query Match 4.0%; Score 54.2; DB 13; Length 110000;  
 Best Local Similarity 43.5%; Pred. No. 0.45;  
 RESULT 673  
 ID AAS46430 standard; DNA; 6106 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #152.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 4.0%; Score 54; DB 4; Length 6106;  
 Best Local Similarity 46.7%; Pred. No. 0.32;  
 RESULT 674

ID ABK40032 standard; DNA; 6106 BP.  
DE Human chemically pretreated gene sequence #57 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.0%; Score 54; DB 6; Length 6106;  
Best Local Similarity 46.7%; Pred. No. 0.32;  
RESULT 675  
ID ABL33473 standard; DNA; 6106 BP.  
DE Human immune system associated gene SEQ ID NO: 1446.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.0%; Score 54; DB 6; Length 6106;  
Best Local Similarity 46.7%; Pred. No. 0.32;  
RESULT 676  
ID AAO90512 standard; DNA; 11288 BP.  
DE CEA clone HindIII-Sau3A fragment.  
PN WO9514100-A2.  
PD 26-MAY-1995.  
PA (WELL) WELLCOME FOUND LTD.  
Query Match 4.0%; Score 54; DB 2; Length 11288;  
Best Local Similarity 62.1%; Pred. No. 0.35;  
RESULT 677  
ID AAS14778 standard; DNA; 11288 BP.  
DE Human carcinoembryonic antigen (CEA) genomic DNA.  
PN WO200174861-A2.  
PD 11-OCT-2001.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Query Match 4.0%; Score 54; DB 5; Length 11288;  
Best Local Similarity 62.1%; Pred. No. 0.35;  
RESULT 678  
ID AAV52967 standard; DNA; 15056 BP.  
DE Carcinoembryonic antigen gene 5' flanking region.  
PN WO9839467-A2.  
PD 11-SEP-1998.  
PA (CALY-) CALYDON INC.  
Query Match 4.0%; Score 54; DB 2; Length 15056;  
Best Local Similarity 62.1%; Pred. No. 0.37;  
RESULT 679  
ID AAZ99933 standard; DNA; 15056 BP.  
DE DNA sequence of comprising a carcinoembryonic antigen TRE.  
PN WO200015820-A1.  
PD 23-MAR-2000.  
PA (CALY-) CALYDON INC.  
Query Match 4.0%; Score 54; DB 3; Length 15056;  
Best Local Similarity 62.1%; Pred. No. 0.37;  
RESULT 680  
ID RAA46851 standard; DNA; 15056 BP.  
DE Nucleotide sequence of a CEA-TRE.  
PN WO200039319-A2.  
PD 06-JUL-2000.  
PA (CALY-) CALYDON INC.  
Query Match 4.0%; Score 54; DB 3; Length 15056;  
Best Local Similarity 62.1%; Pred. No. 0.37;  
RESULT 681  
ID AAH43620 standard; cDNA; 15056 BP.  
DE CEA-TRE.  
PN WO200173093-A2.  
PD 04-OCT-2001.  
PA (CALY-) CALYDON INC.  
Query Match 4.0%; Score 54; DB 5; Length 15056;  
Best Local Similarity 62.1%; Pred. No. 0.37;  
RESULT 682  
ID AAF87238 standard; DNA; 15056 BP.  
DE CEA-TRE fusion protein coding sequence.  
PN WO200172341-A2.  
PD 04-OCT-2001.  
PA (CALY-) CALYDON INC.  
Query Match 4.0%; Score 54; DB 5; Length 15056;  
Best Local Similarity 62.1%; Pred. No. 0.37;  
RESULT 683  
ID ABK99582 standard; DNA; 15056 BP.  
DE Prostate-specific antigen transcriptional regulatory element (TRE).  
PN US2002088049-A1.  
PD 06-JUN-2002.  
PA (HEND/) HENDERSON D R.  
PA (SCHU/) SCHUR E R.  
Query Match 4.0%; Score 54; DB 6; Length 15056;  
Best Local Similarity 62.1%; Pred. No. 0.37;  
RESULT 684  
ID ACD07309 standard; DNA; 15056 BP.  
DE Human carcinoembryonic antigen (CEA) TRE.  
PN US2003044383-A1.  
PD 06-MAR-2003.  
PA (HEND/) HENDERSON D R.  
PA (SCHU/) SCHUR E R.  
Query Match 4.0%; Score 54; DB 8; Length 15056;  
Best Local Similarity 62.1%; Pred. No. 0.37;  
RESULT 685  
ID ABL32315 standard; DNA; 6641 BP.  
DE Human immune system associated gene SEQ ID NO: 288.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.0%; Score 53.4; DB 6; Length 6641;  
Best Local Similarity 44.3%; Pred. No. 0.43;  
RESULT 686  
ID ABL54336 standard; DNA; 6641 BP.  
DE Chemically treated apoptosis gene complementary to gene #18.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.0%; Score 53.4; DB 6; Length 6641;  
Best Local Similarity 44.3%; Pred. No. 0.43;  
RESULT 687  
ID ABL32356 standard; DNA; 9642 BP.  
DE Human immune system associated gene SEQ ID NO: 329.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 4.0%; Score 53.4; DB 6; Length 9642;  
Best Local Similarity 44.9%; Pred. No. 0.46;  
RESULT 688  
ID AAK73166 standard; DNA; 19965 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 27978.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.0%; Score 53.4; DB 4; Length 19965;  
Best Local Similarity 47.2%; Pred. No. 0.51;  
RESULT 689  
ID ABK69932 standard; DNA; 19965 BP.  
DE Human secreted protein gene 68 genomic DNA fragment #20.  
PN WO200226931-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 4.0%; Score 53.4; DB 6; Length 19965;  
Best Local Similarity 47.2%; Pred. No. 0.51;  
RESULT 690  
ID ABD32659 standard; DNA; 163382 BP.  
DE Human cancer-associated genomic DNA HD13-065.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 4.0%; Score 53.4; DB 13; Length 163382;  
Best Local Similarity 46.9%; Pred. No. 0.7;  
RESULT 691  
ID ADI72552 standard; DNA; 530 BP.  
DE Human ovarian cancer DNA marker #5294.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.9%; Score 53; DB 5; Length 530;  
Best Local Similarity 46.1%; Pred. No. 0.36;  
RESULT 692

ID ADL37691 standard; DNA; 530 BP.  
DE Human ovarian cancer DNA marker #11581.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.9%; Score 53; DB 5; Length 530;  
Best Local Similarity 46.1%; Pred. No. 0.36;  
RESULT 693  
ID ABL34495 standard; DNA; 18817 BP.  
DE Human metastasis associated gene SEQ ID NO: 48.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.9%; Score 53; DB 6; Length 18817;  
Best Local Similarity 45.9%; Pred. No. 0.61;  
RESULT 694  
ID ABL70162 standard; DNA; 18817 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #26.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.9%; Score 53; DB 6; Length 18817;  
Best Local Similarity 45.9%; Pred. No. 0.61;  
RESULT 695  
ID ADS99756 standard; DNA; 18817 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #24.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 3.9%; Score 53; DB 7; Length 18817;  
Best Local Similarity 45.9%; Pred. No. 0.61;  
RESULT 696  
ID AAQ24134 standard; DNA; 1671 BP.  
DE 50 kD subunit of SecI.  
PN JP04104793-A.  
PD 07-APR-1992.  
PA (RIKA) RIKAGAKU KENKYUSHO.  
Query Match 3.9%; Score 52.8; DB 2; Length 1671;  
Best Local Similarity 44.7%; Pred. No. 0.46;  
RESULT 697  
ID AAK86271 standard; DNA; 9599 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41083.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.9%; Score 52.8; DB 4; Length 9599;  
Best Local Similarity 47.3%; Pred. No. 0.6;  
RESULT 698  
ID AAD52172 standard; DNA; 26000 BP.  
DE Human interferon gamma receptor 1 (IFNGR1) gene.  
PN WO200288162-A1.  
PD 07-NOV-2002.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 3.9%; Score 52.8; DB 10; Length 26000;  
Best Local Similarity 47.3%; Pred. No. 0.7;  
RESULT 699  
ID ABL34174 standard; DNA; 113515 BP.  
DE Human immune system associated gene SEQ ID NO: 2147.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.9%; Score 52.6; DB 6; Length 113515;  
Best Local Similarity 44.5%; Pred. No. 0.96;  
RESULT 700  
ID AHN80031 standard; DNA; 5942 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 48.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.9%; Score 52.4; DB 6; Length 5942;  
Best Local Similarity 45.1%; Pred. No. 0.68;

RESULT 701  
ID AAS45395 standard; DNA; 11836 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #50.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.9%; Score 52.4; DB 4; Length 11836;  
Best Local Similarity 47.3%; Pred. No. 0.75;  
RESULT 702  
ID ABK28240 standard; DNA; 11836 BP.  
DE DNA transcription associated complementary genomic DNA #57.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.9%; Score 52.4; DB 6; Length 11836;  
Best Local Similarity 47.3%; Pred. No. 0.75;  
RESULT 703  
ID AAS45620 standard; DNA; 15872 BP.  
DE Tumour suppressor gene derived chemically modified sequence #242.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.9%; Score 52.2; DB 4; Length 15872;  
Best Local Similarity 47.8%; Pred. No. 0.86;  
RESULT 704  
ID ABL33165 standard; DNA; 6134 BP.  
DE Human immune system associated gene SEQ ID NO: 1138.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.9%; Score 52; DB 6; Length 6134;  
Best Local Similarity 47.3%; Pred. No. 0.82;  
RESULT 705  
ID ABL33013 standard; DNA; 7597 BP.  
DE Human immune system associated gene SEQ ID NO: 986.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.9%; Score 52; DB 6; Length 7597;  
Best Local Similarity 45.2%; Pred. No. 0.84;  
RESULT 706  
ID ABL33307 standard; DNA; 6175 BP.  
DE Human immune system associated gene SEQ ID NO: 1280.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.8; DB 6; Length 6175;  
Best Local Similarity 47.1%; Pred. No. 0.9;  
RESULT 707  
ID ABZ10100 standard; DNA; 8056 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #240.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.8; DB 8; Length 8056;  
Best Local Similarity 44.1%; Pred. No. 0.93;  
RESULT 708  
ID ABL32348 standard; DNA; 5145 BP.  
DE Human immune system associated gene SEQ ID NO: 321.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.6; DB 6; Length 5145;  
Best Local Similarity 44.5%; Pred. No. 0.96;  
RESULT 709  
ID ABL34464 standard; DNA; 5145 BP.  
DE Human metastasis associated gene SEQ ID NO: 17.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.6; DB 6; Length 5145;  
Best Local Similarity 44.5%; Pred. No. 0.96;  
RESULT 710

ID ADS99725 standard; DNA; 5145 BP.  
DE Bisulphite treated human gene associated with metastasis #9.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 3.8%; Score 51.6; DB 7; Length 5145;  
Best Local Similarity 44.5%; Pred. No. 0.96;  
RESULT 711  
ID ABL32594 standard; DNA; 11976 BP.  
DE Human immune system associated gene SEQ ID NO: 567.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.6; DB 6; Length 11976;  
Best Local Similarity 45.2%; Pred. No. 1.1;  
RESULT 712  
ID ABL34469 standard; DNA; 16173 BP.  
DE Human metastasis associated gene SEQ ID NO: 22.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.6; DB 6; Length 16173;  
Best Local Similarity 46.0%; Pred. No. 1.1;  
RESULT 713  
ID ADS99730 standard; DNA; 16173 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #11.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 3.8%; Score 51.6; DB 7; Length 16173;  
Best Local Similarity 46.0%; Pred. No. 1.1;  
RESULT 714  
ID AAH21613 standard; DNA; 168575 BP.  
DE Human hypocretin receptor 2 (HCRTR2) gene SEQ ID NO:1.  
PN WO200130591-A2.  
PD 03-MAY-2001.  
PA (DECO-) DECODE GENETICS EHF.  
Query Match 3.8%; Score 51.6; DB 4; Length 168575;  
Best Local Similarity 47.5%; Pred. No. 1.6;  
RESULT 715  
ID ABL33393 standard; DNA; 6494 BP.  
DE Human immune system associated gene SEQ ID NO: 1366.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.4; DB 6; Length 6494;  
Best Local Similarity 42.8%; Pred. No. 1.1;  
RESULT 716  
ID AAD28391 standard; DNA; 6494 BP.  
DE Human chemically treated genomic DNA #32.  
PN WO200202809-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.4; DB 6; Length 6494;  
Best Local Similarity 42.8%; Pred. No. 1.1;  
RESULT 717  
ID ABL33568 standard; DNA; 8305 BP.  
DE Human immune system associated gene SEQ ID NO: 1541.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.4; DB 6; Length 8305;  
Best Local Similarity 46.4%; Pred. No. 1.1;  
RESULT 718  
ID ABL33937 standard; DNA; 11422 BP.  
DE Human chemically pretreated gene sequence #9 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 3.8%; Score 51.4; DB 6; Length 11422;  
Best Local Similarity 46.9%; Pred. No. 1.2;  
RESULT 719  
ID ABL32219 standard; DNA; 11422 BP.  
DE Human immune system associated gene SEQ ID NO: 192.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.4; DB 6; Length 11422;  
Best Local Similarity 46.9%; Pred. No. 1.2;  
RESULT 720  
ID ABL31423 standard; DNA; 13123 BP.  
DE Signal transduction associated gene modified complementary DNA #133.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.4; DB 6; Length 13123;  
Best Local Similarity 42.9%; Pred. No. 1.2;  
RESULT 721  
ID ABL54364 standard; DNA; 13123 BP.  
DE Chemically treated apoptosis gene complementary to gene #32.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.4; DB 6; Length 13123;  
Best Local Similarity 42.9%; Pred. No. 1.2;  
RESULT 722  
ID ABL28395 standard; DNA; 15743 BP.  
DE DNA transcription associated genomic DNA #135.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.4; DB 6; Length 15743;  
Best Local Similarity 49.1%; Pred. No. 1.2;  
RESULT 723  
ID ABL92249 standard; DNA; 13131 BP.  
DE Chemically treated DNA repair gene fragment complementary to #29.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.2; DB 6; Length 13131;  
Best Local Similarity 44.9%; Pred. No. 1.3;  
RESULT 724  
ID ABL70544 standard; DNA; 15649 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #217.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51.2; DB 6; Length 15649;  
Best Local Similarity 43.9%; Pred. No. 1.4;  
RESULT 725  
ID ABL33776 standard; DNA; 6239 BP.  
DE Human immune system associated gene SEQ ID NO: 1749.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51; DB 6; Length 6239;  
Best Local Similarity 47.4%; Pred. No. 1.3;  
RESULT 726  
ID ABL28297 standard; DNA; 6239 BP.  
DE DNA transcription associated genomic DNA #86.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51; DB 6; Length 6239;  
Best Local Similarity 47.4%; Pred. No. 1.3;  
RESULT 727  
ID AAS46541 standard; DNA; 10595 BP.  
DE Tumour suppressor gene derived chemically modified sequence #263.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.8%; Score 51; DB 4; Length 10595;

Best Local Similarity 50.6%; Pred. No. 1.4;  
 RESULT 728  
 ID ABL33514 standard; DNA; 15399 BP.  
 DE Human immune system associated gene SEQ ID NO: 1487.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.8%; Score 51; DB 6; Length 15399;  
 Best Local Similarity 47.0%; Pred. No. 1.5;  
 RESULT 729  
 ID ABL34609 standard; DNA; 18585 BP.  
 DE Human metastasis associated gene SEQ ID NO: 162.  
 PN WO200177376-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.8%; Score 51; DB 6; Length 18585;  
 Best Local Similarity 44.3%; Pred. No. 1.5;  
 RESULT 730  
 ID ADS99870 standard; DNA; 18585 BP.  
 DE Complement of bisulphite treated metastasis-associated human gene #81.  
 PN US2003148327-A1.  
 PD 07-AUG-2003.  
 PA (OLEK/) OLEK A.  
 PA (PIEP/) PIEPENBROCK C.  
 PA (BERL/) BERLIN K.  
 Query Match 3.8%; Score 51; DB 7; Length 18585;  
 Best Local Similarity 44.3%; Pred. No. 1.5;  
 RESULT 731  
 ID ABL32326 standard; DNA; 6109 BP.  
 DE Human immune system associated gene SEQ ID NO: 299.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.8%; Score 50.8; DB 6; Length 6109;  
 Best Local Similarity 44.8%; Pred. No. 1.4;  
 RESULT 732  
 ID AAS61077 standard; DNA; 6109 BP.  
 DE Human gene regulation-associated gene oligonucleotide #32.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.8%; Score 50.8; DB 6; Length 6109;  
 Best Local Similarity 44.8%; Pred. No. 1.4;  
 RESULT 733  
 ID ABL32983 standard; DNA; 7143 BP.  
 DE Human immune system associated gene SEQ ID NO: 956.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.8%; Score 50.8; DB 6; Length 7143;  
 Best Local Similarity 45.7%; Pred. No. 1.5;  
 RESULT 734  
 ID AAS46591 standard; DNA; 6286 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #313.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.7%; Score 49.8; DB 3; Length 2010;  
 Best Local Similarity 45.8%; Pred. No. 1.9;  
 RESULT 744  
 ID ABL32853 standard; DNA; 5999 BP.  
 DE Human immune system associated gene SEQ ID NO: 826.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.7%; Score 49.8; DB 6; Length 5999;  
 Best Local Similarity 44.9%; Pred. No. 2.3;  
 RESULT 745

Query Match 3.7%; Score 50.4; DB 13; Length 337344;  
 Best Local Similarity 48.0%; Pred. No. 3.1;  
 RESULT 737  
 ID ABZ10188 standard; DNA; 1501 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #328.  
 PN WO200277272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.7%; Score 50.2; DB 8; Length 1501;  
 Best Local Similarity 45.6%; Pred. No. 1.5;  
 RESULT 738  
 ID ADE84162 standard; DNA; 1501 BP.  
 DE Human lymphoid cell proliferative disorder gene derived DNA #98.  
 PN WO2003044226-A2.  
 PD 30-MAY-2003.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.7%; Score 50.2; DB 10; Length 1501;  
 Best Local Similarity 45.6%; Pred. No. 1.5;  
 RESULT 739  
 ID ABK31511 standard; DNA; 47108 BP.  
 DE Signal transduction associated gene modified complementary DNA #177.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.7%; Score 50.2; DB 6; Length 47108;  
 Best Local Similarity 42.8%; Pred. No. 2.6;  
 RESULT 740  
 ID ABL56201 standard; DNA; 50000 BP.  
 DE AnEPV genome fragment#3.  
 PN WO200212526-A2.  
 PD 14-FEB-2002.  
 PA (UYFL) UNIV FLORIDA.  
 Query Match 3.7%; Score 50.2; DB 6; Length 50000;  
 Best Local Similarity 46.7%; Pred. No. 2.6;  
 RESULT 741  
 ID ABV08149 standard; cDNA; 391 BP.  
 DE Human prostate expression marker cDNA 8140.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 3.7%; Score 50; DB 5; Length 391;  
 Best Local Similarity 49.7%; Pred. No. 1.4;  
 RESULT 742  
 ID ACN47472 standard; cDNA; 560 BP.  
 DE Cotton primed seed EST Clone ID: LfB3825-011-Q1-N6-C9, SEQ:2253.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (FENG/) FENG P C C.  
 PA (FING/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Query Match 3.7%; Score 50; DB 13; Length 560;  
 Best Local Similarity 55.9%; Pred. No. 1.4;  
 RESULT 743  
 ID AAA70201 standard; DNA; 2010 BP.  
 DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:334.  
 PN WO200025728-A2.  
 PD 11-MAY-2000.  
 PA (HOFF/) HOFFMAN S.  
 PA (CARU/) CARUCCI D.  
 PA (GARD/) GARDNER M.  
 PA (VENT/) VENTER J C.  
 Query Match 3.7%; Score 49.8; DB 3; Length 2010;  
 Best Local Similarity 45.8%; Pred. No. 1.9;  
 RESULT 744  
 ID ABL32853 standard; DNA; 5999 BP.  
 DE Human immune system associated gene SEQ ID NO: 826.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.7%; Score 49.8; DB 6; Length 5999;  
 Best Local Similarity 44.9%; Pred. No. 2.3;  
 RESULT 745

ID ABK28192 standard; DNA; 5999 BP.  
DE DNA transcription associated complementary genomic DNA #33.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.8; DB 6; Length 5999;  
Best Local Similarity 44.9%; Pred. No. 2.3;  
RESULT 746  
ID AAS46608 standard; DNA; 6767 BP.  
DE Tumour suppressor gene derived chemically modified sequence #330.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.8; DB 4; Length 6767;  
Best Local Similarity 44.8%; Pred. No. 2.3;  
RESULT 747  
ID ABL16590 standard; DNA; 8786 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1243.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Query Match 3.7%; Score 49.8; DB 4; Length 8786;  
Best Local Similarity 46.7%; Pred. No. 2.4;  
RESULT 748  
ID ABX46069 standard; cDNA; 419 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #11234.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 3.7%; Score 49.6; DB 8; Length 419;  
Best Local Similarity 54.3%; Pred. No. 1.7;  
RESULT 749  
ID ACN85018 standard; DNA; 994 BP.  
DE Breast cancer related marker, seq id 6968.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 3.7%; Score 49.6; DB 11; Length 994;  
Best Local Similarity 27.9%; Pred. No. 1.9;  
RESULT 750  
ID AAZ37082 standard; DNA; 1431 BP.  
DE DNA sequence encoding a yeast SteI endonuclease.  
PN EP972836-A2.  
PD 19-JAN-2000.  
PA (RIKA ) INST PHYSICAL & CHEM RES.  
Query Match 3.7%; Score 49.6; DB 3; Length 1431;  
Best Local Similarity 44.3%; Pred. No. 2;  
RESULT 751  
ID ABL32445 standard; DNA; 5388 BP.  
DE Human immune system associated gene SEQ ID NO: 218.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.6; DB 6; Length 5388;  
Best Local Similarity 45.3%; Pred. No. 2.4;  
RESULT 752  
ID AAS46283 standard; DNA; 6591 BP.  
DE Tumour suppressor gene derived chemically modified sequence #5.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.6; DB 4; Length 6591;  
Best Local Similarity 47.3%; Pred. No. 2.5;  
RESULT 753  
ID ABL32400 standard; DNA; 7167 BP.  
DE Human immune system associated gene SEQ ID NO: 373.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.4; DB 6; Length 7167;

Best Local Similarity 45.0%; Pred. No. 2.8;  
RESULT 754  
ID ABL33748 standard; DNA; 11805 BP.  
DE Human immune system associated gene SEQ ID NO: 1721.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.4; DB 6; Length 11805;  
Best Local Similarity 44.2%; Pred. No. 3;  
RESULT 755  
ID ABL32185 standard; DNA; 15387 BP.  
DE Human immune system associated gene SEQ ID NO: 158.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.4; DB 6; Length 15387;  
Best Local Similarity 45.3%; Pred. No. 3.1;  
RESULT 756  
ID ABL32570 standard; DNA; 18997 BP.  
DE Human immune system associated gene SEQ ID NO: 543.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.4; DB 6; Length 18997;  
Best Local Similarity 43.7%; Pred. No. 3.2;  
RESULT 757  
ID ARK33948 standard; DNA; 18997 BP.  
DE Human DNA for staging of Astrocytomas #16.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.4; DB 6; Length 18997;  
Best Local Similarity 43.7%; Pred. No. 3.2;  
RESULT 758  
ID ADA20352 standard; DNA; 18997 BP.  
DE Prostate tumour related genomic DNA sample #9.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.4; DB 8; Length 18997;  
Best Local Similarity 43.7%; Pred. No. 3.2;  
RESULT 759  
ID ADA84159 standard; DNA; 18997 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:17.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.4; DB 8; Length 18997;  
Best Local Similarity 43.7%; Pred. No. 3.2;  
RESULT 760  
ID ADL37109 standard; DNA; 476 BP.  
DE Human ovarian cancer DNA marker #10999.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.7%; Score 49.2; DB 5; Length 476;  
Best Local Similarity 38.1%; Pred. No. 2;  
RESULT 761  
ID ADI71958 standard; DNA; 476 BP.  
DE Human ovarian cancer DNA marker #4700.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.7%; Score 49.2; DB 5; Length 476;  
Best Local Similarity 38.1%; Pred. No. 2;  
RESULT 762  
ID AAS46429 standard; DNA; 6106 BP.  
DE Tumour suppressor gene derived chemically modified sequence #151.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.2; DB 4; Length 6106;  
Best Local Similarity 45.5%; Pred. No. 3;



RESULT 763  
ID ABL40031 standard; DNA; 6106 BP.  
DE Human chemically pretreated gene sequence #57 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.2; DB 6; Length 6106;  
Best Local Similarity 45.5%; Pred. No. 3;  
RESULT 764  
ID ABL33472 standard; DNA; 6106 BP.  
DE Human immune system associated gene SEQ ID NO: 1445.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.2; DB 6; Length 6106;  
Best Local Similarity 45.5%; Pred. No. 3;  
RESULT 765  
ID AAS46617 standard; DNA; 6863 BP.  
DE Tumour suppressor gene derived chemically modified sequence #339.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.2; DB 4; Length 6863;  
Best Local Similarity 48.6%; Pred. No. 3.1;  
RESULT 766  
ID ABL34155 standard; DNA; 15548 BP.  
DE Human immune system associated gene SEQ ID NO: 2128.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.2; DB 6; Length 15548;  
Best Local Similarity 43.0%; Pred. No. 3.5;  
RESULT 767  
ID ABL32486 standard; DNA; 17183 BP.  
DE Human immune system associated gene SEQ ID NO: 459.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.7%; Score 49.2; DB 6; Length 17183;  
Best Local Similarity 46.8%; Pred. No. 3.5;  
RESULT 768  
ID ABL55643 standard; DNA; 50000 BP.  
DE AMEPV genome fragment#1.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UVFL) UNIV FLORIDA.  
Query Match 3.7%; Score 49.2; DB 6; Length 50000;  
Best Local Similarity 43.7%; Pred. No. 4.1;  
RESULT 769  
ID ACN44010 standard; DNA; 198522 BP.  
DE Human genomic sequence hCG1643869.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 3.7%; Score 49.2; DB 11; Length 198522;  
Best Local Similarity 46.8%; Pred. No. 5.1;  
RESULT 770  
ID ABL32029 standard; DNA; 7351 BP.  
DE Human immune system associated gene SEQ ID NO: 2.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 49; DB 6; Length 7351;  
Best Local Similarity 45.4%; Pred. No. 3.4;  
RESULT 771  
ID ACN44010 standard; DNA; 198522 BP.  
DE Human genomic sequence hCG1643869.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 3.6%; Score 49; DB 11; Length 198522;  
Best Local Similarity 49.4%; Pred. No. 5.6;  
RESULT 772

ID ACF05254 standard; cDNA; 3197 BP.  
DE Plasmodium falciparum cGMP dependent protein kinase cDNA.  
PN WO2003054157-A2.  
PD 03-JUL-2003.  
PA (MERI) MERCK & CO INC.  
Query Match 3.6%; Score 48.8; DB 9; Length 3197;  
Best Local Similarity 48.1%; Pred. No. 3.3;  
RESULT 773  
ID ABL32142 standard; DNA; 5398 BP.  
DE Human immune system associated gene SEQ ID NO: 115.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 6; Length 5398;  
Best Local Similarity 45.5%; Pred. No. 3.6;  
RESULT 774  
ID ABQ67070 standard; DNA; 5611 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 100.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 6; Length 5611;  
Best Local Similarity 44.8%; Pred. No. 3.6;  
RESULT 775  
ID ABL32693 standard; DNA; 6222 BP.  
DE Human immune system associated gene SEQ ID NO: 666.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 6; Length 6222;  
Best Local Similarity 44.5%; Pred. No. 3.6;  
RESULT 776  
ID ABL33761 standard; DNA; 7851 BP.  
DE Human immune system associated gene SEQ ID NO: 1734.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 6; Length 7851;  
Best Local Similarity 48.5%; Pred. No. 3.8;  
RESULT 777  
ID ACF62816 standard; DNA; 8222 BP.  
DE Colon cancer analysis related genomic DNA SEQ ID NO:65.  
PN WO2003014388-A2.  
PD 20-FEB-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 8; Length 8222;  
Best Local Similarity 43.2%; Pred. No. 3.8;  
RESULT 778  
ID ACF62794 standard; DNA; 8222 BP.  
DE Colon cancer analysis related genomic DNA SEQ ID NO:43.  
PN WO2003014388-A2.  
PD 20-FEB-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 8; Length 8222;  
Best Local Similarity 43.2%; Pred. No. 3.8;  
RESULT 779  
ID ABL33569 standard; DNA; 8305 BP.  
DE Human immune system associated gene SEQ ID NO: 1542.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 6; Length 8305;  
Best Local Similarity 49.2%; Pred. No. 3.8;  
RESULT 780  
ID ABL33591 standard; DNA; 10279 BP.  
DE Human immune system associated gene SEQ ID NO: 1564.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 6; Length 10279;  
Best Local Similarity 47.2%; Pred. No. 3.9;  
RESULT 781  
ID ABL92277 standard; DNA; 10279 BP.

DE Chemically treated DNA repair gene fragment complementary to#43.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 6; Length 10279;  
Best Local Similarity 47.2%; Pred. No. 3.9;  
RESULT 782  
ID AD22328 standard; DNA; 10279 BP.  
DE Chemically treated human genomic DNA #18 associated with DNA adducts.  
PN WO200177378-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 6; Length 10279;  
Best Local Similarity 47.2%; Pred. No. 3.9;  
RESULT 783  
ID ADB54190 standard; DNA; 11222 BP.  
DE Pretreated genomic DNA region 114.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 10; Length 11222;  
Best Local Similarity 43.2%; Pred. No. 4;  
RESULT 784  
ID ADB54318 standard; DNA; 11222 BP.  
DE Pretreated genomic DNA region 242.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 10; Length 11222;  
Best Local Similarity 43.2%; Pred. No. 4;  
RESULT 785  
ID ABL32342 standard; DNA; 11534 BP.  
DE Human immune system associated gene SEQ ID NO: 315.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 6; Length 11534;  
Best Local Similarity 46.6%; Pred. No. 4;  
RESULT 786  
ID ABL32467 standard; DNA; 15373 BP.  
DE Human immune system associated gene SEQ ID NO: 440.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 6; Length 15373;  
Best Local Similarity 45.3%; Pred. No. 4.2;  
RESULT 787  
ID AAS46771 standard; DNA; 17280 BP.  
DE Tumour suppressor gene derived chemically modified sequence #495.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.8; DB 4; Length 17280;  
Best Local Similarity 46.4%; Pred. No. 4.2;  
RESULT 788  
ID ABZ09999 standard; DNA; 5033 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #139.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 8; Length 5033;  
Best Local Similarity 47.9%; Pred. No. 3.9;  
RESULT 789  
ID ABK33920 standard; DNA; 7001 BP.  
DE Human DNA for staging of Astrocytomas, complement, #1.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 6; Length 7001;  
Best Local Similarity 43.4%; Pred. No. 4.1;  
RESULT 790  
ID ADA20395 standard; DNA; 7001 BP.  
DE Prostate tumour related genomic DNA complement sample #30.

PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 8; Length 7001;  
Best Local Similarity 43.4%; Pred. No. 4.1;  
RESULT 791  
ID ADA84202 standard; DNA; 7001 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:60.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 8; Length 7001;  
Best Local Similarity 43.4%; Pred. No. 4.1;  
RESULT 792  
ID AAS46307 standard; DNA; 8033 BP.  
DE Tumour suppressor gene derived chemically modified sequence #29.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 4; Length 8033;  
Best Local Similarity 47.9%; Pred. No. 4.1;  
RESULT 793  
ID ABK31202 standard; DNA; 8033 BP.  
DE Signal transduction associated gene modified DNA #23.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 6; Length 8033;  
Best Local Similarity 47.9%; Pred. No. 4.1;  
RESULT 794  
ID ABL70169 standard; DNA; 8033 BP.  
DE Chemically treated cell signalling DNA sequence#30.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 6; Length 8033;  
Best Local Similarity 47.9%; Pred. No. 4.1;  
RESULT 795  
ID AAS61116 standard; DNA; 8033 BP.  
DE Human gene regulation-associated gene oligonucleotide #71.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 6; Length 8033;  
Best Local Similarity 47.9%; Pred. No. 4.1;  
RESULT 796  
ID ADB54330 standard; DNA; 11787 BP.  
DE Pretreated genomic DNA region 254.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 10; Length 11787;  
Best Local Similarity 47.1%; Pred. No. 4.4;  
RESULT 797  
ID ABL33032 standard; DNA; 14798 BP.  
DE Human immune system associated gene SEQ ID NO: 1005.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 6; Length 14798;  
Best Local Similarity 50.2%; Pred. No. 4.5;  
RESULT 798  
ID AAS61426 standard; DNA; 19380 BP.  
DE Human gene regulation-associated gene oligonucleotide #381.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.6; DB 6; Length 19380;  
Best Local Similarity 44.2%; Pred. No. 4.7;  
RESULT 799  
ID ABL55644 standard; DNA; 50000 BP.  
DE AnePV genome fragment#2.  
PN WO200212526-A2.

PD 14-FEB-2002.  
PA (UTFL) UNIV FLORIDA.  
Query Match 3.6%; Score 48.6; DB 6; Length 50000;  
Best Local Similarity 44.7%; Pred. No. 5.5;  
RESULT 800  
ID ABL33036 standard; DNA; 6123 BP.  
DE Human immune system associated gene SEQ ID NO: 1009.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.4; DB 6; Length 6123;  
Best Local Similarity 50.4%; Pred. No. 4.4;  
RESULT 801  
ID ABL32257 standard; DNA; 7498 BP.  
DE Human immune system associated gene SEQ ID NO: 230.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.4; DB 6; Length 7498;  
Best Local Similarity 44.8%; Pred. No. 4.5;  
RESULT 802  
ID ABL31275 standard; DNA; 10205 BP.  
DE Signal transduction associated gene modified complementary DNA #59.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.4; DB 6; Length 10205;  
Best Local Similarity 51.4%; Pred. No. 4.7;  
RESULT 803  
ID ABL70236 standard; DNA; 10205 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #63.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.4; DB 6; Length 10205;  
Best Local Similarity 51.4%; Pred. No. 4.7;  
RESULT 804  
ID AAK73165 standard; DNA; 20420 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 27977.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.6%; Score 48.4; DB 4; Length 20420;  
Best Local Similarity 51.4%; Pred. No. 5.2;  
RESULT 805  
ID ABL65933 standard; DNA; 20420 BP.  
DE Human secreted protein gene 68 genomic DNA fragment #21.  
PN WO200226931-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.6%; Score 48.4; DB 6; Length 20420;  
Best Local Similarity 51.4%; Pred. No. 5.2;  
RESULT 806  
ID ADQ97050 standard; DNA; 687411 BP.  
DE Human cancer associated sequence HD08-001, SEQ ID 26.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 3.6%; Score 48.4; DB 12; Length 110000;  
Best Local Similarity 42.2%; Pred. No. 6.7;  
RESULT 807  
ID ADA71938 standard; DNA; 2000 BP.  
DE Rice gene, SEQ ID 5263.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Query Match 3.6%; Score 48.2; DB 8; Length 2000;  
Best Local Similarity 14.5%; Pred. No. 4;  
RESULT 808  
ID ADL63811 standard; DNA; 4240 BP.  
DE Human ovarian cancer DNA marker #22023.  
PN WO200170979-A2.  
PD 27-SEP-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.6%; Score 48.2; DB 5; Length 4240;  
Best Local Similarity 46.5%; Pred. No. 4.5;  
RESULT 809  
ID AAS45456 standard; DNA; 6030 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #81.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.2; DB 4; Length 6030;  
Best Local Similarity 44.4%; Pred. No. 4.8;  
RESULT 810  
ID ABR28312 standard; DNA; 6030 BP.  
DE DNA transcription associated complementary genomic DNA #93.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.2; DB 6; Length 6030;  
Best Local Similarity 44.4%; Pred. No. 4.8;  
RESULT 811  
ID AAS61348 standard; DNA; 6030 BP.  
DE Human gene regulation-associated gene oligonucleotide #303.  
PN WO200177175-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.2; DB 6; Length 6030;  
Best Local Similarity 44.4%; Pred. No. 4.8;  
RESULT 812  
ID ABL54314 standard; DNA; 6314 BP.  
DE Chemically treated apoptosis gene complementary to gene #7.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.2; DB 6; Length 6314;  
Best Local Similarity 45.0%; Pred. No. 4.8;  
RESULT 813  
ID ABR39963 standard; DNA; 6731 BP.  
DE Human chemically pretreated gene sequence #22 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.2; DB 6; Length 6731;  
Best Local Similarity 51.3%; Pred. No. 4.9;  
RESULT 814  
ID ABL34240 standard; DNA; 11691 BP.  
DE Human immune system associated gene SEQ ID NO: 2213.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.2; DB 6; Length 11691;  
Best Local Similarity 44.4%; Pred. No. 5.3;  
RESULT 815  
ID ADB54330 standard; DNA; 11787 BP.  
DE Pretreated genomic DNA region 254.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.2; DB 10; Length 11787;  
Best Local Similarity 44.4%; Pred. No. 5.3;  
RESULT 816  
ID ABR39920 standard; DNA; 17869 BP.  
DE Human chemically pretreated gene sequence #1 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.2; DB 6; Length 17869;  
Best Local Similarity 49.8%; Pred. No. 5.6;  
RESULT 817  
ID ABL32104 standard; DNA; 17869 BP.  
DE Human immune system associated gene SEQ ID NO: 77.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 3.6%; Score 48.2; DB 6; Length 17869;  
Best Local Similarity 49.8%; Pred. No. 5.6;  
RESULT 818  
ID ADE43862 standard; DNA; 40178 BP.  
DE Human LIPA genomic sequence, SEQ ID 467.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 3.6%; Score 48.2; DB 10; Length 40178;  
Best Local Similarity 44.3%; Pred. No. 6.4;  
RESULT 819  
ID ADE43863 standard; DNA; 40178 BP.  
DE Polymorphic human LIPA genomic sequence, SEQ ID 468.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 3.6%; Score 48.2; DB 10; Length 40178;  
Best Local Similarity 44.3%; Pred. No. 6.4;  
RESULT 820  
ID ADH54341 standard; DNA; 40178 BP.  
DE Human LIPA gene variant DNA sequence SeqID468.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 3.6%; Score 48.2; DB 12; Length 40178;  
Best Local Similarity 44.3%; Pred. No. 6.4;  
RESULT 821  
ID ADH54340 standard; DNA; 40178 BP.  
DE Human LIPA gene DNA sequence SeqID467.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 3.6%; Score 48.2; DB 12; Length 40178;  
Best Local Similarity 44.3%; Pred. No. 6.4;  
RESULT 822  
ID ABL34073 standard; DNA; 40862 BP.  
DE Human immune system associated gene SEQ ID NO: 2046.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48.2; DB 6; Length 40862;  
Best Local Similarity 45.0%; Pred. No. 6.4;  
RESULT 823  
Query Match 3.6%; Score 48.2; DB 13; Length 110000;  
Best Local Similarity 43.7%; Pred. No. 7.4;  
RESULT 824  
ID ABN53251 standard; DNA; 65 BP.  
DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:259999.  
PN WO200210449-A2.  
PD 07-FEB-2002.  
PA (COMP-) COMPUGEN INC.  
Query Match 3.6%; Score 48; DB 6; Length 65;  
Best Local Similarity 84.4%; Pred. No. 2.7;  
RESULT 825  
ID ABK63918 standard; cDNA; 800 BP.  
DE cDNA encoding human secreted protein sequence #3.  
PN WO200216388-A1.  
PD 28-FEB-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.6%; Score 48; DB 6; Length 800;  
Best Local Similarity 60.9%; Pred. No. 3.9;  
RESULT 826  
ID ABK63942 standard; cDNA; 801 BP.  
DE cDNA encoding human secreted protein sequence #27.  
PN WO200216388-A1.  
PD 28-FEB-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.6%; Score 48; DB 6; Length 801;  
Best Local Similarity 60.9%; Pred. No. 3.9;  
RESULT 827  
ID ACC62484 standard; cDNA; 834 BP.

DE Human secreted protein #10 coding sequence SEQ ID 20.  
PN WO20029066-A2.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.6%; Score 48; DB 8; Length 834;  
Best Local Similarity 60.9%; Pred. No. 3.9;  
RESULT 828  
ID AAV73003 standard; cDNA; 3076 BP.  
DE Human adult brain secreted protein dm26\_2 cDNA.  
PN WO9842741-A2.  
PD 01-OCT-1998.  
PA (GEMY) GENETICS INST INC.  
Query Match 3.6%; Score 48; DB 2; Length 3076;  
Best Local Similarity 60.9%; Pred. No. 4.7;  
RESULT 829  
ID ABQ92028 standard; cDNA; 3076 BP.  
DE Human polynucleotide SEQ ID NO 25.  
PN US2002065394-A1.  
PD 30-MAY-2002.  
PA (JACO/) JACOBS K.  
PA (MCCO/) MCCOY J M.  
PA (LAVA/) LAVALLIE E R.  
PA (COLL/) COLLINS-RACIE L A.  
PA (EVAN/) EVANS C.  
PA (MERB/) MERBERG D.  
PA (TREA/) TREACY M.  
PA (SPAU/) SPAULDING V.  
Query Match 3.6%; Score 48; DB 6; Length 3076;  
Best Local Similarity 60.9%; Pred. No. 4.7;  
RESULT 830  
ID ABL32400 standard; DNA; 7167 BP.  
DE Human immune system associated gene SEQ ID NO: 373.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48; DB 6; Length 7167;  
Best Local Similarity 43.6%; Pred. No. 5.4;  
RESULT 831  
ID ABL34105 standard; DNA; 14023 BP.  
DE Human immune system associated gene SEQ ID NO: 2078.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48; DB 6; Length 14023;  
Best Local Similarity 48.2%; Pred. No. 6;  
RESULT 832  
ID ABL70576 standard; DNA; 19576 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#233.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48; DB 6; Length 19576;  
Best Local Similarity 46.6%; Pred. No. 6.3;  
RESULT 833  
ID AAS61259 standard; DNA; 19576 BP.  
DE Human gene regulation-associated gene oligonucleotide #214.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48; DB 6; Length 19576;  
Best Local Similarity 46.6%; Pred. No. 6.3;  
RESULT 834  
ID ABQ66998 standard; DNA; 37515 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 28.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48; DB 6; Length 37515;  
Best Local Similarity 44.3%; Pred. No. 6.9;  
RESULT 835  
ID ABQ67094 standard; DNA; 83391 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 124.  
PN WO200246454-A2.

PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 48; DB 6; Length 83391;  
Best Local Similarity 44.7%; Pred. No. 7.8;  
RESULT 836  
ID AC64845 standard; DNA; 115218 BP.  
DE Human HNRNP GP43 DNA corresponding to AL034397.  
PN DE10127572-A1.  
PD 05-DEC-2002.  
PA (PATH-) PATHOARRAY GMBH.  
Query Match 3.6%; Score 48; DB 8; Length 115218;  
Best Local Similarity 44.8%; Pred. No. 8.2;  
RESULT 837  
ID ADR02445 standard; DNA; 636 BP.  
DE A. gossypii genomic DNA PAG1692RP.  
PN US6239264-B1.  
PD 29-MAY-2001.  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 3.6%; Score 47.8; DB 2; Length 636;  
Best Local Similarity 43.2%; Pred. No. 4.1;  
RESULT 838  
ID AAS63366 standard; DNA; 3586 BP.  
DE Chemically pretreated metabolism associated gene #61.  
PN WO200176451-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 47.8; DB 6; Length 3586;  
Best Local Similarity 47.0%; Pred. No. 5.3;  
RESULT 839  
ID ABX31451 standard; DNA; 7131 BP.  
DE Signal transduction associated gene modified complementary DNA #147.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 47.8; DB 6; Length 7131;  
Best Local Similarity 44.7%; Pred. No. 5.9;  
RESULT 840  
ID AB170428 standard; DNA; 7131 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #159.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 47.8; DB 6; Length 7131;  
Best Local Similarity 44.7%; Pred. No. 5.9;  
RESULT 841  
ID AAS61361 standard; DNA; 7131 BP.  
DE Human gene regulation-associated gene oligonucleotide #316.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 47.8; DB 6; Length 7131;  
Best Local Similarity 44.7%; Pred. No. 5.9;  
RESULT 842  
ID AB133989 standard; DNA; 8238 BP.  
DE Human immune system associated gene SEQ ID NO: 1962.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 47.8; DB 6; Length 8238;  
Best Local Similarity 45.6%; Pred. No. 6;  
RESULT 843  
ID AAS63349 standard; DNA; 8238 BP.  
DE Chemically pretreated metabolism associated gene #44.  
PN WO200176451-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 47.8; DB 6; Length 8238;  
Best Local Similarity 45.6%; Pred. No. 6;  
RESULT 844  
ID ABL34293 standard; DNA; 10020 BP.  
DE Human immune system associated gene SEQ ID NO: 2266.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 47.8; DB 6; Length 10020;  
Best Local Similarity 47.6%; Pred. No. 6.2;  
RESULT 845  
ID ABO67149 standard; DNA; 40324 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 179.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.6%; Score 47.8; DB 6; Length 40324;  
Best Local Similarity 45.6%; Pred. No. 7.7;  
RESULT 846  
ID AAA01920 standard; cDNA; 875 BP.  
DE Human colon cancer cell line polynucleotide sequence SEQ ID NO:1911.  
PN WO9958675-A2.  
PD 18-NOV-1999.  
PA (CHIR ) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Query Match 3.5%; Score 47.6; DB 3; Length 875;  
Best Local Similarity 39.7%; Pred. No. 4.7;  
RESULT 847  
ID ABU56243 standard; DNA; 1830 BP.  
DE AmEPV metalloprotease (AMV256) encoding sequence.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL ) UNIV FLORIDA.  
Query Match 3.5%; Score 47.6; DB 6; Length 1830;  
Best Local Similarity 44.1%; Pred. No. 5.3;  
RESULT 848  
ID ADR07247 standard; cDNA; 2187 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 753.  
PN EPI447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 3.5%; Score 47.6; DB 13; Length 2187;  
Best Local Similarity 46.7%; Pred. No. 5.4;  
RESULT 849  
ID ABL55640 standard; DNA; 4152 BP.  
DE AmEPV ABC transporter-like protein (AMV130) coding sequence.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL ) UNIV FLORIDA.  
Query Match 3.5%; Score 47.6; DB 6; Length 4152;  
Best Local Similarity 46.6%; Pred. No. 6;  
RESULT 850  
ID AAS46429 standard; DNA; 6106 BP.  
DE Tumour suppressor gene derived chemically modified sequence #151.  
PN WO200168312-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.6; DB 4; Length 6106;  
Best Local Similarity 45.4%; Pred. No. 6.3;  
RESULT 851  
ID ABK40031 standard; DNA; 6106 BP.  
DE Human chemically pretreated gene sequence #57 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.6; DB 6; Length 6106;  
Best Local Similarity 45.4%; Pred. No. 6.3;  
RESULT 852  
ID ABL33472 standard; DNA; 6106 BP.  
DE Human immune system associated gene SEQ ID NO: 1445.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.6; DB 6; Length 6106;  
Best Local Similarity 45.4%; Pred. No. 6.3;  
RESULT 853  
ID ABL34358 standard; DNA; 12237 BP.  
DE Human immune system associated gene SEQ ID NO: 2331.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.6; DB 6; Length 12237;  
Best Local Similarity 44.1%; Pred. No. 7;  
RESULT 854  
ID ABL33531 standard; DNA; 13712 BP.  
DE Human immune system associated gene SEQ ID NO: 1504.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.6; DB 6; Length 13712;  
Best Local Similarity 47.0%; Pred. No. 7.1;  
RESULT 855  
ID ABL41803 standard; DNA; 15567 BP.  
DE Nucleotide sequence of mutacin I operon.  
PN US6342385-B1.  
PD 29-JAN-2002.  
PA (UABR-) UAB RES FOUND.  
Query Match 3.5%; Score 47.6; DB 6; Length 15567;  
Best Local Similarity 49.2%; Pred. No. 7.3;  
RESULT 856  
ID ABS58318 standard; DNA; 15567 BP.  
DE DNA sequence encoding Streptococcus mutans mutacin (MutA) operon.  
PN US2002123105-A1.  
PD 05-SEP-2002.  
PA (QIFE/) QI F.  
PA (CAUF/) CAUFIELD P W.  
PA (CHEN/) CHEN P.  
Query Match 3.5%; Score 47.6; DB 8; Length 15567;  
Best Local Similarity 49.2%; Pred. No. 7.3;  
RESULT 857  
ID ABL33999 standard; DNA; 21537 BP.  
DE Human immune system associated gene SEQ ID NO: 1972.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.6; DB 6; Length 21537;  
Best Local Similarity 42.6%; Pred. No. 7.6;  
RESULT 858  
ID ABL56203 standard; DNA; 32392 BP.  
DE AMEPV genome fragment#5.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UVFL) UNIV FLORIDA.  
Query Match 3.5%; Score 47.6; DB 6; Length 32392;  
Best Local Similarity 44.1%; Pred. No. 8.1;  
RESULT 859  
ID AAI61371 standard; DNA; 335913 BP.  
DE Soybean 240017 region G3, SEQ ID NO: 2.  
PN WO200151627-A2.  
PD 19-JUL-2001.  
PA (MONS) MONSANTO CO.  
Query Match 3.5%; Score 47.6; DB 5; Length 335913;  
Best Local Similarity 46.8%; Pred. No. 12;  
RESULT 860  
ID AAI61372 standard; DNA; 335913 BP.  
DE Soybean 240017 region G3, SEQ ID NO: 3.  
PN WO200151627-A2.  
PD 19-JUL-2001.  
PA (MONS) MONSANTO CO.  
Query Match 3.5%; Score 47.6; DB 5; Length 335913;  
Best Local Similarity 46.8%; Pred. No. 12;  
RESULT 861  
ID AAH93353 standard; DNA; 402 BP.  
DE Human chromosome 16 BAC clone CIT987SK-A-248F7 SEQ ID NO 74.  
PN WO200152616-A2.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 3.5%; Score 47.4; DB 4; Length 402;  
Best Local Similarity 45.9%; Pred. No. 4.6;  
RESULT 862  
ID ADN04895 standard; cDNA; 2559 BP.  
DE Antisporiatric cDNA sequence #662.  
PN WO2004028479-A2.

PD 08-APR-2004.  
PA (GETH) GENENTECH INC.  
Query Match 3.5%; Score 47.4; DB 12; Length 2559;  
Best Local Similarity 49.4%; Pred. No. 6.1;  
RESULT 863  
ID ABK31193 standard; DNA; 5768 BP.  
DE Signal transduction associated gene modified complementary DNA #18.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.4; DB 6; Length 5768;  
Best Local Similarity 47.1%; Pred. No. 6.9;  
RESULT 864  
ID ABL70518 standard; DNA; 5768 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#204.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.4; DB 6; Length 5768;  
Best Local Similarity 47.1%; Pred. No. 6.9;  
RESULT 865  
ID AAS45477 standard; DNA; 7657 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #91.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.4; DB 4; Length 7657;  
Best Local Similarity 48.7%; Pred. No. 7.2;  
RESULT 866  
ID ABL34022 standard; DNA; 7657 BP.  
DE Human immune system associated gene SEQ ID NO: 1995.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.4; DB 6; Length 7657;  
Best Local Similarity 48.7%; Pred. No. 7.2;  
RESULT 867  
ID ABL70458 standard; DNA; 15161 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#174.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.4; DB 6; Length 15161;  
Best Local Similarity 48.0%; Pred. No. 8;  
RESULT 868  
ID AAS61423 standard; DNA; 15161 BP.  
DE Human gene regulation-associated gene oligonucleotide #378.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.4; DB 6; Length 15161;  
Best Local Similarity 48.0%; Pred. No. 8;  
RESULT 869  
ID ABL32467 standard; DNA; 15373 BP.  
DE Human immune system associated gene SEQ ID NO: 440.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.4; DB 6; Length 15373;  
Best Local Similarity 46.5%; Pred. No. 8;  
RESULT 870  
ID ABD32715 standard; DNA; 337344 BP.  
DE Human cancer-associated genomic DNA HD14-044.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 3.5%; Score 47.4; DB 13; Length 337344;  
Best Local Similarity 45.4%; Pred. No. 13;  
RESULT 871  
ID ADM82157 standard; cDNA; 1219 BP.  
DE Goldfish testis development factor Tdf2-encoding cDNA.  
PN CN1401657-A.  
PD 12-MAR-2003.

PA (HYDR-) INST HYDROBIOLOGY CHINESE ACAD SCI.  
Query Match 3.5%; Score 47.2; DB 11; Length 1219;  
Best Local Similarity 50.9%; Pred. No. 6;  
RESULT 872  
ID ABL32821 standard; DNA; 6123 BP.  
DE Human immune system associated gene SEQ ID NO: 794.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 6; Length 6123;  
Best Local Similarity 45.8%; Pred. No. 7.6;  
RESULT 873  
ID ABL32315 standard; DNA; 6641 BP.  
DE Human immune system associated gene SEQ ID NO: 288.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 6; Length 6641;  
Best Local Similarity 43.7%; Pred. No. 7.7;  
RESULT 874  
ID ABL54336 standard; DNA; 6641 BP.  
DE Chemically treated apoptosis gene complementary to gene #18.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 6; Length 6641;  
Best Local Similarity 43.7%; Pred. No. 7.7;  
RESULT 875  
ID ABK40010 standard; DNA; 7445 BP.  
DE Human chemically pretreated gene sequence #46 strand 2.  
PN WO200202866-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 6; Length 7445;  
Best Local Similarity 50.4%; Pred. No. 7.9;  
RESULT 876  
ID ABL32851 standard; DNA; 7445 BP.  
DE Human immune system associated gene SEQ ID NO: 824.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 6; Length 7445;  
Best Local Similarity 50.4%; Pred. No. 7.9;  
RESULT 877  
ID ADB54312 standard; DNA; 7833 BP.  
DE Pretreated genomic DNA region 236.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 10; Length 7833;  
Best Local Similarity 45.7%; Pred. No. 7.9;  
RESULT 878  
ID ADE37779 standard; DNA; 7833 BP.  
DE Human chemically treated EYA4 nucleotide sequence SEQ ID NO:25.  
PN WO2003072820-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 10; Length 7833;  
Best Local Similarity 45.7%; Pred. No. 7.9;  
RESULT 879  
ID ADS89608 standard; DNA; 7833 BP.  
DE Oligonucleotide of the invention SEQ ID NO:624.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 13; Length 7833;  
Best Local Similarity 45.7%; Pred. No. 7.9;  
RESULT 880  
ID ABL70227 standard; DNA; 8897 BP.  
DE Chemically treated cell signalling DNA sequence#59.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 3.5%; Score 47.2; DB 6; Length 8897;  
Best Local Similarity 47.3%; Pred. No. 8.1;  
RESULT 881  
ID ABL32669 standard; DNA; 11049 BP.  
DE Human immune system associated gene SEQ ID NO: 642.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 6; Length 11049;  
Best Local Similarity 44.7%; Pred. No. 8.3;  
RESULT 882  
ID ABL92219 standard; DNA; 11049 BP.  
DE Chemically treated DNA repair gene fragment complementary to#14.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 6; Length 11049;  
Best Local Similarity 44.7%; Pred. No. 8.3;  
RESULT 883  
ID ABL49322 standard; DNA; 11049 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO 22.  
PN WO200177377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 6; Length 11049;  
Best Local Similarity 44.7%; Pred. No. 8.3;  
RESULT 884  
ID ABL32624 standard; DNA; 16217 BP.  
DE Human immune system associated gene SEQ ID NO: 597.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 6; Length 16217;  
Best Local Similarity 45.5%; Pred. No. 8.8;  
RESULT 885  
ID ABL34006 standard; DNA; 18434 BP.  
DE Human immune system associated gene SEQ ID NO: 1979.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47.2; DB 6; Length 18434;  
Best Local Similarity 45.2%; Pred. No. 9;  
RESULT 886  
ID ABL32875 standard; DNA; 5273 BP.  
DE Human immune system associated gene SEQ ID NO: 848.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47; DB 6; Length 5273;  
Best Local Similarity 45.0%; Pred. No. 8.2;  
RESULT 887  
ID ABN80294 standard; DNA; 6661 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 311.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47; DB 6; Length 6661;  
Best Local Similarity 48.1%; Pred. No. 8.5;  
RESULT 888  
ID ABL92243 standard; DNA; 11787 BP.  
DE Chemically treated DNA repair gene fragment complementary to#26.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47; DB 6; Length 11787;  
Best Local Similarity 46.9%; Pred. No. 9.2;  
RESULT 889  
ID ADB54202 standard; DNA; 11787 BP.  
DE Pretreated genomic DNA region 126.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47; DB 10; Length 11787;

Best Local Similarity 46.9%; Pred. No. 9.2;  
RESULT 890  
ID ABL33927 standard; DNA; 13427 BP.  
DE Human immune system associated gene SEQ ID NO: 1900.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 47; DB 6; Length 13427;  
Best Local Similarity 42.3%; Pred. No. 9.4;  
RESULT 891  
ID AAH70049 standard; cDNA; 300 BP.  
DE Human cervical cancer marker nucleic acid 1323.  
PN WO200142467-A2.  
PD 14-JUN-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.5%; Score 46.8; DB 4; Length 300;  
Best Local Similarity 53.8%; Pred. No. 5.8;  
RESULT 892  
ID AAL15924 standard; cDNA; 422 BP.  
DE Human breast cancer expressed polynucleotide 8381.  
PN WO200151628-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.5%; Score 46.8; DB 4; Length 422;  
Best Local Similarity 43.5%; Pred. No. 6.1;  
RESULT 893  
ID ACN85885 standard; DNA; 858 BP.  
DE Breast cancer related marker, seq id 7035.  
PN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 3.5%; Score 46.8; DB 11; Length 858;  
Best Local Similarity 43.5%; Pred. No. 6.8;  
RESULT 894  
ID ABK31517 standard; DNA; 1335 BP.  
DE Signal transduction associated gene modified complementary DNA #180.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 46.8; DB 6; Length 1335;  
Best Local Similarity 50.0%; Pred. No. 7.3;  
RESULT 895  
ID ABL70486 standard; DNA; 1335 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#188.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 46.8; DB 6; Length 1335;  
Best Local Similarity 50.0%; Pred. No. 7.3;  
RESULT 896  
ID ABQ54403 standard; cDNA; 2911 BP.  
DE Human ovarian antigen HAPOE30 cDNA, SEQ ID NO:283.  
PN WO200200677-A1.  
PD 03-JAN-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.5%; Score 46.8; DB 6; Length 2911;  
Best Local Similarity 63.2%; Pred. No. 8.2;  
RESULT 897  
ID AAV42653 standard; cDNA to mRNA; 4358 BP.  
DE Nucleotide sequence of p102, a protein present in SA-17S complex.  
PN WO9828419-A2.  
PD 02-JUL-1998.  
PA (STRD-) UNIV LELAND STANFORD JUNIOR.  
Query Match 3.5%; Score 46.8; DB 2; Length 4358;  
Best Local Similarity 67.3%; Pred. No. 8.7;  
RESULT 898  
ID ABL70494 standard; DNA; 5126 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#192.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 46.8; DB 6; Length 5126;  
Best Local Similarity 46.1%; Pred. No. 8.9;

RESULT 899  
ID ABL33614 standard; DNA; 6127 BP.  
DE Human immune system associated gene SEQ ID NO: 1587.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 46.8; DB 6; Length 6127;  
Best Local Similarity 48.5%; Pred. No. 9.2;  
RESULT 900  
ID ABL33303 standard; DNA; 6609 BP.  
DE Human immune system associated gene SEQ ID NO: 1276.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 46.8; DB 6; Length 6609;  
Best Local Similarity 45.7%; Pred. No. 9.3;  
RESULT 901  
ID AAZ29911 standard; DNA; 8310 BP.  
DE cDNA encoding a SC4 protein of soybean.  
PN WO953087-A2.  
PD 21-OCT-1999.  
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.  
Query Match 3.5%; Score 46.8; DB 2; Length 8310;  
Best Local Similarity 46.7%; Pred. No. 9.6;  
RESULT 902  
ID ABL32426 standard; DNA; 9810 BP.  
DE Human immune system associated gene SEQ ID NO: 399.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 46.8; DB 6; Length 9810;  
Best Local Similarity 47.9%; Pred. No. 9.9;  
RESULT 903  
ID ABK39964 standard; DNA; 15479 BP.  
DE Human chemically pretreated gene sequence #23 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 46.8; DB 6; Length 15479;  
Best Local Similarity 44.9%; Pred. No. 11;  
RESULT 904  
ID ABL33728 standard; DNA; 17721 BP.  
DE Human immune system associated gene SEQ ID NO: 1701.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.5%; Score 46.8; DB 6; Length 17721;  
Best Local Similarity 58.7%; Pred. No. 11;  
RESULT 905  
ID ABD32992 standard; DNA; 99764 BP.  
DE Human cancer-associated genomic DNA HD21-017.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 3.5%; Score 46.8; DB 13; Length 99764;  
Best Local Similarity 42.8%; Pred. No. 14;  
RESULT 906  
ID ADH10017 standard; DNA; 365186 BP.  
DE Human chromosome 2p21-22 fragment containing the DRIP gene.  
PN WO2003093310-A1.  
PD 13-NOV-2003.  
PA (UYER-) UNIV BREMEN.  
Query Match 3.5%; Score 46.8; DB 10; Length 110000;  
Best Local Similarity 47.4%; Pred. No. 14;  
RESULT 907  
ID ADD34713 standard; DNA; 300 BP.  
DE Mouse mitochondrial DNA sequence SEQ ID NO:2492.  
PN WO2003020220-A2.  
PD 13-MAR-2003.  
PA (UYEN-) UNIV EMORY.  
Query Match 3.5%; Score 46.6; DB 10; Length 300;  
Best Local Similarity 62.4%; Pred. No. 6.4;  
RESULT 908



ID ACN85231 standard; DNA; 960 BP.  
 DE Breast cancer related marker, seq id 6381.  
 PN US2003099974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 3.5%; Score 46.6; DB 11; Length 960;  
 Best Local Similarity 40.3%; Pred. No. 7.6;  
 RESULT 909  
 ID ABL92243 standard; DNA; 11787 BP.  
 DE Chemically treated DNA repair gene fragment complementary to#26.  
 PN WO200181622-A2.  
 PD 01-NOV-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.5%; Score 46.6; DB 6; Length 11787;  
 Best Local Similarity 44.2%; Pred. No. 11;  
 RESULT 910  
 ID ADB54202 standard; DNA; 11787 BP.  
 DE Pretreated genomic DNA region 126.  
 PN WO2003072821-A2.  
 PD 04-SEP-2003.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.5%; Score 46.6; DB 10; Length 11787;  
 Best Local Similarity 44.2%; Pred. No. 11;  
 RESULT 911  
 ID ABL32298 standard; DNA; 12507 BP.  
 DE Human immune system associated gene SEQ ID NO: 271.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.5%; Score 46.6; DB 6; Length 12507;  
 Best Local Similarity 46.3%; Pred. No. 11;  
 RESULT 912  
 ID ABL32729 standard; DNA; 14307 BP.  
 DE Human immune system associated gene SEQ ID NO: 702.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.5%; Score 46.6; DB 6; Length 14307;  
 Best Local Similarity 44.0%; Pred. No. 11;  
 RESULT 913  
 ID ABL92212 standard; DNA; 18060 BP.  
 DE Chemically treated DNA repair gene fragment#11.  
 PN WO2003181622-A2.  
 PD 01-NOV-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.5%; Score 46.6; DB 6; Length 18060;  
 Best Local Similarity 45.3%; Pred. No. 12;  
 RESULT 914  
 ID AAD22313 standard; DNA; 18060 BP.  
 DE Chemically treated human genomic DNA #3 associated with DNA adducts.  
 PN WO200177378-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.5%; Score 46.6; DB 6; Length 18060;  
 Best Local Similarity 45.3%; Pred. No. 12;  
 RESULT 915  
 ID AAL15210 standard; cDNA; 883 BP.  
 DE Human breast cancer expressed polynucleotide 7667.  
 PN WO200151628-A2.  
 PD 19-JUL-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 3.4%; Score 46.4; DB 4; Length 883;  
 Best Local Similarity 40.5%; Pred. No. 8.3;  
 RESULT 916  
 ID ADS89680 standard; DNA; 4394 BP.  
 DE Oligonucleotide of the invention SEQ ID NO:696.  
 PN WO2004035803-A2.  
 PD 29-APR-2004.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.4%; Score 46.4; DB 13; Length 4394;  
 Best Local Similarity 46.8%; Pred. No. 11;  
 RESULT 917  
 ID ABK28306 standard; DNA; 5518 BP.

DE DNA transcription associated complementary genomic DNA #90.  
 PN WO200192565-A2.  
 PD 06-DEC-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.4%; Score 46.4; DB 6; Length 5518;  
 Best Local Similarity 45.1%; Pred. No. 11;  
 RESULT 918  
 ID ABL70157 standard; DNA; 5551 BP.  
 DE Chemically treated cell signalling DNA sequence#24.  
 PN WO200202807-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.4%; Score 46.4; DB 6; Length 5551;  
 Best Local Similarity 45.2%; Pred. No. 11;  
 RESULT 919  
 ID AAS61099 standard; DNA; 5551 BP.  
 DE Human gene regulation-associated gene oligonucleotide #54.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.4%; Score 46.4; DB 6; Length 5551;  
 Best Local Similarity 45.2%; Pred. No. 11;  
 RESULT 920  
 ID ABL33567 standard; DNA; 5647 BP.  
 DE Human immune system associated gene SEQ ID NO: 1540.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.4%; Score 46.4; DB 6; Length 5647;  
 Best Local Similarity 43.8%; Pred. No. 11;  
 RESULT 921  
 ID ABL70356 standard; DNA; 5647 BP.  
 DE Chemically treated cell signalling DNA sequence complementary to#123.  
 PN WO200202807-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.4%; Score 46.4; DB 6; Length 5647;  
 Best Local Similarity 43.8%; Pred. No. 11;  
 RESULT 922  
 ID AAS61321 standard; DNA; 5647 BP.  
 DE Human gene regulation-associated gene oligonucleotide #276.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.4%; Score 46.4; DB 6; Length 5647;  
 Best Local Similarity 43.8%; Pred. No. 11;  
 RESULT 923  
 ID ABL33106 standard; DNA; 5696 BP.  
 DE Human immune system associated gene SEQ ID NO: 1079.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.4%; Score 46.4; DB 6; Length 5696;  
 Best Local Similarity 49.6%; Pred. No. 11;  
 RESULT 924  
 ID ABK31288 standard; DNA; 5696 BP.  
 DE Signal transduction associated gene modified DNA #66.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.4%; Score 46.4; DB 6; Length 5696;  
 Best Local Similarity 49.6%; Pred. No. 11;  
 RESULT 925  
 ID AAN50530 standard; DNA; 5760 BP.  
 DE Sequence encoding the P195 protein of Plasmodium falciparum.  
 PN EPI54454-A.  
 PD 11-SEP-1985.  
 PA (WELL) WELLCOME FOUND LTD.  
 Query Match 3.4%; Score 46.4; DB 1; Length 5760;  
 Best Local Similarity 45.0%; Pred. No. 11;  
 RESULT 926  
 ID AAD46980 standard; DNA; 5917 BP.  
 DE Plasmodium falciparum merozoite surface protein-1 (MSP-1) DNA.

PN WO200270542-A2.  
PD 12-SEP-2002.  
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.  
Query Match 3.4%; Score 46.4; DB 6; Length 5917;  
Best Local Similarity 45.0%; Pred. No. 11;  
RESULT 927  
ID ABL32088 standard; DNA; 6283 BP.  
DE Human immune system associated gene SEQ ID NO: 61.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 6283;  
Best Local Similarity 44.6%; Pred. No. 11;  
RESULT 928  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 929  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 930  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 931  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 932  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 933  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 934  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 935  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 936  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 937  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 938  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 939  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 940  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 941  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 942  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 943  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;  
RESULT 944  
ID ABL3549 standard; DNA; 7503 BP.  
DE Human immune system associated gene SEQ ID NO: 1522.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.4; DB 6; Length 7503;  
Best Local Similarity 45.7%; Pred. No. 11;

RESULT 935  
ID ABL55643 standard; DNA; 50000 BP.  
DE AMEPV genome fragment#1.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UYFL ) UNIV FLORIDA.  
Query Match 3.4%; Score 46.4; DB 6; Length 50000;  
Best Local Similarity 44.0%; Pred. No. 15;  
RESULT 936  
ID ADL44075 standard; DNA; 469 BP.  
DE Human ovarian cancer DNA marker #17965.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.4%; Score 46.2; DB 5; Length 469;  
Best Local Similarity 54.1%; Pred. No. 8.2;  
RESULT 937  
ID AAS45384 standard; DNA; 5689 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #45.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.2; DB 4; Length 5689;  
Best Local Similarity 44.3%; Pred. No. 12;  
RESULT 938  
ID AAS46426 standard; DNA; 5689 BP.  
DE Tumour suppressor gene derived chemically modified sequence #148.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.2; DB 4; Length 5689;  
Best Local Similarity 44.3%; Pred. No. 12;  
RESULT 939  
ID ABK28226 standard; DNA; 5689 BP.  
DE DNA transcription associated complementary genomic DNA #50.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.2; DB 6; Length 5689;  
Best Local Similarity 44.3%; Pred. No. 12;  
RESULT 940  
ID ABL70598 standard; DNA; 5706 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#244.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.2; DB 6; Length 5706;  
Best Local Similarity 48.3%; Pred. No. 12;  
RESULT 941  
ID AAS61319 standard; DNA; 5706 BP.  
DE Human gene regulation-associated gene oligonucleotide #274.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.2; DB 6; Length 5706;  
Best Local Similarity 48.3%; Pred. No. 12;  
RESULT 942  
ID AAS61176 standard; DNA; 6223 BP.  
DE Human gene regulation-associated gene oligonucleotide #131.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.2; DB 6; Length 6223;  
Best Local Similarity 44.9%; Pred. No. 12;  
RESULT 943  
ID ABL32281 standard; DNA; 13511 BP.  
DE Human immune system associated gene SEQ ID NO: 254.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.2; DB 6; Length 13511;  
Best Local Similarity 45.8%; Pred. No. 14;  
RESULT 944

ID ABQ66975 standard; DNA; 13627 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 5.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46.2; DB 6; Length 13627;  
Best Local Similarity 44.5%; Pred. No. 14;  
RESULT 945  
ID AAK73166 standard; DNA; 19965 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:27978.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 46.2; DB 4; Length 19965;  
Best Local Similarity 48.8%; Pred. No. 15;  
RESULT 946  
ID ABK69932 standard; DNA; 19965 BP.  
DE Human secreted protein gene 68 genomic DNA fragment #20.  
PN WO200226931-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 46.2; DB 6; Length 19965;  
Best Local Similarity 48.8%; Pred. No. 15;  
RESULT 947  
ID ABK35839 standard; cDNA; 298 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #1004.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 3.4%; Score 46; DB 8; Length 298;  
Best Local Similarity 53.6%; Pred. No. 8.5;  
RESULT 948  
ID ABN80073 standard; DNA; 5771 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 90.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 6; Length 5771;  
Best Local Similarity 46.6%; Pred. No. 13;  
RESULT 949  
ID ABLJ3155 standard; DNA; 5807 BP.  
DE Human immune system associated gene SEQ ID NO: 1128.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 6; Length 5807;  
Best Local Similarity 44.9%; Pred. No. 13;  
RESULT 950  
ID ABLJ3216 standard; DNA; 6191 BP.  
DE Human immune system associated gene SEQ ID NO: 1189.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 6; Length 6191;  
Best Local Similarity 43.6%; Pred. No. 13;  
RESULT 951  
ID ABK31306 standard; DNA; 6191 BP.  
DE Signal transduction associated gene modified DNA #75.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 6; Length 6191;  
Best Local Similarity 43.6%; Pred. No. 13;  
RESULT 952  
ID ABL70281 standard; DNA; 6191 BP.  
DE Chemically treated cell signalling DNA sequence#86.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 6; Length 6191;

Best Local Similarity 43.6%; Pred. No. 13;  
RESULT 953  
ID ABN80160 standard; DNA; 6191 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 177.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 6; Length 6191;  
Best Local Similarity 43.6%; Pred. No. 13;  
RESULT 954  
ID ABL33380 standard; DNA; 6881 BP.  
DE Human immune system associated gene SEQ ID NO: 1353.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 6; Length 6881;  
Best Local Similarity 44.0%; Pred. No. 14;  
RESULT 955  
ID ABK28249 standard; DNA; 6881 BP.  
DE DNA transcription associated genomic DNA #62.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 6; Length 6881;  
Best Local Similarity 44.0%; Pred. No. 14;  
RESULT 956  
ID AAS46530 standard; DNA; 7814 BP.  
DE Tumour suppressor gene derived chemically modified sequence #252.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 4; Length 7814;  
Best Local Similarity 43.3%; Pred. No. 14;  
RESULT 957  
ID ABK28257 standard; DNA; 8170 BP.  
DE DNA transcription associated genomic DNA #66.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 6; Length 8170;  
Best Local Similarity 44.9%; Pred. No. 14;  
RESULT 958  
ID AAK86270 standard; DNA; 9706 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41082.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 46; DB 4; Length 9706;  
Best Local Similarity 51.7%; Pred. No. 14;  
RESULT 959  
ID ABLJ2793 standard; DNA; 19087 BP.  
DE Human immune system associated gene SEQ ID NO: 766.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 46; DB 6; Length 19087;  
Best Local Similarity 47.4%; Pred. No. 16;  
RESULT 960  
ID ABD32684 standard; DNA; 41991 BP.  
DE Human cancer-associated genomic DNA HD13-117.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 3.4%; Score 46; DB 13; Length 41991;  
Best Local Similarity 51.7%; Pred. No. 18;  
RESULT 961  
ID ABL93743 standard; cDNA; 457 BP.  
DE Arabidopsis thaliana nucleic acid sequence Ref:2027508 SEQ ID NO:508.  
PN US2002023280-A1.  
PD 21-FEB-2002.  
PA (GORL/) GORLACH J.  
PA (ANYI/) AN Y.  
PA (HAMI/) HAMILTON C M.

PA (PRIC/) PRICE J L.  
PA (RAIN/) RAINES T M.  
PA (YUY/) YU Y.  
PA (NAME/) NAMEKA J G.  
PA (PAGE/) PAGE A.  
PA (MATH/) MATHAW A V.  
PA (LEDF/) LEDFORD B L.  
PA (WOES/) WOESSNER J P.  
PA (HAAS/) HAAS W D.  
PA (GARC/) GARCIA C A.  
PA (KRIC/) KRICKER M.  
PA (SLAT/) SLATER T.  
PA (DAVI/) DAVIS K R.  
PA (ALLE/) ALLEN K.  
PA (HOPE/) HOFFMAN N.  
PA (HURB/) HURBAN P.  
Query Match 3.4%; Score 45.8; DB 6; Length 457;  
Best Local Similarity 61.2%; Pred. No. 9.9;  
RESULT 962  
ID ADL45106 standard; DNA; 531 BP.  
DE Human ovarian cancer DNA marker #18996.  
PN WO200170979-A2.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.4%; Score 45.8; DB 5; Length 531;  
Best Local Similarity 59.7%; Pred. No. 10;  
RESULT 963  
ID AAH93026 standard; DNA; 700 BP.  
DE Human inflammatory bowel disease related gene fragment IGR3319a.  
PN WO200142511-A2.  
PA (WHEH) WHITEHEAD INST BIOMEDICAL RES.  
PA (ELLI-) ELLIPSIS BIOTHERAPEUTICS CORP.  
Query Match 3.4%; Score 45.8; DB 4; Length 700;  
Best Local Similarity 45.2%; Pred. No. 11;  
RESULT 964  
ID AAA26377 standard; cDNA; 1559 BP.  
DE Human secreted protein gene 32 SEQ ID NO:42.  
PN WO200006698-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.8; DB 3; Length 1559;  
Best Local Similarity 57.2%; Pred. No. 12;  
RESULT 965  
ID ADL71438 standard; cDNA; 1559 BP.  
DE Novel human secreted protein cDNA seqid 42.  
PN US2004034196-A1.  
PA (KOMA/) KOMATSOU LIS G A.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (DUAN/) DUAN D R.  
PA (MOOR/) MOORE P A.  
PA (SHIY/) SHI Y.  
PA (LAFI/) LAFLEUR D W.  
PA (WEIY/) WEI Y.  
Query Match 3.4%; Score 45.8; DB 12; Length 1559;  
Best Local Similarity 57.2%; Pred. No. 12;  
RESULT 966  
ID AAS01496 standard; DNA; 2056 BP.  
DE Human secreted protein gene #37.  
PN WO200123402-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.8; DB 4; Length 2056;  
Best Local Similarity 57.2%; Pred. No. 12;  
RESULT 967  
ID AAH34935 standard; cDNA; 2056 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2017.  
PN WO200122920-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.8; DB 4; Length 2056;

Best Local Similarity 57.2%; Pred. No. 12;  
RESULT 968  
ID RAD08390 standard; cDNA; 2166 BP.  
DE Human secreted protein-encoding gene 46 cDNA clone HCQCC96, SEQ ID NO:56.  
PN WO200077022-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.8; DB 4; Length 2166;  
Best Local Similarity 57.2%; Pred. No. 13;  
RESULT 969  
ID ABZ73348 standard; cDNA; 2166 BP.  
DE Secreted protein-encoding gene 68 cDNA clone HCQCC96, SEQ ID NO:78.  
PN WO200277013-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.8; DB 8; Length 2166;  
Best Local Similarity 57.2%; Pred. No. 13;  
RESULT 970  
ID ADA97953 standard; cDNA; 2166 BP.  
DE Human secreted protein cDNA sequence #47.  
PN WO2003004623-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.8; DB 8; Length 2166;  
Best Local Similarity 57.2%; Pred. No. 13;  
RESULT 971  
ID ADA43859 standard; cDNA; 2166 BP.  
DE Human secreted protein cDNA SEQ ID 47.  
PN WO2003000865-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.8; DB 8; Length 2166;  
Best Local Similarity 57.2%; Pred. No. 13;  
RESULT 972  
ID ADC20109 standard; DNA; 2166 BP.  
DE Human secreted protein coding sequence #48.  
PN WO200292787-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.8; DB 10; Length 2166;  
Best Local Similarity 57.2%; Pred. No. 13;  
RESULT 973  
ID ADF10572 standard; DNA; 2166 BP.  
DE Human secreted protein encoding sequence #25.  
PN WO200299085-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.8; DB 10; Length 2166;  
Best Local Similarity 57.2%; Pred. No. 13;  
RESULT 974  
ID AAC89670 standard; DNA; 2500 BP.  
DE P. gallinaceum chitinase coding sequence SEQ ID NO: 5.  
PN WO200073488-A1.  
PA (TEXA) UNIV TEXAS SYSTEM.  
Query Match 3.4%; Score 45.8; DB 4; Length 2500;  
Best Local Similarity 42.7%; Pred. No. 13;  
RESULT 975  
ID ABL17264 standard; DNA; 3296 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3265.  
PN WO200171042-A2.  
PA (PEKE) PE CORP NY.  
Query Match 3.4%; Score 45.8; DB 4; Length 3296;  
Best Local Similarity 45.8%; Pred. No. 13;  
RESULT 976  
ID ABL33768 standard; DNA; 5795 BP.  
DE Human immune system associated gene SEQ ID NO: 1741.  
PN WO200200928-A2.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 6; Length 5795;  
Best Local Similarity 51.1%; Pred. No. 15;

RESULT 977  
ID ABL33326 standard; DNA; 15592 BP.  
DE Human immune system associated gene SEQ ID NO: 1299.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 6; Length 5795;  
Best Local Similarity 51.1%; Pred. No. 15;  
RESULT 978  
ID ABL32267 standard; DNA; 6419 BP.  
DE Human immune system associated gene SEQ ID NO: 240.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 6; Length 6419;  
Best Local Similarity 46.6%; Pred. No. 15;  
RESULT 979  
ID ABL32463 standard; DNA; 9155 BP.  
DE Human immune system associated gene SEQ ID NO: 436.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 6; Length 9155;  
Best Local Similarity 47.9%; Pred. No. 16;  
RESULT 980  
ID ABL33421 standard; DNA; 9707 BP.  
DE Human immune system associated gene SEQ ID NO: 1394.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 6; Length 9707;  
Best Local Similarity 44.8%; Pred. No. 16;  
RESULT 981  
ID ABK31173 standard; DNA; 11178 BP.  
DE Signal transduction associated gene modified complementary DNA #8.  
FN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 6; Length 11178;  
Best Local Similarity 46.9%; Pred. No. 16;  
RESULT 982  
ID ABL70508 standard; DNA; 11178 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#199.  
FN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 6; Length 11178;  
Best Local Similarity 46.9%; Pred. No. 16;  
RESULT 983  
ID AAS61060 standard; DNA; 11178 BP.  
DE Human gene regulation-associated gene oligonucleotide #15.  
FN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 6; Length 11178;  
Best Local Similarity 46.9%; Pred. No. 16;  
RESULT 984  
ID ABK31320 standard; DNA; 11907 BP.  
DE Signal transduction associated gene modified DNA #82.  
FN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 6; Length 11907;  
Best Local Similarity 45.7%; Pred. No. 16;  
RESULT 985  
ID AAS46453 standard; DNA; 15592 BP.  
DE Tumour suppressor gene derived chemically modified sequence #175.  
FN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 4; Length 15592;  
Best Local Similarity 43.6%; Pred. No. 17;  
RESULT 986

ID ABL33326 standard; DNA; 15592 BP.  
DE Human immune system associated gene SEQ ID NO: 1299.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.8; DB 6; Length 15592;  
Best Local Similarity 43.6%; Pred. No. 17;  
RESULT 987  
ID ADL02342 standard; DNA; 255 BP.  
DE DNA encoding a M. catarrhalis protein #28.  
FN U6673910-B1.  
PD 06-JAN-2004.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Query Match 3.4%; Score 45.6; DB 12; Length 255;  
Best Local Similarity 47.1%; Pred. No. 9.9;  
RESULT 988  
ID AAL15484 standard; cDNA; 711 BP.  
DE Human breast cancer expressed polynucleotide 7941.  
FN WO200151828-A2.  
PD 19-JUL-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.4%; Score 45.6; DB 4; Length 711;  
Best Local Similarity 51.2%; Pred. No. 12;  
RESULT 989  
ID ACN85475 standard; DNA; 950 BP.  
DE Breast cancer related marker, seq id 6625.  
FN US200309974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 3.4%; Score 45.6; DB 11; Length 950;  
Best Local Similarity 51.2%; Pred. No. 12;  
RESULT 990  
ID ADS0927 standard; cDNA; 1730 BP.  
DE Bacterial polynucleotide #5670.  
FN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 3.4%; Score 45.6; DB 13; Length 1730;  
Best Local Similarity 43.6%; Pred. No. 13;  
RESULT 991  
ID AAS46781 standard; DNA; 4654 BP.  
DE Tumour suppressor gene derived chemically modified sequence #506.  
FN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 4; Length 4654;  
Best Local Similarity 44.9%; Pred. No. 15;  
RESULT 992  
ID ABL34223 standard; DNA; 4654 BP.  
DE Human immune system associated gene SEQ ID NO: 2196.  
FN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 4654;  
Best Local Similarity 44.9%; Pred. No. 15;  
RESULT 993  
ID ABQ75107 standard; cDNA; 4985 BP.  
DE Anopheles gambiae odourant receptor 2 genomic DNA SEQ ID NO:10.  
FN WO200259274-A2.  
PD 01-AUG-2002.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 3.4%; Score 45.6; DB 6; Length 4985;  
Best Local Similarity 43.3%; Pred. No. 16;  
RESULT 994  
ID ACF79720 standard; DNA; 4985 BP.  
DE Mosquito odorant receptor 2 genomic DNA.  
FN WO2003076590-A2.  
PD 18-SEP-2003.  
PA (UYVA-) UNIV VANDERBILT.

Query Match 3.4%; Score 45.6; DB 10; Length 4985;  
Best Local Similarity 43.3%; Pred. No. 16;  
RESULT 995  
ID ABK31344 standard; DNA; 5388 BP.  
DE Signal transduction associated gene modified DNA #94.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 5388;  
Best Local Similarity 43.1%; Pred. No. 16;  
RESULT 996  
ID ABL70305 standard; DNA; 5388 BP.  
DE Chemically treated cell signalling DNA sequence#98.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 5388;  
Best Local Similarity 43.1%; Pred. No. 16;  
RESULT 997  
ID RAS61239 standard; DNA; 5388 BP.  
DE Human gene regulation-associated gene oligonucleotide #194.  
PN WO20017375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 5388;  
Best Local Similarity 43.1%; Pred. No. 16;  
RESULT 998  
ID ABL32712 standard; DNA; 5427 BP.  
DE Human immune system associated gene SEQ ID NO: 685.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 5427;  
Best Local Similarity 49.6%; Pred. No. 16;  
RESULT 999  
ID ABL32676 standard; DNA; 6015 BP.  
DE Human immune system associated gene SEQ ID NO: 649.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 6015;  
Best Local Similarity 45.7%; Pred. No. 16;  
RESULT 1000  
ID RAS46439 standard; DNA; 7040 BP.  
DE Tumour suppressor gene derived chemically modified sequence #161.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 4; Length 7040;  
Best Local Similarity 44.2%; Pred. No. 16;  
RESULT 1001  
ID ABK33963 standard; DNA; 7040 BP.  
DE Human DNA for staging of Astrocytomas #24.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 7040;  
Best Local Similarity 44.2%; Pred. No. 16;  
RESULT 1002  
ID ABZ10179 standard; DNA; 7040 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #319.  
PN WO20027272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 8; Length 7040;  
Best Local Similarity 44.2%; Pred. No. 16;  
RESULT 1003  
ID ABZ10033 standard; DNA; 7040 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #173.  
PN WO20027272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 8; Length 7040;  
Best Local Similarity 44.2%; Pred. No. 17;  
RESULT 1004  
ID ADA20348 standard; DNA; 7040 BP.  
DE Prostate tumour related genomic DNA sample #7.  
PN WO2002103042-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 8; Length 7040;  
Best Local Similarity 44.2%; Pred. No. 16;  
RESULT 1005  
ID ADA84155 standard; DNA; 7040 BP.  
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:13.  
PN WO2002103041-A2.  
PD 27-DEC-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 8; Length 7040;  
Best Local Similarity 44.2%; Pred. No. 16;  
RESULT 1006  
ID ADE84191 standard; DNA; 7040 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #127.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 10; Length 7040;  
Best Local Similarity 44.2%; Pred. No. 16;  
RESULT 1007  
ID ADE84115 standard; DNA; 7040 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #51.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 10; Length 7040;  
Best Local Similarity 44.2%; Pred. No. 16;  
RESULT 1008  
ID ADB54184 standard; DNA; 7833 BP.  
DE Pretreated genomic DNA region 108.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 10; Length 7833;  
Best Local Similarity 45.5%; Pred. No. 17;  
RESULT 1009  
ID ADE37769 standard; DNA; 7833 BP.  
DE Human chemically treated EXA4 nucleotide sequence SEQ ID NO:15.  
PN WO2003072820-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 10; Length 7833;  
Best Local Similarity 45.5%; Pred. No. 17;  
RESULT 1010  
ID ADS89334 standard; DNA; 7833 BP.  
DE Oligonucleotide of the invention SEQ ID NO:350.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 13; Length 7833;  
Best Local Similarity 45.5%; Pred. No. 17;  
RESULT 1011  
ID ABL32158 standard; DNA; 7990 BP.  
DE Human immune system associated gene SEQ ID NO: 131.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 7990;  
Best Local Similarity 44.2%; Pred. No. 17;  
RESULT 1012  
ID ABL54307 standard; DNA; 7990 BP.  
DE Chemically treated apoptosis gene #4.  
PN WO20017164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 7990;  
Best Local Similarity 44.2%; Pred. No. 17;

RESULT 1013  
ID ABL33568 standard; DNA; 8305 BP.  
DE Human immune system associated gene SEQ ID NO: 1541.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 8305;  
Best Local Similarity 47.7%; Pred. No. 17;  
RESULT 1014  
ID AAS45314 standard; DNA; 11260 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #10.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 4; Length 11260;  
Best Local Similarity 68.5%; Pred. No. 18;  
RESULT 1015  
ID ABK28153 standard; DNA; 11260 BP.  
DE DNA transcription associated genomic DNA #14.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 11260;  
Best Local Similarity 68.5%; Pred. No. 18;  
RESULT 1016  
ID ABR80038 standard; DNA; 11260 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 55.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 11260;  
Best Local Similarity 68.5%; Pred. No. 18;  
RESULT 1017  
ID ABL33262 standard; DNA; 12393 BP.  
DE Human immune system associated gene SEQ ID NO: 1235.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 12393;  
Best Local Similarity 44.1%; Pred. No. 18;  
RESULT 1018  
ID ABL33453 standard; DNA; 14032 BP.  
DE Human immune system associated gene SEQ ID NO: 1426.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 14032;  
Best Local Similarity 45.3%; Pred. No. 18;  
RESULT 1019  
ID AAS46506 standard; DNA; 14919 BP.  
DE Tumour suppressor gene derived chemically modified sequence #228.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 4; Length 14919;  
Best Local Similarity 45.0%; Pred. No. 18;  
RESULT 1020  
ID AAS45348 standard; DNA; 17421 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #27.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 4; Length 17421;  
Best Local Similarity 46.8%; Pred. No. 19;  
RESULT 1021  
ID ABK28181 standard; DNA; 17421 BP.  
DE DNA transcription associated genomic DNA #28.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 17421;  
Best Local Similarity 46.8%; Pred. No. 19;  
RESULT 1022

ID ABK31212 standard; DNA; 19459 BP.  
DE Signal transduction associated gene modified DNA #28.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 19459;  
Best Local Similarity 45.2%; Pred. No. 19;  
RESULT 1023  
ID ABL70527 standard; DNA; 19459 BP.  
DE Chemically treated cell signalling DNA sequence#209.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 19459;  
Best Local Similarity 45.2%; Pred. No. 19;  
RESULT 1024  
ID ABL70527 standard; DNA; 19459 BP.  
DE Chemically treated cell signalling DNA sequence#209.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 19459;  
Best Local Similarity 45.2%; Pred. No. 19;  
RESULT 1025  
ID ABL70527 standard; DNA; 19459 BP.  
DE Chemically treated cell signalling DNA sequence#209.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.6; DB 6; Length 19459;  
Best Local Similarity 45.2%; Pred. No. 19;  
RESULT 1026  
ID ADL37508 standard; DNA; 294 BP.  
DE Human ovarian cancer DNA marker #11398.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.4%; Score 45.4; DB 5; Length 294;  
Best Local Similarity 47.6%; Pred. No. 11;  
RESULT 1027  
ID ADI72364 standard; DNA; 294 BP.  
DE Human ovarian cancer DNA marker #5106.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.4%; Score 45.4; DB 5; Length 294;  
Best Local Similarity 47.6%; Pred. No. 11;  
RESULT 1028  
ID ABV05431 standard; cDNA; 445 BP.  
DE Human prostate expression marker cDNA 5422.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.4%; Score 45.4; DB 5; Length 445;  
Best Local Similarity 47.5%; Pred. No. 12;  
RESULT 1029  
ID ADI72375 standard; DNA; 614 BP.  
DE Human ovarian cancer DNA marker #5117.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.4%; Score 45.4; DB 5; Length 614;  
Best Local Similarity 43.0%; Pred. No. 12;  
RESULT 1030  
ID ADL37519 standard; DNA; 614 BP.  
DE Human ovarian cancer DNA marker #11409.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.4%; Score 45.4; DB 5; Length 614;  
Best Local Similarity 43.0%; Pred. No. 12;  
RESULT 1031  
ID ADR01494 standard; DNA; 615 BP.  
DE A. Gossypii genomic DNA PAG1074RP.  
PN US6239264-B1.  
PD 29-MAY-2001.  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 3.4%; Score 45.4; DB 2; Length 615;

Best Local Similarity 44.2%; Pred. No. 12;  
RESULT 1032  
ID AAL01672 standard; cDNA; 622 BP.  
DE Human reproductive system related antigen cDNA SEQ ID NO: 1673.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.4; DB 4; Length 622;  
Best Local Similarity 70.1%; Pred. No. 12;  
RESULT 1033  
ID ABA07591 standard; cDNA; 622 BP.  
DE Human ovarian and breast cancer associated polynucleotide SEQ ID NO 148.  
PN WO200155325-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.4; DB 4; Length 622;  
Best Local Similarity 70.1%; Pred. No. 12;  
RESULT 1034  
ID AAX37474 standard; cDNA; 1014 BP.  
DE Human secreted protein cDNA fragment containing gene 24.  
PN WO9918208-A1.  
PD 15-APR-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.4; DB 2; Length 1014;  
Best Local Similarity 51.2%; Pred. No. 13;  
RESULT 1035  
ID AAS92198 standard; cDNA; 2482 BP.  
DE DNA encoding novel human diagnostic protein #28002.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 3.4%; Score 45.4; DB 5; Length 2482;  
Best Local Similarity 49.4%; Pred. No. 15;  
RESULT 1036  
ID ABL17264 standard; DNA; 3296 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 3265.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 3.4%; Score 45.4; DB 4; Length 3296;  
Best Local Similarity 45.8%; Pred. No. 16;  
RESULT 1037  
ID AAV52396 standard; DNA; 3744 BP.  
DE Streptococcus pneumoniae genome fragment SEQ ID NO:263.  
PN WO9818931-A2.  
PD 07-MAY-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.4%; Score 45.4; DB 2; Length 3744;  
Best Local Similarity 47.7%; Pred. No. 16;  
RESULT 1038  
ID AUS89612 standard; DNA; 4930 BP.  
DE Oligonucleotide of the invention SEQ ID NO:628.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 13; Length 4930;  
Best Local Similarity 47.2%; Pred. No. 17;  
RESULT 1039  
ID ABQ75107 standard; cDNA; 4985 BP.  
DE Anopheles gambiae odourant receptor 2 genomic DNA SEQ ID NO:10.  
PN WO200259274-A2.  
PD 01-AUG-2002.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 3.4%; Score 45.4; DB 6; Length 4985;  
Best Local Similarity 45.8%; Pred. No. 17;  
RESULT 1040  
ID ACF79720 standard; DNA; 4985 BP.  
DE Mosquito odorant receptor 2 genomic DNA.  
PN WO2003076590-A2.  
PD 18-SEP-2003.  
PA (UYVA-) UNIV VANDERBILT.  
Query Match 3.4%; Score 45.4; DB 10; Length 4985;  
Best Local Similarity 45.8%; Pred. No. 17;

RESULT 1041  
ID ABZ10145 standard; DNA; 5033 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #285.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 8; Length 5033;  
Best Local Similarity 47.3%; Pred. No. 17;  
RESULT 1042  
ID ABL33266 standard; DNA; 5218 BP.  
DE Human immune system associated gene SEQ ID NO: 1239.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 5218;  
Best Local Similarity 43.5%; Pred. No. 17;  
RESULT 1043  
ID ABL34150 standard; DNA; 5376 BP.  
DE Human immune system associated gene SEQ ID NO: 2123.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 5376;  
Best Local Similarity 50.2%; Pred. No. 17;  
RESULT 1044  
ID ABL32713 standard; DNA; 5427 BP.  
DE Human immune system associated gene SEQ ID NO: 686.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 5427;  
Best Local Similarity 45.5%; Pred. No. 17;  
RESULT 1045  
ID ABL33276 standard; DNA; 5675 BP.  
DE Human immune system associated gene SEQ ID NO: 1249.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 5675;  
Best Local Similarity 44.0%; Pred. No. 17;  
RESULT 1046  
ID AEN80142 standard; DNA; 5721 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 159.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 5721;  
Best Local Similarity 43.8%; Pred. No. 17;  
RESULT 1047  
ID ABL33159 standard; DNA; 5909 BP.  
DE Human immune system associated gene SEQ ID NO: 1132.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 5909;  
Best Local Similarity 55.3%; Pred. No. 18;  
RESULT 1048  
ID ADS89769 standard; DNA; 6001 BP.  
DE Oligonucleotide of the invention SEQ ID NO:785.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 13; Length 6001;  
Best Local Similarity 47.2%; Pred. No. 18;  
RESULT 1049  
ID ABL32913 standard; DNA; 6621 BP.  
DE Human immune system associated gene SEQ ID NO: 886.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 6621;  
Best Local Similarity 47.6%; Pred. No. 18;  
RESULT 1050



ID AAV70132 standard; DNA; 7620 BP.  
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:265.  
PN WO20025728-A2.  
PD 11-MAY-2000.  
PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Query Match 3.4%; Score 45.4; DB 3; Length 7620;  
Best Local Similarity 47.3%; Pred. No. 18;  
RESULT 1051  
ID AAS45391 standard; DNA; 7906 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #48.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 4; Length 7906;  
Best Local Similarity 48.2%; Pred. No. 18;  
RESULT 1052  
ID ABK28236 standard; DNA; 7906 BP.  
DE DNA transcription associated complementary genomic DNA #55.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 7906;  
Best Local Similarity 48.2%; Pred. No. 18;  
RESULT 1053  
ID ABN80179 standard; DNA; 7906 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 196.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 7906;  
Best Local Similarity 48.2%; Pred. No. 18;  
RESULT 1054  
ID ABQ67125 standard; DNA; 8227 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 155.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 8227;  
Best Local Similarity 46.4%; Pred. No. 18;  
RESULT 1055  
ID AAS46588 standard; DNA; 8524 BP.  
DE Tumour suppressor gene derived chemically modified sequence #310.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 4; Length 8524;  
Best Local Similarity 48.6%; Pred. No. 19;  
RESULT 1056  
ID ABL33841 standard; DNA; 8524 BP.  
DE Human immune system associated gene SEQ ID NO: 1814.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 8524;  
Best Local Similarity 48.6%; Pred. No. 19;  
RESULT 1057  
ID ABL33317 standard; DNA; 13574 BP.  
DE Human immune system associated gene SEQ ID NO: 1290.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 13574;  
Best Local Similarity 46.9%; Pred. No. 20;  
RESULT 1058  
ID ABL70466 standard; DNA; 15853 BP.  
DE Chemically treated cell signalling DNA sequence complementary to #178.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 15853;

Best Local Similarity 44.8%; Pred. No. 20;  
RESULT 1059  
ID AAS61457 standard; DNA; 15853 BP.  
DE Human gene regulation-associated gene oligonucleotide #412.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 15853;  
Best Local Similarity 44.8%; Pred. No. 20;  
RESULT 1060  
ID ABL33949 standard; DNA; 18218 BP.  
DE Human immune system associated gene SEQ ID NO: 1922.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 18218;  
Best Local Similarity 46.4%; Pred. No. 21;  
RESULT 1061  
ID ABL32610 standard; DNA; 18855 BP.  
DE Human immune system associated gene SEQ ID NO: 583.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.4; DB 6; Length 18855;  
Best Local Similarity 48.3%; Pred. No. 21;  
RESULT 1062  
Query Match 3.4%; Score 45.4; DB 10; Length 110000;  
Best Local Similarity 47.7%; Pred. No. 27;  
RESULT 1063  
Query Match 3.4%; Score 45.4; DB 10; Length 110000;  
Best Local Similarity 46.8%; Pred. No. 27;  
RESULT 1064  
ID ADL17884 standard; cDNA; 158001 BP.  
DE Human phosphotyrosyl phosphatase activator, PTPA, gene.  
PN US2004023906-A1.  
PD 05-FEB-2004.  
PA (ISIS-) ISIS PHARM INC.  
Query Match 3.4%; Score 45.4; DB 12; Length 158001;  
Best Local Similarity 45.1%; Pred. No. 29;  
RESULT 1065  
ID ADL38882 standard; DNA; 420 BP.  
DE Human ovarian cancer DNA marker #12772.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.4%; Score 45.2; DB 5; Length 420;  
Best Local Similarity 41.7%; Pred. No. 13;  
RESULT 1066  
ID ADI72427 standard; DNA; 421 BP.  
DE Human ovarian cancer DNA marker #5169.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.4%; Score 45.2; DB 5; Length 421;  
Best Local Similarity 41.7%; Pred. No. 13;  
RESULT 1067  
ID ABV97199 standard; cDNA; 505 BP.  
DE Human pancreatic cancer expressed cDNA SEQ ID NO 2607.  
PN WO200260317-A2.  
PD 08-AUG-2002.  
PA (CORI-) CORIXA CORP.  
Query Match 3.4%; Score 45.2; DB 6; Length 505;  
Best Local Similarity 57.5%; Pred. No. 13;  
RESULT 1068  
ID ABK33950 standard; DNA; 5001 BP.  
DE Human DNA for staging of Astrocytomas #17.  
PN WO200202808-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.4%; Score 45.2; DB 6; Length 5001;  
Best Local Similarity 46.3%; Pred. No. 19;  
RESULT 1069  
ID ABL54373 standard; DNA; 5001 BP.

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DE Chemically treated apoptosis gene #37.
PN WO20017164-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 5001;
  Best Local Similarity 46.3%; Pred. No. 19;
RESULT 1070
ID ADA20404 standard; DNA; 5001 BP.
DE Prostate tumour related genomic DNA sample #35.
PN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 8; Length 5001;
  Best Local Similarity 46.3%; Pred. No. 19;
RESULT 1071
ID ADA84211 standard; DNA; 5001 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:69.
PN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 8; Length 5001;
  Best Local Similarity 46.3%; Pred. No. 19;
RESULT 1072
ID ABL32560 standard; DNA; 5328 BP.
DE Human immune system associated gene SEQ ID NO: 533.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 5328;
  Best Local Similarity 46.1%; Pred. No. 19;
RESULT 1073
ID ABK39970 standard; DNA; 5519 BP.
DE Human chemically pretreated gene sequence #26 strand 1.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 5519;
  Best Local Similarity 42.3%; Pred. No. 19;
RESULT 1074
ID ABL32517 standard; DNA; 5930 BP.
DE Human immune system associated gene SEQ ID NO: 490.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 5930;
  Best Local Similarity 44.3%; Pred. No. 19;
RESULT 1075
ID ABL32788 standard; DNA; 6171 BP.
DE Human immune system associated gene SEQ ID NO: 761.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 6171;
  Best Local Similarity 53.2%; Pred. No. 19;
RESULT 1076
ID ABL34215 standard; DNA; 6200 BP.
DE Human immune system associated gene SEQ ID NO: 2188.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 6200;
  Best Local Similarity 44.8%; Pred. No. 19;
RESULT 1077
ID ABL32345 standard; DNA; 7346 BP.
DE Human immune system associated gene SEQ ID NO: 318.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 7346;
  Best Local Similarity 46.5%; Pred. No. 20;
RESULT 1078
ID ABK40056 standard; DNA; 7892 BP.
DE Human chemically pretreated gene sequence #69 strand 2.
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PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 7892;
  Best Local Similarity 49.4%; Pred. No. 20;
RESULT 1079
ID ABL34152 standard; DNA; 9255 BP.
DE Human immune system associated gene SEQ ID NO: 2125.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 9255;
  Best Local Similarity 45.9%; Pred. No. 21;
RESULT 1080
ID AAS63354 standard; DNA; 9265 BP.
DE Chemically pretreated metabolism associated gene #49.
PN WO200176451-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 9265;
  Best Local Similarity 45.9%; Pred. No. 21;
RESULT 1081
ID AAS61102 standard; DNA; 12592 BP.
DE Human gene regulation-associated gene oligonucleotide #57.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 12592;
  Best Local Similarity 50.0%; Pred. No. 22;
RESULT 1082
ID AAS61427 standard; DNA; 19380 BP.
DE Human gene regulation-associated gene oligonucleotide #382.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 19380;
  Best Local Similarity 43.9%; Pred. No. 23;
RESULT 1083
ID ABQ67150 standard; DNA; 40324 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 180.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
  Query Match 3.4%; Score 45.2; DB 6; Length 40324;
  Best Local Similarity 44.2%; Pred. No. 26;
RESULT 1084
  Query Match 3.4%; Score 45.2; DB 6; Length 110000;
  Best Local Similarity 45.9%; Pred. No. 30;
RESULT 1085
ID ABD32659 standard; DNA; 163382 BP.
DE Human cancer-associated genomic DNA HD13-065.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
  Query Match 3.4%; Score 45.2; DB 13; Length 163382;
  Best Local Similarity 45.7%; Pred. No. 32;
RESULT 1086
ID AAL13342 standard; cDNA; 297 BP.
DE Human breast cancer expressed polynucleotide 5799.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
  Query Match 3.3%; Score 45; DB 4; Length 297;
  Best Local Similarity 42.5%; Pred. No. 13;
RESULT 1087
ID AAI82669 standard; cDNA; 350 BP.
DE Human polynucleotide SEQ ID NO 2729.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
  Query Match 3.3%; Score 45; DB 4; Length 350;
  Best Local Similarity 60.0%; Pred. No. 14;
RESULT 1088
```

ID AAI87168 standard; cDNA; 361 BP.  
 DE Human polynucleotide SEQ ID NO 7228.  
 PN WO200164835-A2.  
 PD 07-SEP-2001.  
 PA (HYSE-) HYSEQ INC. 3.3%; Score 45; DB 4; Length 361;  
 Query Match Best Local Similarity 60.0%; Pred. No. 14;  
 RESULT 1089  
 ID ACN83440 standard; DNA; 411 BP.  
 DE Breast cancer related marker, seq id 4590.  
 PN US200309974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC. 3.3%; Score 45; DB 11; Length 411;  
 Query Match Best Local Similarity 42.5%; Pred. No. 14;  
 RESULT 1090  
 ID AB210188 standard; DNA; 1501 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #328.  
 PN WO200277272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG. 3.3%; Score 45; DB 8; Length 1501;  
 Query Match Best Local Similarity 46.5%; Pred. No. 17;  
 RESULT 1091  
 ID AD884162 standard; DNA; 1501 BP.  
 DE Human lymphoid cell proliferative disorder gene derived DNA #98.  
 PN WO2003044226-A2.  
 PD 30-MAY-2003.  
 PA (EPIG-) EPIGENOMICS AG. 3.3%; Score 45; DB 10; Length 1501;  
 Query Match Best Local Similarity 46.5%; Pred. No. 17;  
 RESULT 1092  
 ID ADQ22191 standard; DNA; 1758 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5011.  
 PN WO200404838-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC. 3.3%; Score 45; DB 12; Length 1758;  
 Query Match Best Local Similarity 57.4%; Pred. No. 18;  
 RESULT 1093  
 ID AB216379 standard; DNA; 2000 BP.  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 4184.  
 PN WO200216655-A2.  
 PD 28-FEB-2002.  
 PA (SCRI) SCRIPPS RES INST. 3.3%; Score 45; DB 6; Length 2000;  
 Query Match Best Local Similarity 46.4%; Pred. No. 18;  
 RESULT 1094  
 ID ABK31379 standard; DNA; 5338 BP.  
 DE Signal transduction associated gene modified complementary DNA #111.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG. 3.3%; Score 45; DB 6; Length 5338;  
 Query Match Best Local Similarity 46.9%; Pred. No. 21;  
 RESULT 1095  
 ID ABL70330 standard; DNA; 5338 BP.  
 DE Chemically treated cell signalling DNA sequence complementary to #110.  
 PN WO200202807-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG. 3.3%; Score 45; DB 6; Length 5338;  
 Query Match Best Local Similarity 46.9%; Pred. No. 21;  
 RESULT 1096  
 ID AAS61281 standard; DNA; 5338 BP.  
 DE Human gene regulation-associated gene oligonucleotide #236.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG. 3.3%; Score 45; DB 6; Length 5338;  
 Query Match Best Local Similarity 46.9%; Pred. No. 21;  
 RESULT 1097

ID AAA70105 standard; DNA; 5940 BP.  
 DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:238.  
 PN WO20025728-A2.  
 PD 11-MAY-2000.  
 PA (HOFF/) HOFFMAN S. 3.3%; Score 45; DB 3; Length 5940;  
 Query Match Best Local Similarity 44.9%; Pred. No. 21;  
 RESULT 1098  
 ID ABL32194 standard; DNA; 6208 BP.  
 DE Human immune system associated gene SEQ ID NO: 167.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG. 3.3%; Score 45; DB 6; Length 6208;  
 Query Match Best Local Similarity 50.2%; Pred. No. 21;  
 RESULT 1099  
 ID ABL32087 standard; DNA; 8178 BP.  
 DE Human immune system associated gene SEQ ID NO: 60.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG. 3.3%; Score 45; DB 6; Length 8178;  
 Query Match Best Local Similarity 46.1%; Pred. No. 22;  
 RESULT 1100  
 ID AAS46421 standard; DNA; 13321 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #143.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG. 3.3%; Score 45; DB 4; Length 13321;  
 Query Match Best Local Similarity 44.2%; Pred. No. 24;  
 RESULT 1101  
 ID ABL32254 standard; DNA; 18154 BP.  
 DE Human immune system associated gene SEQ ID NO: 227.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG. 3.3%; Score 45; DB 6; Length 18154;  
 Query Match Best Local Similarity 45.4%; Pred. No. 25;  
 RESULT 1102  
 ID ACA64845 standard; DNA; 115218 BP.  
 DE Human HNRNP GP43 DNA corresponding to AL034397.  
 PN DE10127572-A1.  
 PD 05-DEC-2002.  
 PA (PATH-) PATHOARRAY GMBH. 3.3%; Score 45; DB 8; Length 115218;  
 Query Match Best Local Similarity 45.6%; Pred. No. 33;  
 RESULT 1103  
 ID AAC94795 standard; cDNA; 549 BP.  
 DE Cat flea hindgut and Malpighian tubule (HMT) cDNA, SEQ ID NO:1290.  
 PN WO200061621-A2.  
 PD 19-OCT-2000.  
 PA (HESK-) HESKA CORP. 3.3%; Score 44.8; DB 3; Length 549;  
 Query Match Best Local Similarity 49.6%; Pred. No. 16;  
 RESULT 1104  
 ID AAC99867 standard; cDNA; 551 BP.  
 DE Human secreted protein gene 50 SEQ ID NO:60.  
 PN WO200070042-A1.  
 PD 23-NOV-2000.  
 PA (HUMA-) HUMAN GENOME SCI INC. 3.3%; Score 44.8; DB 3; Length 551;  
 Query Match Best Local Similarity 59.4%; Pred. No. 16;  
 RESULT 1105  
 ID ADR01596 standard; DNA; 837 BP.  
 DE A. gossypii genomic DNA PAG1241RP.  
 PN US6239264-B1.  
 PD 29-MAY-2001.  
 PA (SYNG-) SYNGENTA PARTICIPATIONS AG. 3.3%; Score 44.8; DB 2; Length 837;  
 Query Match

Best Local Similarity 44.9%; Pred. No. 17;  
RESULT 1106  
ID ADF82206 standard; DNA; 1114 BP.  
DE Leukemia-related DNA sequence #2762.  
PN WO2003039443-A2.  
PD 15-MAY-2003.  
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAFF-) HAFERLACH T.  
PA (SCHO-) SCHOCH C.  
PA (KERN-) KERN W.  
Query Match 3.3%; Score 44.8; DB 10; Length 1114;  
Best Local Similarity 56.6%; Pred. No. 18;  
RESULT 1107  
ID AAA97037 standard; DNA; 2486 BP.  
DE Nucleotide sequence encoding 48kD i-antigen.  
PN WO200046373-A1.  
PD 10-AUG-2000.  
PA (UYGE-) UNIV GEORGIA RES FOUND INC.  
PA (CORR-) CORNELL RES FOUND INC.  
PA (CLAR-) CLARK T G.  
PA (DICK-) DICKERSON H W.  
PA (LINT-) LIN T.  
Query Match 3.3%; Score 44.8; DB 3; Length 2486;  
Best Local Similarity 46.2%; Pred. No. 20;  
RESULT 1108  
ID ADS89406 standard; DNA; 4394 BP.  
DE Oligonucleotide of the invention SEQ ID NO:422.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 13; Length 4394;  
Best Local Similarity 46.5%; Pred. No. 22;  
RESULT 1109  
ID ABZ09959 standard; DNA; 5020 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #99.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 8; Length 5020;  
Best Local Similarity 46.8%; Pred. No. 23;  
RESULT 1110  
ID ABZ10105 standard; DNA; 5020 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #245.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 8; Length 5020;  
Best Local Similarity 46.8%; Pred. No. 23;  
RESULT 1111  
ID AAA70189 standard; DNA; 5454 BP.  
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:322.  
PN WO200025728-A2.  
PD 11-MAY-2000.  
PA (HOFF-) HOFFMAN S.  
PA (CARU-) CARUCCI D.  
PA (GARD-) GARDNER M.  
PA (VENT-) VENTER J C.  
Query Match 3.3%; Score 44.8; DB 3; Length 5454;  
Best Local Similarity 47.5%; Pred. No. 23;  
RESULT 1112  
ID AAN50530 standard; DNA; 5760 BP.  
DE Sequence encoding the P195 protein of Plasmodium falciparum.  
PN EP154454-A.  
PD 11-SEP-1985.  
PA (WELL-) WELLCOME FOUND LTD.  
Query Match 3.3%; Score 44.8; DB 1; Length 5760;  
Best Local Similarity 62.9%; Pred. No. 23;  
RESULT 1113  
ID ABL32288 standard; DNA; 5875 BP.  
DE Human immune system associated gene SEQ ID NO: 261.  
PN WO200200928-A2.  
PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 5875;  
Best Local Similarity 43.8%; Pred. No. 23;  
RESULT 1114  
ID AAD46980 standard; DNA; 5917 BP.  
DE Plasmodium falciparum merozoite surface protein-1 (MSP-1) DNA.  
PN WO200270542-A2.  
PD 12-SEP-2002.  
PA (SELI-) ST ELIZABETH'S MEDICAL CENT INC.  
Query Match 3.3%; Score 44.8; DB 6; Length 5917;  
Best Local Similarity 62.9%; Pred. No. 23;  
RESULT 1115  
ID ABL32238 standard; DNA; 6222 BP.  
DE Human immune system associated gene SEQ ID NO: 211.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 6222;  
Best Local Similarity 55.0%; Pred. No. 23;  
RESULT 1116  
ID ABK31496 standard; DNA; 6228 BP.  
DE Signal transduction associated gene modified DNA #170.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 6228;  
Best Local Similarity 55.0%; Pred. No. 23;  
RESULT 1117  
ID ABL70469 standard; DNA; 6228 BP.  
DE Chemically treated cell signalling DNA sequence#180.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 6228;  
Best Local Similarity 55.0%; Pred. No. 23;  
RESULT 1118  
ID AAS61430 standard; DNA; 6228 BP.  
DE Human gene regulation-associated gene oligonucleotide #385.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 6228;  
Best Local Similarity 55.0%; Pred. No. 23;  
RESULT 1119  
ID ABL32819 standard; DNA; 6397 BP.  
DE Human immune system associated gene SEQ ID NO: 792.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 6397;  
Best Local Similarity 49.0%; Pred. No. 23;  
RESULT 1120  
ID ABL33574 standard; DNA; 6627 BP.  
DE Human immune system associated gene SEQ ID NO: 1547.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 6627;  
Best Local Similarity 47.5%; Pred. No. 24;  
RESULT 1121  
ID ABL32398 standard; DNA; 6662 BP.  
DE Human immune system associated gene SEQ ID NO: 371.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 6662;  
Best Local Similarity 45.0%; Pred. No. 24;  
RESULT 1122  
ID ABQ67014 standard; DNA; 6676 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 44.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.

Query Match 3.3%; Score 44.8; DB 6; Length 6676;  
Best Local Similarity 49.7%; Pred. No. 24;  
RESULT 1123  
ID ABL32212 standard; DNA; 6904 BP.  
DE Human immune system associated gene SEQ ID NO: 185.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 6904;  
Best Local Similarity 46.2%; Pred. No. 24;  
RESULT 1124  
ID ABL32336 standard; DNA; 7201 BP.  
DE Human immune system associated gene SEQ ID NO: 309.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 7201;  
Best Local Similarity 45.8%; Pred. No. 24;  
RESULT 1125  
ID ABL34045 standard; DNA; 7319 BP.  
DE Human immune system associated gene SEQ ID NO: 2018.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 7319;  
Best Local Similarity 49.0%; Pred. No. 24;  
RESULT 1126  
ID AAS45490 standard; DNA; 7823 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #98.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 4; Length 7823;  
Best Local Similarity 45.1%; Pred. No. 24;  
RESULT 1127  
ID ABL34061 standard; DNA; 7823 BP.  
DE Human immune system associated gene SEQ ID NO: 2034.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 7823;  
Best Local Similarity 45.1%; Pred. No. 24;  
RESULT 1128  
ID ABK31493 standard; DNA; 7823 BP.  
DE Signal transduction associated gene modified complementary DNA #168.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 7823;  
Best Local Similarity 45.1%; Pred. No. 24;  
RESULT 1129  
ID ABK28418 standard; DNA; 7823 BP.  
DE DNA transduction associated complementary genomic DNA #146.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 7823;  
Best Local Similarity 45.1%; Pred. No. 24;  
RESULT 1130  
ID ADE84209 standard; DNA; 8020 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #145.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 10; Length 8020;  
Best Local Similarity 46.8%; Pred. No. 24;  
RESULT 1131  
ID ADE84133 standard; DNA; 8020 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #69.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 10; Length 8020;

Best Local Similarity 46.8%; Pred. No. 24;  
RESULT 1132  
ID ADS89617 standard; DNA; 8020 BP.  
DE Oligonucleotide of the invention SEQ ID NO:633.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 13; Length 8020;  
Best Local Similarity 46.8%; Pred. No. 24;  
RESULT 1133  
ID ADS89343 standard; DNA; 8020 BP.  
DE Oligonucleotide of the invention SEQ ID NO:359.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 13; Length 8020;  
Best Local Similarity 46.8%; Pred. No. 24;  
RESULT 1134  
ID AAS46445 standard; DNA; 8952 BP.  
DE Tumour suppressor gene derived chemically modified sequence #167.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 4; Length 8952;  
Best Local Similarity 43.4%; Pred. No. 25;  
RESULT 1135  
ID ABL32687 standard; DNA; 8962 BP.  
DE Human immune system associated gene SEQ ID NO: 660.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 8962;  
Best Local Similarity 43.3%; Pred. No. 25;  
RESULT 1136  
ID ABL33513 standard; DNA; 11092 BP.  
DE Human immune system associated gene SEQ ID NO: 1486.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 11092;  
Best Local Similarity 44.5%; Pred. No. 25;  
RESULT 1137  
ID ABL70570 standard; DNA; 24939 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#230.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.8; DB 6; Length 24939;  
Best Local Similarity 41.8%; Pred. No. 29;  
RESULT 1138  
ID ADE43582 standard; DNA; 128034 BP.  
DE Polymorphic human IDE genomic sequence, SEQ ID 187.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 3.3%; Score 44.8; DB 10; Length 128034;  
Best Local Similarity 58.1%; Pred. No. 37;  
RESULT 1139  
ID ADE43581 standard; DNA; 128034 BP.  
DE Human IDE genomic sequence, SEQ ID 186.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
PA (GEO) GEN HOSPITAL CORP.  
Query Match 3.3%; Score 44.8; DB 10; Length 128034;  
Best Local Similarity 58.1%; Pred. No. 37;  
RESULT 1140  
ID ADH54059 standard; DNA; 128034 BP.  
DE Human IDE gene DNA sequence SeqID186.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GEO) GEN HOSPITAL CORP.

Query Match 3.3%; Score 44.8; DB 12; Length 128034;  
Best Local Similarity 58.1%; Pred. No. 37;  
RESULT 1141  
ID ADH54060 standard; DNA; 128034 BP.  
DE Human IDE gene variant DNA sequence SeqID187.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GHEO ) GEN HOSPITAL CORP.  
Query Match 3.3%; Score 44.8; DB 12; Length 128034;  
Best Local Similarity 58.1%; Pred. No. 37;  
RESULT 1142  
ID ADE43315 standard; DNA; 202100 BP.  
DE Human IDE/ KNSL1 genomic sequence, SEQ ID 484.  
PN WO2003054143-A2.  
PD 03-JUL-2003.  
PA (NEUR-) NEUROGENETICS INC.  
PA (GHEO ) GEN HOSPITAL CORP.  
Query Match 3.3%; Score 44.8; DB 10; Length 202100;  
Best Local Similarity 58.1%; Pred. No. 39;  
RESULT 1143  
ID ADH54357 standard; DNA; 202100 BP.  
DE Human IDE/ KNSL1 gene DNA sequence SeqID484.  
PN US2003224380-A1.  
PD 04-DEC-2003.  
PA (GHEO ) GEN HOSPITAL CORP.  
Query Match 3.3%; Score 44.8; DB 12; Length 202100;  
Best Local Similarity 58.1%; Pred. No. 39;  
RESULT 1144  
ID ADI71847 standard; DNA; 363 BP.  
DE Human ovarian cancer DNA marker #4589.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 44.6; DB 5; Length 363;  
Best Local Similarity 43.2%; Pred. No. 17;  
RESULT 1145  
ID ADL36998 standard; DNA; 363 BP.  
DE Human ovarian cancer DNA marker #10888.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 44.6; DB 5; Length 363;  
Best Local Similarity 43.2%; Pred. No. 17;  
RESULT 1146  
ID ABX39417 standard; cDNA; 393 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #4582.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
Query Match 3.3%; Score 44.6; DB 8; Length 393;  
Best Local Similarity 48.0%; Pred. No. 17;  
RESULT 1147  
ID ADL43858 standard; DNA; 465 BP.  
DE Human ovarian cancer DNA marker #17748.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 44.6; DB 5; Length 465;  
Best Local Similarity 53.8%; Pred. No. 17;  
RESULT 1148  
ID AAS46621 standard; DNA; 6031 BP.  
DE Tumour suppressor gene derived chemically modified sequence #343.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.6; DB 4; Length 6031;  
Best Local Similarity 49.2%; Pred. No. 25;  
RESULT 1149  
ID ABN80275 standard; DNA; 6452 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 292.

PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.6; DB 6; Length 6452;  
Best Local Similarity 46.9%; Pred. No. 26;  
RESULT 1150  
ID ABL32310 standard; DNA; 6853 BP.  
DE Human immune system associated gene SEQ ID NO: 283.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.6; DB 6; Length 6853;  
Best Local Similarity 46.0%; Pred. No. 26;  
RESULT 1151  
ID ABL54331 standard; DNA; 6853 BP.  
DE Chemically treated apoptosis gene #16.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.6; DB 6; Length 6853;  
Best Local Similarity 46.0%; Pred. No. 26;  
RESULT 1152  
ID ABL32028 standard; DNA; 7351 BP.  
DE Human immune system associated gene SEQ ID NO: 1.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.6; DB 6; Length 7351;  
Best Local Similarity 44.4%; Pred. No. 26;  
RESULT 1153  
ID ABZ10245 standard; DNA; 8056 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #385.  
PN WO20027272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.6; DB 8; Length 8056;  
Best Local Similarity 45.5%; Pred. No. 27;  
RESULT 1154  
ID ABL92302 standard; DNA; 8607 BP.  
DE Chemically treated DNA repair gene fragment#56.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.6; DB 6; Length 8607;  
Best Local Similarity 53.8%; Pred. No. 27;  
RESULT 1155  
ID ABL49371 standard; DNA; 8607 BP.  
DE Human polynucleotide associated with DNA replication SEQ ID NO 71.  
PN WO200177377-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.6; DB 6; Length 8607;  
Best Local Similarity 53.8%; Pred. No. 27;  
RESULT 1156  
ID ABQ67026 standard; DNA; 11964 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 56.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.6; DB 6; Length 11964;  
Best Local Similarity 50.2%; Pred. No. 28;  
RESULT 1157  
ID ABL32631 standard; DNA; 14987 BP.  
DE Human immune system associated gene SEQ ID NO: 604.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.6; DB 6; Length 14987;  
Best Local Similarity 46.3%; Pred. No. 29;  
RESULT 1158  
ID AAS45388 standard; DNA; 15732 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #47.  
PN WO200168911-A2.

PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 4; Length 15732;  
 Best Local Similarity 44.6%; Pred. No. 29;  
 RESULT 1159  
 ID ABK28233 standard; DNA; 15732 BP.  
 DE DNA transcription associated genomic DNA #54.  
 PN WO200192585-A2.  
 PD 06-DEC-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 6; Length 15732;  
 Best Local Similarity 44.6%; Pred. No. 29;  
 RESULT 1160  
 ID ABL33681 standard; DNA; 15951 BP.  
 DE Human immune system associated gene SEQ ID NO: 1654.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 6; Length 15951;  
 Best Local Similarity 44.3%; Pred. No. 30;  
 RESULT 1161  
 ID ABL34581 standard; DNA; 15951 BP.  
 DE Human metastasis associated gene SEQ ID NO: 134.  
 PN WO200177376-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 6; Length 15951;  
 Best Local Similarity 44.3%; Pred. No. 30;  
 RESULT 1162  
 ID ABL70374 standard; DNA; 15951 BP.  
 DE Chemically treated cell signalling DNA sequence complementary to #132.  
 PN WO200202807-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 6; Length 15951;  
 Best Local Similarity 44.3%; Pred. No. 30;  
 RESULT 1163  
 ID ADS99842 standard; DNA; 17959 BP.  
 DE Complement of bisulphite treated metastasis-associated human gene #67.  
 PN US2003148327-A1.  
 PD 07-AUG-2003.  
 PA (OLEK/) OLEK A.  
 PA (PIEP/) PIEPENBROCK C.  
 PA (BERL/) BERLIN K.  
 Query Match 3.3%; Score 44.6; DB 7; Length 15951;  
 Best Local Similarity 44.3%; Pred. No. 30;  
 RESULT 1164  
 ID ABL32575 standard; DNA; 17959 BP.  
 DE Human immune system associated gene SEQ ID NO: 548.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 6; Length 17959;  
 Best Local Similarity 47.1%; Pred. No. 30;  
 RESULT 1165  
 ID ABL54342 standard; DNA; 17959 BP.  
 DE Chemically treated apoptosis gene complementary to gene #21.  
 PN WO200177164-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 6; Length 17959;  
 Best Local Similarity 47.1%; Pred. No. 30;  
 RESULT 1166  
 ID ABL32626 standard; DNA; 19082 BP.  
 DE Human immune system associated gene SEQ ID NO: 599.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 6; Length 19082;  
 Best Local Similarity 46.7%; Pred. No. 30;  
 RESULT 1167  
 ID AAT72882 standard; cDNA; 19124 BP.  
 DE Plasmodium var-7 gene.

PN WO9640766-A2.  
 PD 19-DEC-1996.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 3.3%; Score 44.6; DB 2; Length 19124;  
 Best Local Similarity 46.1%; Pred. No. 30;  
 RESULT 1168  
 ID AAZ98287 standard; DNA; 19124 BP.  
 DE Plasmodium var-7 polypeptide encoding DNA.  
 PN US5993827-A.  
 PD 30-NOV-1999.  
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.  
 Query Match 3.3%; Score 44.6; DB 3; Length 19124;  
 Best Local Similarity 46.1%; Pred. No. 30;  
 RESULT 1169  
 ID ABL34124 standard; DNA; 73334 BP.  
 DE Human immune system associated gene SEQ ID NO: 2097.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 6; Length 73334;  
 Best Local Similarity 43.9%; Pred. No. 37;  
 RESULT 1170  
 ID ABL92318 standard; DNA; 73334 BP.  
 DE Chemically treated DNA repair gene fragment #64.  
 PN WO200181622-A2.  
 PD 01-NOV-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 6; Length 73334;  
 Best Local Similarity 43.9%; Pred. No. 37;  
 RESULT 1171  
 ID ABL34175 standard; DNA; 113515 BP.  
 DE Human immune system associated gene SEQ ID NO: 2148.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.6; DB 6; Length 113515;  
 Best Local Similarity 43.3%; Pred. No. 40;  
 RESULT 1172  
 ID ADO59452 standard; DNA; 168198 BP.  
 DE Human cancer-associated (CA) gene sequence SEQ ID NO: 88.  
 PN WO2004058288-A1.  
 PD 15-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 3.3%; Score 44.6; DB 12; Length 168198;  
 Best Local Similarity 46.6%; Pred. No. 42;  
 RESULT 1173  
 ID ABX48619 standard; cDNA; 397 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #13784.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHALAGAN N.  
 PA (TAOW/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 3.3%; Score 44.4; DB 8; Length 397;  
 Best Local Similarity 52.7%; Pred. No. 19;  
 RESULT 1174  
 ID ADI72227 standard; DNA; 647 BP.  
 DE Human ovarian cancer DNA marker #4969.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 3.3%; Score 44.4; DB 5; Length 647;  
 Best Local Similarity 42.9%; Pred. No. 20;  
 RESULT 1175  
 ID ADI37372 standard; DNA; 647 BP.  
 DE Human ovarian cancer DNA marker #11262.  
 PN WO200170979-A2.  
 PD 27-SEP-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 3.3%; Score 44.4; DB 5; Length 647;  
 Best Local Similarity 42.9%; Pred. No. 20;  
 RESULT 1176

ID ADB59228 standard; DNA; 2217 BP.  
DE Toxicity-related gene, SEQ ID 4254.  
PN WO2003064624-A2.  
PD 07-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Query Match 3.3%; Score 44.4; DB 10; Length 2217;  
Best Local Similarity 54.2%; Pred. No. 24;  
RESULT 1177  
ID ABT42483 standard; DNA; 2217 BP.  
DE Toxicity modelling related rat gene SEQ ID No 2185.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Query Match 3.3%; Score 44.4; DB 10; Length 2217;  
Best Local Similarity 54.2%; Pred. No. 24;  
RESULT 1178  
ID ADS89709 standard; DNA; 2526 BP.  
DE Oligonucleotide of the invention SEQ ID NO:725.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 13; Length 2526;  
Best Local Similarity 45.6%; Pred. No. 25;  
RESULT 1179  
ID ADS91270 standard; DNA; 2648 BP.  
DE alpha-1 tubulin coding sequence, SEQ ID 166.  
PN WO2004074479-A1.  
PD 02-SEP-2004.  
PA (PHYL-) PHYLOGICA LTD.  
Query Match 3.3%; Score 44.4; DB 13; Length 2648;  
Best Local Similarity 44.9%; Pred. No. 25;  
RESULT 1180  
ID ABL33598 standard; DNA; 5487 BP.  
DE Human immune system associated gene SEQ ID NO: 1571.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 5487;  
Best Local Similarity 47.2%; Pred. No. 28;  
RESULT 1181  
ID ABL32603 standard; DNA; 5912 BP.  
DE Human immune system associated gene SEQ ID NO: 576.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 5912;  
Best Local Similarity 45.4%; Pred. No. 28;  
RESULT 1182  
ID ABL32862 standard; DNA; 6132 BP.  
DE Human immune system associated gene SEQ ID NO: 835.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 6132;  
Best Local Similarity 46.4%; Pred. No. 28;  
RESULT 1183  
ID ABL33587 standard; DNA; 6227 BP.  
DE Human immune system associated gene SEQ ID NO: 1560.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 6227;  
Best Local Similarity 46.8%; Pred. No. 28;  
RESULT 1184  
ID ABL92261 standard; DNA; 6227 BP.  
DE Chemically treated DNA repair gene fragment complementary to#35.  
PN WO200181622-A2.  
PD 01-NOV-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 6227;  
Best Local Similarity 46.8%; Pred. No. 28;  
RESULT 1185  
ID ABL34025 standard; DNA; 6375 BP.

DE Human immune system associated gene SEQ ID NO: 1998.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 6375;  
Best Local Similarity 43.3%; Pred. No. 28;  
RESULT 1186  
ID ABL32985 standard; DNA; 6465 BP.  
DE Human immune system associated gene SEQ ID NO: 958.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 6465;  
Best Local Similarity 44.5%; Pred. No. 28;  
RESULT 1187  
ID ABK40036 standard; DNA; 7374 BP.  
DE Human chemically pretreated gene sequence #59 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 7374;  
Best Local Similarity 48.4%; Pred. No. 29;  
RESULT 1188  
ID ABL70602 standard; DNA; 7374 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#246.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 7374;  
Best Local Similarity 48.4%; Pred. No. 29;  
RESULT 1189  
ID ABX77219 standard; DNA; 10094 BP.  
DE 5' sequence flanking human MDR1 contig.  
PN WO200283897-A1.  
PD 24-OCT-2002.  
PA (GENE-) GENE STREAM PTY LTD.  
Query Match 3.3%; Score 44.4; DB 10; Length 10094;  
Best Local Similarity 45.5%; Pred. No. 30;  
RESULT 1190  
ID ABL34122 standard; DNA; 10329 BP.  
DE Human immune system associated gene SEQ ID NO: 2095.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 10329;  
Best Local Similarity 46.9%; Pred. No. 30;  
RESULT 1191  
ID AAS63313 standard; DNA; 12409 BP.  
DE Chemically pretreated metabolism associated gene #8.  
PN WO200176451-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 12409;  
Best Local Similarity 46.0%; Pred. No. 31;  
RESULT 1192  
ID ABL33926 standard; DNA; 13427 BP.  
DE Human immune system associated gene SEQ ID NO: 1899.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 13427;  
Best Local Similarity 46.2%; Pred. No. 32;  
RESULT 1193  
ID ABL32615 standard; DNA; 13584 BP.  
DE Human immune system associated gene SEQ ID NO: 588.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 13584;  
Best Local Similarity 45.4%; Pred. No. 32;  
RESULT 1194  
ID ABL32362 standard; DNA; 15674 BP.  
DE Human immune system associated gene SEQ ID NO: 335.



PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 15674;  
Best Local Similarity 48.6%; Pred. No. 32;  
RESULT 1195  
ID ABL34476 standard; DNA; 15674 BP.  
DE Human metastasis associated gene SEQ ID NO: 29.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 15674;  
Best Local Similarity 48.6%; Pred. No. 32;  
RESULT 1196  
ID ABL70513 standard; DNA; 15674 BP.  
DE Chemically treated cell signalling DNA sequence#202.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 15674;  
Best Local Similarity 48.6%; Pred. No. 32;  
RESULT 1197  
ID ADS99737 standard; DNA; 15674 BP.  
DE Bisulphite treated human gene associated with metastasis #15.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 3.3%; Score 44.4; DB 7; Length 15674;  
Best Local Similarity 48.6%; Pred. No. 32;  
RESULT 1198  
ID ADB54118 standard; DNA; 16579 BP.  
DE Pretreated genomic DNA region 42.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 10; Length 16579;  
Best Local Similarity 46.0%; Pred. No. 33;  
RESULT 1199  
ID ADB54246 standard; DNA; 16579 BP.  
DE Pretreated genomic DNA region 170.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 10; Length 16579;  
Best Local Similarity 46.0%; Pred. No. 33;  
RESULT 1200  
ID ADE37773 standard; DNA; 16579 BP.  
DE Human chemically treated TPEF nucleotide sequence SEQ ID NO:19.  
PN WO2003072820-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 10; Length 16579;  
Best Local Similarity 46.0%; Pred. No. 33;  
RESULT 1201  
ID ADE37763 standard; DNA; 16579 BP.  
DE Human chemically treated TPEF nucleotide sequence SEQ ID NO:9.  
PN WO2003072820-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 10; Length 16579;  
Best Local Similarity 46.0%; Pred. No. 33;  
RESULT 1202  
ID ADS89274 standard; DNA; 16579 BP.  
DE Oligonucleotide of the invention SEQ ID NO:290.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 13; Length 16579;  
Best Local Similarity 46.0%; Pred. No. 33;  
RESULT 1203  
ID ADS89548 standard; DNA; 16579 BP.

DE Oligonucleotide of the invention SEQ ID NO:564.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 13; Length 16579;  
Best Local Similarity 46.0%; Pred. No. 33;  
RESULT 1204  
ID AAS46314 standard; DNA; 16750 BP.  
DE Tumour suppressor gene derived chemically modified sequence #36.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 4; Length 16750;  
Best Local Similarity 46.0%; Pred. No. 33;  
RESULT 1205  
ID ABL32521 standard; DNA; 16750 BP.  
DE Human immune system associated gene SEQ ID NO: 494.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 16750;  
Best Local Similarity 46.0%; Pred. No. 33;  
RESULT 1206  
ID ABL33053 standard; DNA; 17131 BP.  
DE Human immune system associated gene SEQ ID NO: 1026.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 17131;  
Best Local Similarity 46.7%; Pred. No. 33;  
RESULT 1207  
ID ABL34027 standard; DNA; 17594 BP.  
DE Human immune system associated gene SEQ ID NO: 2000.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 17594;  
Best Local Similarity 47.4%; Pred. No. 33;  
RESULT 1208  
ID AAS45323 standard; DNA; 17848 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #14.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 4; Length 17848;  
Best Local Similarity 44.6%; Pred. No. 33;  
RESULT 1209  
ID ASK39976 standard; DNA; 17848 BP.  
DE Human chemically pretreated gene sequence #29 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 17848;  
Best Local Similarity 44.6%; Pred. No. 33;  
RESULT 1210  
ID ASK28164 standard; DNA; 17848 BP.  
DE DNA transcription associated complementary genomic DNA #19.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 17848;  
Best Local Similarity 44.6%; Pred. No. 33;  
RESULT 1211  
ID ABL32313 standard; DNA; 18683 BP.  
DE Human immune system associated gene SEQ ID NO: 286.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 18683;  
Best Local Similarity 44.3%; Pred. No. 33;  
RESULT 1212  
ID ABL54334 standard; DNA; 18683 BP.  
DE Chemically treated apoptosis gene complementary to gene #17.

PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 18683;  
Best Local Similarity 44.3%; Pred. No. 33;  
RESULT 1213  
ID ABN80016 standard; DNA; 19345 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 33.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.4; DB 6; Length 19345;  
Best Local Similarity 46.5%; Pred. No. 33;  
RESULT 1214  
ID ABN85767 standard; cDNA; 83698 BP.  
DE Arabidopsis yellow striped-like 4 encoding cDNA SEQ ID NO 9.  
PN WO200240688-A2.  
PD 23-MAY-2002.  
PA (UYUA) UNIV YALE.  
Query Match 3.3%; Score 44.4; DB 6; Length 83698;  
Best Local Similarity 62.7%; Pred. No. 42;  
RESULT 1215  
ID ADQ97050 standard; DNA; 687411 BP.  
DE Human cancer associated sequence HD08-001, SEQ ID 26.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 3.3%; Score 44.4; DB 12; Length 110000;  
Best Local Similarity 46.5%; Pred. No. 43;  
RESULT 1216  
ID ACF62751 standard; DNA; 177380 BP.  
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.  
PN WO2003013534-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
Query Match 3.3%; Score 44.4; DB 8; Length 177380;  
Best Local Similarity 45.5%; Pred. No. 47;  
RESULT 1217  
ID ADB20870 standard; DNA; 177380 BP.  
DE MRP1 based cancer related nucleic acid SEQ ID NO:683.  
PN WO2003013533-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
Query Match 3.3%; Score 44.4; DB 8; Length 177380;  
Best Local Similarity 45.5%; Pred. No. 47;  
RESULT 1218  
ID ADB87959 standard; DNA; 177380 BP.  
DE Human UGT1A1 gene sequence SEQ ID NO:683.  
PN WO2003013536-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
Query Match 3.3%; Score 44.4; DB 10; Length 177380;  
Best Local Similarity 45.5%; Pred. No. 47;  
RESULT 1219  
ID ADB96942 standard; DNA; 177380 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:683.  
PN WO2003013537-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
Query Match 3.3%; Score 44.4; DB 10; Length 177380;  
Best Local Similarity 45.5%; Pred. No. 47;  
RESULT 1220  
ID ADB92133 standard; DNA; 177380 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:683.  
PN WO2003013535-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
Query Match 3.3%; Score 44.4; DB 10; Length 177380;  
Best Local Similarity 45.5%; Pred. No. 47;  
RESULT 1221  
ID ADL37087 standard; DNA; 410 BP.  
DE Human ovarian cancer DNA marker #10977.  
PN WO200170979-A2.

PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 44.2; DB 5; Length 410;  
Best Local Similarity 43.1%; Pred. No. 20;  
RESULT 1222  
ID ADI71936 standard; DNA; 410 BP.  
DE Human ovarian cancer DNA marker #4678.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 44.2; DB 5; Length 410;  
Best Local Similarity 43.1%; Pred. No. 20;  
RESULT 1223  
ID ADL43834 standard; DNA; 461 BP.  
DE Human ovarian cancer DNA marker #17724.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 44.2; DB 5; Length 461;  
Best Local Similarity 61.4%; Pred. No. 21;  
RESULT 1224  
ID ADL10644 standard; cDNA; 495 BP.  
DE Cat flea hindgut and malpighian tubule (HMT) protein cDNA #1049.  
PN US2004067516-A1.  
PD 08-APR-2004.  
PA (BRAN/) BRANDT K S.  
PA (GAIN/) GAINES P J.  
PA (STIN/) STINCHCOMB D T.  
PA (WISN/) WISNEWSKI N.  
Query Match 3.3%; Score 44.2; DB 12; Length 495;  
Best Local Similarity 48.0%; Pred. No. 21;  
RESULT 1225  
ID ADC20845 standard; DNA; 1238 BP.  
DE Human secreted protein-related DNA sequence #263.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.3%; Score 44.2; DB 10; Length 1238;  
Best Local Similarity 60.3%; Pred. No. 24;  
RESULT 1226  
ID ABT16982 standard; DNA; 1238 BP.  
DE Human secreted protein-related DNA sequence - SEQ ID NO 336.  
PN WO200277188-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.3%; Score 44.2; DB 10; Length 1238;  
Best Local Similarity 60.3%; Pred. No. 24;  
RESULT 1227  
ID ABZ67930 standard; DNA; 1238 BP.  
DE Human secreted protein encoding genomic DNA SEQ ID NO 1453.  
PN WO200277186-A2.  
PD 03-OCT-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.3%; Score 44.2; DB 10; Length 1238;  
Best Local Similarity 60.3%; Pred. No. 24;  
RESULT 1228  
ID ACA8992 standard; DNA; 1425 BP.  
DE Prokaryotic essential gene #10849.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Query Match 3.3%; Score 44.2; DB 8; Length 1425;  
Best Local Similarity 50.7%; Pred. No. 25;  
RESULT 1229  
ID AAN80917 standard; cDNA; 1540 BP.  
DE Sequence of the 3'-end of the human glucocorticoid receptor beta cDNA (beta-hGR).  
PN WO8803168-A.  
PD 05-MAY-1988.  
PA (SALK) SALK INST BIOLOGICAL STUDIES.  
Query Match 3.3%; Score 44.2; DB 1; Length 1540;  
Best Local Similarity 75.3%; Pred. No. 25;  
RESULT 1230

ID AAV38740 standard; cDNA; 1584 BP.  
 DE Complementary strand of cDNA nfsP11-1584 encoding a SPI protein.  
 PN WO9820034-A2.  
 PD 14-MAY-1998.  
 PA (HESK-) HESKA CORP.  
 Query Match 3.3%; Score 44.2; DB 2; Length 1584;  
 Best Local Similarity 47.7%; Pred. No. 25;  
 RESULT 1231  
 ID AAV38739 standard; cDNA; 1584 BP.  
 DE cDNA nfsP11-1584 encoding a flea serine protease inhibitor protein.  
 PN WO9820034-A2.  
 PD 14-MAY-1998.  
 PA (HESK-) HESKA CORP.  
 Query Match 3.3%; Score 44.2; DB 2; Length 1584;  
 Best Local Similarity 47.7%; Pred. No. 25;  
 RESULT 1232  
 ID ADQ25468 standard; DNA; 2341 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8288.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 3.3%; Score 44.2; DB 12; Length 2341;  
 Best Local Similarity 68.5%; Pred. No. 27;  
 RESULT 1233  
 ID ADQ24153 standard; DNA; 2341 BP.  
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6973.  
 PN WO2004048938-A2.  
 PD 10-JUN-2004.  
 PA (PROT-) PROTEIN DESIGN LABS INC.  
 Query Match 3.3%; Score 44.2; DB 12; Length 2341;  
 Best Local Similarity 68.5%; Pred. No. 27;  
 RESULT 1234  
 ID AAS46320 standard; DNA; 2865 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #42.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 4; Length 2865;  
 Best Local Similarity 44.9%; Pred. No. 27;  
 RESULT 1235  
 ID AEN80051 standard; DNA; 2865 BP.  
 DE Human chemically modified disease associated gene SEQ ID NO 68.  
 PN WO200200927-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 6; Length 2865;  
 Best Local Similarity 44.9%; Pred. No. 27;  
 RESULT 1236  
 ID ABQ67051 standard; DNA; 3046 BP.  
 DE Human angiogenesis associated polynucleotide SEQ ID NO 81.  
 PN WO200246454-A2.  
 PD 13-JUN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 6; Length 3046;  
 Best Local Similarity 46.8%; Pred. No. 28;  
 RESULT 1237  
 ID ABL32133 standard; DNA; 5421 BP.  
 DE Human immune system associated gene SEQ ID NO: 106.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 6; Length 5421;  
 Best Local Similarity 49.8%; Pred. No. 30;  
 RESULT 1238  
 ID AAD28388 standard; DNA; 6123 BP.  
 DE Human chemically treated genomic DNA #29.  
 PN WO200202809-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 6; Length 6123;  
 Best Local Similarity 44.5%; Pred. No. 31;  
 RESULT 1239  
 ID ABL32972 standard; DNA; 6145 BP.

DE Human immune system associated gene SEQ ID NO: 945.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 6; Length 6145;  
 Best Local Similarity 51.4%; Pred. No. 31;  
 RESULT 1240  
 ID ABZ10060 standard; DNA; 6289 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #200.  
 PN WO200277272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 8; Length 6289;  
 Best Local Similarity 46.8%; Pred. No. 31;  
 RESULT 1241  
 ID ABZ10194 standard; DNA; 6343 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #334.  
 PN WO200277272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 8; Length 6343;  
 Best Local Similarity 49.8%; Pred. No. 31;  
 RESULT 1242  
 ID ADS89670 standard; DNA; 6343 BP.  
 DE Oligonucleotide of the invention SEQ ID NO:686.  
 PN WO2004035803-A2.  
 PD 29-APR-2004.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 13; Length 6343;  
 Best Local Similarity 49.8%; Pred. No. 31;  
 RESULT 1243  
 ID ABQ66987 standard; DNA; 6652 BP.  
 DE Human angiogenesis associated polynucleotide SEQ ID NO 17.  
 PN WO200246454-A2.  
 PD 13-JUN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 6; Length 6652;  
 Best Local Similarity 45.3%; Pred. No. 31;  
 RESULT 1244  
 ID ABL33602 standard; DNA; 6821 BP.  
 DE Human immune system associated gene SEQ ID NO: 1575.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 6; Length 6821;  
 Best Local Similarity 53.1%; Pred. No. 31;  
 RESULT 1245  
 ID AEN80025 standard; DNA; 8453 BP.  
 DE Human chemically modified disease associated gene SEQ ID NO 42.  
 PN WO200200927-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 6; Length 8453;  
 Best Local Similarity 46.8%; Pred. No. 32;  
 RESULT 1246  
 ID ABL32210 standard; DNA; 8889 BP.  
 DE Human immune system associated gene SEQ ID NO: 183.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 6; Length 8889;  
 Best Local Similarity 44.7%; Pred. No. 33;  
 RESULT 1247  
 ID AAS46502 standard; DNA; 9289 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #224.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44.2; DB 4; Length 9289;  
 Best Local Similarity 46.8%; Pred. No. 33;  
 RESULT 1248  
 ID ADE84122 standard; DNA; 9289 BP.  
 DE Human lymphoid cell proliferative disorder gene derived DNA #58.

PN WO2003044226-A2.  
PD 30-MAY-2003  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.2; DB 10; Length 9289;  
Best Local Similarity 46.8%; Pred. No. 33;  
RESULT 1249  
ID ABL33014 standard; DNA; 17967 BP.  
DE Human immune system associated gene SEQ ID NO: 987.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.2; DB 6; Length 17967;  
Best Local Similarity 45.3%; Pred. No. 36;  
RESULT 1250  
ID ABL70502 standard; DNA; 18283 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#196.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.2; DB 6; Length 18283;  
Best Local Similarity 45.1%; Pred. No. 36;  
RESULT 1251  
ID AAS61363 standard; DNA; 18283 BP.  
DE Human gene regulation-associated gene oligonucleotide #318.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44.2; DB 6; Length 18283;  
Best Local Similarity 45.1%; Pred. No. 36;  
RESULT 1252  
ID AAD36834 standard; DNA; 59215 BP.  
DE Human transporter protein genomic DNA.  
Query Match 3.3%; Score 44.2; DB 8; Length 59215;  
Best Local Similarity 48.2%; Pred. No. 43;  
RESULT 1253  
Query Match 3.3%; Score 44.2; DB 6; Length 110000;  
Best Local Similarity 46.8%; Pred. No. 48;  
RESULT 1254  
ID ABD32602 standard; DNA; 277616 BP.  
DE Human cancer-associated genomic DNA HD7-221.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 3.3%; Score 44.2; DB 13; Length 277616;  
Best Local Similarity 44.4%; Pred. No. 55;  
RESULT 1255  
ID ADL37437 standard; DNA; 469 BP.  
DE Human ovarian cancer DNA marker #11327.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 44; DB 5; Length 469;  
Best Local Similarity 60.2%; Pred. No. 23;  
RESULT 1256  
ID ADI72293 standard; DNA; 469 BP.  
DE Human ovarian cancer DNA marker #5035.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 44; DB 5; Length 469;  
Best Local Similarity 60.2%; Pred. No. 23;  
RESULT 1257  
ID ACN47785 standard; cDNA; 557 BP.  
DE Cotton primed seed EST Clone ID: LTB3825-015-Q1-N6-A5, SEQ:2566.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 3.3%; Score 44; DB 13; Length 557;  
Best Local Similarity 52.8%; Pred. No. 24;  
RESULT 1258  
ID AAA70232 standard; DNA; 579 BP.  
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:365.  
PN WO200025728-A2.  
PD 11-MAY-2000.  
PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Query Match 3.3%; Score 44; DB 3; Length 579;  
Best Local Similarity 47.6%; Pred. No. 24;  
RESULT 1259  
ID AAS00668 standard; cDNA; 1909 BP.  
DE Human INTERCEPT 309 cDNA.  
PN WO200125088-A1.  
PD 26-APR-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 3.3%; Score 44; DB 4; Length 1909;  
Best Local Similarity 56.1%; Pred. No. 28;  
RESULT 1260  
ID ACD66731 standard; cDNA; 1909 BP.  
DE Secreted polypeptide-related cDNA #23.  
PN US2003022279-A1.  
PD 30-JAN-2003.  
PA (FRAS/) FRASER C C.  
PA (BARN/) BARNES T M.  
PA (SHAR/) SHARP J D.  
PA (KIRS/) KIRST S J.  
PA (MYER/) MYERS P S.  
PA (LEIB/) LEIBY K R.  
PA (HOLT/) HOLTZMAN D A.  
PA (MCCA/) MCCARTHY S A.  
PA (WRIG/) WRIGHTON N.  
PA (MACK/) MACKAY C R.  
PA (GOOD/) GOODEARL A D J.  
Query Match 3.3%; Score 44; DB 8; Length 1909;  
Best Local Similarity 56.1%; Pred. No. 28;  
RESULT 1261  
ID ADQ10174 standard; cDNA; 1909 BP.  
DE Human polynucleotide #24.  
PN US2004121396-A1.  
PD 24-JUN-2004.  
PA (MILL-) MILLENNIUM PHARM INC.  
Query Match 3.3%; Score 44; DB 12; Length 1909;  
Best Local Similarity 56.1%; Pred. No. 28;  
RESULT 1262  
ID ABV23236 standard; cDNA; 2105 BP.  
DE Human prostate expression marker cDNA 23227.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 44; DB 5; Length 2105;  
Best Local Similarity 56.1%; Pred. No. 29;  
RESULT 1263  
ID ABV29079 standard; cDNA; 2109 BP.  
DE Human prostate expression marker cDNA 29070.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.3%; Score 44; DB 5; Length 2109;  
Best Local Similarity 56.1%; Pred. No. 29;  
RESULT 1264  
ID ABL32178 standard; DNA; 5536 BP.  
DE Human immune system associated gene SEQ ID NO: 151.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 5536;  
Best Local Similarity 50.4%; Pred. No. 33;  
RESULT 1265  
ID AAS45313 standard; DNA; 5979 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #9.  
PN WO200168911-A2.  
PD 20-SEP-2001.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 4; Length 5979;  
Best Local Similarity 45.0%; Pred. No. 34;  
RESULT 1266  
ID ABK28152 standard; DNA; 5979 BP.  
DE DNA transcription associated complementary genomic DNA #13.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 5979;  
Best Local Similarity 45.0%; Pred. No. 34;  
RESULT 1267  
ID ABL33679 standard; DNA; 6070 BP.  
DE Human immune system associated gene SEQ ID NO: 1652.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 6070;  
Best Local Similarity 46.8%; Pred. No. 34;  
RESULT 1268  
ID ABL34579 standard; DNA; 6070 BP.  
DE Human metastasis associated gene SEQ ID NO: 132.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 6070;  
Best Local Similarity 46.8%; Pred. No. 34;  
RESULT 1269  
ID ABL70372 standard; DNA; 6070 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#131.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 6070;  
Best Local Similarity 46.8%; Pred. No. 34;  
RESULT 1270  
ID ASQ67130 standard; DNA; 6070 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 160.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 6070;  
Best Local Similarity 46.8%; Pred. No. 34;  
RESULT 1271  
ID ADS99840 standard; DNA; 6070 BP.  
DE Complement of bisulphite treated metastasis-associated human gene #66.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK)/ OLEK A.  
PA (PIEP)/ PIEPENBROCK C.  
PA (BERL)/ BERLIN K.  
Query Match 3.3%; Score 44; DB 7; Length 6070;  
Best Local Similarity 46.8%; Pred. No. 34;  
RESULT 1272  
ID ABL34218 standard; DNA; 6077 BP.  
DE Human immune system associated gene SEQ ID NO: 2191.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 6077;  
Best Local Similarity 44.8%; Pred. No. 34;  
RESULT 1273  
ID ABL33823 standard; DNA; 6113 BP.  
DE Human immune system associated gene SEQ ID NO: 1796.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 6113;  
Best Local Similarity 45.2%; Pred. No. 34;  
RESULT 1274  
ID ABL33215 standard; DNA; 6249 BP.  
DE Human immune system associated gene SEQ ID NO: 1188.  
PN WO200200928-A2.

PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 6249;  
Best Local Similarity 47.8%; Pred. No. 34;  
RESULT 1275  
ID ABK31305 standard; DNA; 6249 BP.  
DE Signal transduction associated gene modified complementary DNA #74.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 6249;  
Best Local Similarity 47.8%; Pred. No. 34;  
RESULT 1276  
ID ABL70556 standard; DNA; 6249 BP.  
DE Chemically treated cell signalling DNA sequence complementary to#223.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 6249;  
Best Local Similarity 47.8%; Pred. No. 34;  
RESULT 1277  
ID ARN80159 standard; DNA; 6249 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 176.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 6249;  
Best Local Similarity 47.8%; Pred. No. 34;  
RESULT 1278  
ID ABL34117 standard; DNA; 7046 BP.  
DE Human immune system associated gene SEQ ID NO: 2090.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 7046;  
Best Local Similarity 47.8%; Pred. No. 35;  
RESULT 1279  
ID ARN80289 standard; DNA; 7046 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 306.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 7046;  
Best Local Similarity 47.8%; Pred. No. 35;  
RESULT 1280  
ID ARN80224 standard; DNA; 8067 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 241.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 6; Length 8067;  
Best Local Similarity 43.9%; Pred. No. 35;  
RESULT 1281  
ID AAQ62924 standard; cDNA; 8920 BP.  
DE Carbamoyl-phosphate-synthetase II.  
PN WO9412643-A1.  
PD 09-JUN-1994.  
PA (UNIX ) UNISEARCH LTD.  
Query Match 3.3%; Score 44; DB 2; Length 8920;  
Best Local Similarity 50.3%; Pred. No. 36;  
RESULT 1282  
ID AAS45502 standard; DNA; 11812 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #104.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 44; DB 4; Length 11812;  
Best Local Similarity 47.4%; Pred. No. 37;  
RESULT 1283  
ID AAS46742 standard; DNA; 11812 BP.  
DE Tumour suppressor gene derived chemically modified sequence #466.  
PN WO200168912-A2.  
PD 20-SEP-2001.

PA (EPiG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44; DB 4; Length 11812;  
 Best Local Similarity 47.4%; Pred. No. 37;  
 RESULT 1284  
 ID ABL34119 standard; DNA; 11812 BP.  
 DE Human immune system associated gene SEQ ID NO: 2092.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPiG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44; DB 6; Length 11812;  
 Best Local Similarity 47.4%; Pred. No. 37;  
 RESULT 1285  
 ID ABK28432 standard; DNA; 11812 BP.  
 DE DNA transcriptions associated complementary genomic DNA #153.  
 PN WO200192565-A2.  
 PD 06-DEC-2001.  
 PA (EPiG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44; DB 6; Length 11812;  
 Best Local Similarity 47.4%; Pred. No. 37;  
 RESULT 1286  
 ID AAS45395 standard; DNA; 11836 BP.  
 DE Chemically pretreated complementary DNA associated with cell cycle #50.  
 PN WO200168911-A2.  
 PD 20-SEP-2001.  
 PA (EPiG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44; DB 4; Length 11836;  
 Best Local Similarity 44.8%; Pred. No. 37;  
 RESULT 1287  
 ID ABK28240 standard; DNA; 11836 BP.  
 DE DNA transcriptions associated complementary genomic DNA #57.  
 PN WO200192565-A2.  
 PD 06-DEC-2001.  
 PA (EPiG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44; DB 6; Length 11836;  
 Best Local Similarity 44.6%; Pred. No. 37;  
 RESULT 1288  
 ID AAS46660 standard; DNA; 12578 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #382.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPiG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44; DB 4; Length 12578;  
 Best Local Similarity 43.8%; Pred. No. 38;  
 RESULT 1289  
 ID ABL32487 standard; DNA; 17183 BP.  
 DE Human immune system associated gene SEQ ID NO: 460.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPiG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44; DB 6; Length 17183;  
 Best Local Similarity 44.5%; Pred. No. 39;  
 RESULT 1290  
 ID ABL34608 standard; DNA; 18585 BP.  
 DE Human metastasis associated gene SEQ ID NO: 161.  
 PN WO200177376-A2.  
 PD 18-OCT-2001.  
 PA (EPiG-) EPIGENOMICS AG.  
 Query Match 3.3%; Score 44; DB 6; Length 18585;  
 Best Local Similarity 45.0%; Pred. No. 40;  
 RESULT 1291  
 ID ADS99869 standard; DNA; 18585 BP.  
 DE Bisulphite treated human gene associated with metastasis #81.  
 PN US2003148327-A1.  
 PD 07-AUG-2003.  
 PA (OLEK/) OLEK A.  
 PA (PIEP/) PIEPENBROCK C.  
 PA (BERL/) BERLIN K.  
 Query Match 3.3%; Score 44; DB 7; Length 18585;  
 Best Local Similarity 45.0%; Pred. No. 40;  
 RESULT 1292  
 ID ABD33125 standard; DNA; 58320 BP.  
 DE Human cancer-associated (CA) gene HD07-013.  
 PN WO2004058146-A2.

PD 15-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 3.3%; Score 44; DB 13; Length 58320;  
 Best Local Similarity 50.0%; Pred. No. 47;  
 RESULT 1293  
 ID ABV47167 standard; cDNA; 230 BP.  
 DE Human prostate expression marker cDNA 47158.  
 PN WO200160860-A2.  
 PD 23-AUG-2001.  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
 Query Match 3.3%; Score 43.8; DB 5; Length 230;  
 Best Local Similarity 54.7%; Pred. No. 23;  
 RESULT 1294  
 ID AAX99162 standard; DNA; 516 BP.  
 DE DNA encoding N. meningitidis protein ORF82.  
 PN WO9936544-A2.  
 PD 22-JUL-1999.  
 PA (CHIR-) CHIRON SPA.  
 Query Match 3.3%; Score 43.8; DB 2; Length 516;  
 Best Local Similarity 47.9%; Pred. No. 26;  
 RESULT 1295  
 ID AAA81451 standard; DNA; 516 BP.  
 DE N. meningitidis MenB polynucleotide sequence ORF number 122.  
 PN WO200022430-A2.  
 PD 20-APR-2000.  
 PA (CHIR-) CHIRON CORP.  
 Query Match 3.3%; Score 43.8; DB 3; Length 516;  
 Best Local Similarity 47.9%; Pred. No. 26;  
 RESULT 1296  
 ID AAX99163 standard; DNA; 729 BP.  
 DE DNA encoding N. meningitidis protein ORF82-1.  
 PN WO9936544-A2.  
 PD 22-JUL-1999.  
 PA (CHIR-) CHIRON SPA.  
 Query Match 3.3%; Score 43.8; DB 2; Length 729;  
 Best Local Similarity 47.9%; Pred. No. 27;  
 RESULT 1297  
 ID AAX99164 standard; DNA; 729 BP.  
 DE DNA encoding N. meningitidis protein ORF82a.  
 PN WO9936544-A2.  
 PD 22-JUL-1999.  
 PA (CHIR-) CHIRON SPA.  
 Query Match 3.3%; Score 43.8; DB 2; Length 729;  
 Best Local Similarity 47.9%; Pred. No. 27;  
 RESULT 1298  
 ID AAV19304 standard; cDNA; 889 BP.  
 DE Human p26 cDNA sequence.  
 PN JP09299092-A.  
 PD 25-NOV-1997.  
 PA (TAXE-) TAKEDA CHEM IND LTD.  
 Query Match 3.3%; Score 43.8; DB 2; Length 889;  
 Best Local Similarity 81.0%; Pred. No. 28;  
 RESULT 1299  
 ID AAC75917 standard; cDNA; 1501 BP.  
 DE Human ORFX ORF1472 polynucleotide sequence SEQ ID NO:2943.  
 PN WO200058473-A2.  
 PD 05-OCT-2000.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 3.3%; Score 43.8; DB 3; Length 1501;  
 Best Local Similarity 60.5%; Pred. No. 30;  
 RESULT 1300  
 ID ABL56222 standard; DNA; 2619 BP.  
 DE AmEVF mRNA capping large subunit (AMV135) encoding sequence.  
 PN WO200212526-A2.  
 PD 14-FEB-2002.  
 PA (UYFL) UNIV FLORIDA.  
 Query Match 3.3%; Score 43.8; DB 6; Length 2619;  
 Best Local Similarity 44.2%; Pred. No. 33;  
 RESULT 1301  
 ID ABQ67089 standard; DNA; 3873 BP.  
 DE Human angiogenesis associated polynucleotide SEQ ID NO 119.  
 PN WO200246454-A2.  
 PD 13-JUN-2002.

PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 3873;  
Best Local Similarity 41.6%; Pred. No. 35;  
RESULT 1302  
ID ADS89338 standard; DNA; 4930 BP.  
DE Oligonucleotide of the invention SEQ ID NO:354.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 13; Length 4930;  
Best Local Similarity 47.0%; Pred. No. 36;  
RESULT 1303  
ID AAA70189 standard; DNA; 5454 BP.  
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:322.  
PN WO200205728-A2.  
PD 11-MAY-2000.  
PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Query Match 3.3%; Score 43.8; DB 3; Length 5454;  
Best Local Similarity 44.7%; Pred. No. 36;  
RESULT 1304  
ID AB210144 standard; DNA; 5660 BP.  
DE Haematopoietic cell proliferation disorder related DNA sequence #284.  
PN WO200277272-A2.  
PD 03-OCT-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 8; Length 5660;  
Best Local Similarity 47.4%; Pred. No. 37;  
RESULT 1305  
ID ACP62812 standard; DNA; 5666 BP.  
DE Colon cancer analysis related genomic DNA SEQ ID NO:61.  
PN WO2003014388-A2.  
PD 20-FEB-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 8; Length 5666;  
Best Local Similarity 47.4%; Pred. No. 37;  
RESULT 1306  
ID ADS89495 standard; DNA; 6001 BP.  
DE Oligonucleotide of the invention SEQ ID NO:511.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 13; Length 6001;  
Best Local Similarity 47.0%; Pred. No. 37;  
RESULT 1307  
ID ABK31161 standard; DNA; 6013 BP.  
DE Signal transduction associated gene modified complementary DNA #102.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6013;  
Best Local Similarity 50.2%; Pred. No. 37;  
RESULT 1308  
ID AAS61265 standard; DNA; 6013 BP.  
DE Human gene regulation-associated gene oligonucleotide #220.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6013;  
Best Local Similarity 50.2%; Pred. No. 37;  
RESULT 1309  
ID AAS45311 standard; DNA; 6046 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #8.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 4; Length 6046;  
Best Local Similarity 76.1%; Pred. No. 37;  
RESULT 1310  
ID ABK28150 standard; DNA; 6046 BP.  
DE DNA transcription associated complementary genomic DNA #12.

PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6046;  
Best Local Similarity 76.1%; Pred. No. 37;  
RESULT 1311  
ID ABL54343 standard; DNA; 6059 BP.  
DE Chemically treated apoptosis gene #22.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6059;  
Best Local Similarity 46.8%; Pred. No. 37;  
RESULT 1312  
ID ABL32366 standard; DNA; 6071 BP.  
DE Human immune system associated gene SEQ ID NO: 339.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6071;  
Best Local Similarity 45.6%; Pred. No. 37;  
RESULT 1313  
ID ABL34482 standard; DNA; 6071 BP.  
DE Human metastasis associated gene SEQ ID NO: 35.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6071;  
Best Local Similarity 45.6%; Pred. No. 37;  
RESULT 1314  
ID ABL70153 standard; DNA; 6071 BP.  
DE Chemically treated cell signalling DNA sequence#22.  
PN WO200202807-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6071;  
Best Local Similarity 45.6%; Pred. No. 37;  
RESULT 1315  
ID ADS9743 standard; DNA; 6071 BP.  
DE Bisulphite treated human gene associated with metastasis #18.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 3.3%; Score 43.8; DB 7; Length 6071;  
Best Local Similarity 45.6%; Pred. No. 37;  
RESULT 1316  
ID AAS45465 standard; DNA; 6078 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #85.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 4; Length 6078;  
Best Local Similarity 69.0%; Pred. No. 37;  
RESULT 1317  
ID ABL33890 standard; DNA; 6078 BP.  
DE Human immune system associated gene SEQ ID NO: 1863.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6078;  
Best Local Similarity 69.0%; Pred. No. 37;  
RESULT 1318  
ID ASK28321 standard; DNA; 6078 BP.  
DE DNA transcription associated genomic DNA #98.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6078;  
Best Local Similarity 69.0%; Pred. No. 37;  
RESULT 1319  
ID ABL32177 standard; DNA; 6378 BP.

DE Human immune system associated gene SEQ ID NO: 150.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6378;  
Best Local Similarity 44.5%; Pred. No. 37;  
RESULT 1320  
ID A0Q67028 standard; DNA; 6378 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 58.  
PN WO200246454-A2.  
PD 13-JUN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6378;  
Best Local Similarity 44.5%; Pred. No. 37;  
RESULT 1321  
ID ABL33408 standard; DNA; 6948 BP.  
DE Human immune system associated gene SEQ ID NO: 1381.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6948;  
Best Local Similarity 76.1%; Pred. No. 38;  
RESULT 1322  
ID AAS61229 standard; DNA; 6948 BP.  
DE Human gene regulation-associated gene oligonucleotide #184.  
PN WO200177375-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 6948;  
Best Local Similarity 76.1%; Pred. No. 38;  
RESULT 1323  
ID AAS4335 standard; DNA; 7348 BP.  
DE Tumour suppressor gene derived chemically modified sequence #57.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 4; Length 7348;  
Best Local Similarity 54.7%; Pred. No. 38;  
RESULT 1324  
ID AAS45469 standard; DNA; 8588 BP.  
DE Chemically pretreated complementary DNA associated with cell cycle #87.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 4; Length 8588;  
Best Local Similarity 47.0%; Pred. No. 39;  
RESULT 1325  
ID ABK28325 standard; DNA; 8588 BP.  
DE DNA transcription associated genomic DNA #100.  
PN WO200192565-A2.  
PD 06-DEC-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 8588;  
Best Local Similarity 47.0%; Pred. No. 39;  
RESULT 1326  
ID ADB54240 standard; DNA; 8666 BP.  
DE Pretreated genomic DNA region 164.  
PN WO2003072821-A2.  
PD 04-SEP-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 10; Length 8666;  
Best Local Similarity 47.4%; Pred. No. 39;  
RESULT 1327  
ID ADE84178 standard; DNA; 8666 BP.  
DE Human lymphoid cell proliferative disorder gene derived DNA #114.  
PN WO2003044226-A2.  
PD 30-MAY-2003.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 10; Length 8666;  
Best Local Similarity 47.4%; Pred. No. 39;  
RESULT 1328  
ID ADS89542 standard; DNA; 8666 BP.  
DE Oligonucleotide of the invention SEQ ID NO:558.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 13; Length 8666;  
Best Local Similarity 47.4%; Pred. No. 39;  
RESULT 1329  
ID AAS46394 standard; DNA; 9110 BP.  
DE Tumour suppressor gene derived chemically modified sequence #116.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 4; Length 9110;  
Best Local Similarity 45.7%; Pred. No. 39;  
RESULT 1330  
ID AAS46510 standard; DNA; 12356 BP.  
DE Tumour suppressor gene derived chemically modified sequence #232.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 4; Length 12356;  
Best Local Similarity 44.9%; Pred. No. 41;  
RESULT 1331  
ID ABL32298 standard; DNA; 12507 BP.  
DE Human immune system associated gene SEQ ID NO: 271.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 12507;  
Best Local Similarity 46.6%; Pred. No. 41;  
RESULT 1332  
ID ABL34026 standard; DNA; 17594 BP.  
DE Human immune system associated gene SEQ ID NO: 1999.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.3%; Score 43.8; DB 6; Length 17594;  
Best Local Similarity 43.6%; Pred. No. 43;  
RESULT 1333  
ID AAB81455 standard; DNA; 23532 BP.  
DE N. meningitidis partial DNA sequence gnm\_3 SEQ ID NO:3.  
PN WO20022430-A2.  
PD 20-APR-2000.  
PA (CHIR ) CHIRON CORP.  
Query Match 3.3%; Score 43.8; DB 3; Length 23532;  
Best Local Similarity 47.9%; Pred. No. 45;  
RESULT 1334  
ID AAL03263 standard; DNA; 24977 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 5951.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.3%; Score 43.8; DB 4; Length 24977;  
Best Local Similarity 53.9%; Pred. No. 46;  
RESULT 1335  
ID AAL05788 standard; DNA; 24977 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 8476.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.3%; Score 43.8; DB 4; Length 24977;  
Best Local Similarity 53.9%; Pred. No. 46;  
RESULT 1336  
ID ABL98352 standard; DNA; 24977 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3004.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 3.3%; Score 43.8; DB 4; Length 24977;  
Best Local Similarity 53.9%; Pred. No. 46;  
RESULT 1337  
ID AAL05787 standard; DNA; 24983 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 8475.  
PN WO200155320-A2.



PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.3%; Score 43.8; DB 4; Length 24983;  
RESULT 1338  
ID AAL03262 standard; DNA; 24983 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 5950.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.3%; Score 43.8; DB 4; Length 24983;  
RESULT 1339  
ID ABL98351 standard; DNA; 24983 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3003.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.3%; Score 43.8; DB 4; Length 24983;  
RESULT 1340  
ID AAS33462 standard; DNA; 25715 BP.  
DE DNA encoding human secreted protein, Seq ID No 745.  
PN WO200155326-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.3%; Score 43.8; DB 4; Length 25715;  
RESULT 1341  
ID AAG97397 standard; DNA; 25587 BP.  
DE Human cancer associated sequence HD08-043, SEQ ID 374.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match  
Best Local Similarity 3.3%; Score 43.8; DB 12; Length 225587;  
RESULT 1344  
ID ADQ59440 standard; DNA; 347814 BP.  
DE Human cancer-associated (CA) gene sequence SEQ ID NO:76.  
PN WO2004058288-A1.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match  
Best Local Similarity 3.3%; Score 43.8; DB 12; Length 347814;  
RESULT 1345  
ID AAF21610 standard; DNA; 349980 BP.  
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:111.  
PN WO20066791-A1.  
PD 09-NOV-2000.  
PA (CHIR) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Query Match  
Best Local Similarity 3.3%; Score 43.8; DB 3; Length 349980;  
RESULT 1346  
ID ABX45169 standard; CDNA; 228 BP.  
DE Bovine EST associated with lactation/muscle/fat deposition #10334.  
PN US2002137139-A1.  
PD 26-SEP-2002.  
PA (BYAT) BYATT J C.  
PA (MATH) MATHIALAGAN N.  
PA (TAON) TAO N.  
PA (WARR) WARREN W C.  
Query Match  
Best Local Similarity 3.2%; Score 43.6; DB 8; Length 228;  
RESULT 1347  
ID ADL36867 standard; DNA; 293 BP.  
DE Human ovarian cancer DNA marker #10757.

PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 3.2%; Score 43.6; DB 5; Length 293;  
RESULT 1348  
ID ADI71712 standard; DNA; 293 BP.  
DE Human ovarian cancer DNA marker #4454.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match  
Best Local Similarity 3.2%; Score 43.6; DB 5; Length 293;  
RESULT 1349  
ID ACN63020 standard; CDNA; 396 BP.  
DE Cotton carpel wall/septum EST Clone ID: LIB3831-002-Q1-N6-A7, SEQ:17801.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK) DEIKMAN J.  
PA (FENG) FENG P C C.  
PA (FINC) FINCHER K L.  
PA (ZIEG) ZIEGLER T E.  
Query Match  
Best Local Similarity 3.2%; Score 43.6; DB 13; Length 396;  
RESULT 1350  
ID ACN53005 standard; CDNA; 569 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-020-Q1-N6-E7, SEQ:7786.  
PN US2004123340-A1.  
PD 24-JUN-2004.  
PA (DEIK) DEIKMAN J.  
PA (FENG) FENG P C C.  
PA (FINC) FINCHER K L.  
PA (ZIEG) ZIEGLER T E.  
Query Match  
Best Local Similarity 3.2%; Score 43.6; DB 13; Length 569;  
RESULT 1351  
ID AAH33135 standard; CDNA; 858 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:191.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.2%; Score 43.6; DB 4; Length 858;  
RESULT 1352  
ID ADQ23789 standard; DNA; 2116 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6609.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match  
Best Local Similarity 3.2%; Score 43.6; DB 12; Length 2116;  
RESULT 1353  
ID ASL18982 standard; DNA; 2279 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 8419.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match  
Best Local Similarity 3.2%; Score 43.6; DB 4; Length 2279;  
RESULT 1354  
ID AAS27049 standard; CDNA; 2418 BP.  
DE cDNA encoding novel signal transduction pathway protein, Seq ID 84.  
PN WO200154733-A1.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match  
Best Local Similarity 3.2%; Score 43.6; DB 4; Length 2418;  
RESULT 1355  
ID ADB93227 standard; CDNA; 2418 BP.  
DE Human cDNA encoding a novel protein #74.  
PN US2002168711-A1.  
PD 14-NOV-2002.  
PA (ROSE) ROSEN C A.

PA (RUBE/) RUBEN S M.  
 Query Match 3.2%; Score 43.6; DB 10; Length 2418;  
 Best Local Similarity 67.8%; Pred. No. 35;  
 RESULT 1356  
 ID ADH41462 standard; DNA; 3345 BP.  
 DE Novel human nucleic acid NOV3a.  
 PN WO2003102159-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 3.2%; Score 43.6; DB 12; Length 3345;  
 Best Local Similarity 49.1%; Pred. No. 37;  
 RESULT 1357  
 ID ADH41498 standard; DNA; 3345 BP.  
 DE Novel human nucleic acid NOV3b.  
 PN WO2003102159-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 3.2%; Score 43.6; DB 12; Length 3345;  
 Best Local Similarity 49.1%; Pred. No. 37;  
 RESULT 1358  
 ID ADH41494 standard; DNA; 3345 BP.  
 DE Novel human nucleic acid NOV3q.  
 PN WO2003102159-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 3.2%; Score 43.6; DB 12; Length 3345;  
 Best Local Similarity 49.1%; Pred. No. 37;  
 RESULT 1359  
 ID ADH41496 standard; DNA; 3345 BP.  
 DE Novel human nucleic acid NOV3r.  
 PN WO2003102159-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 3.2%; Score 43.6; DB 12; Length 3345;  
 Best Local Similarity 49.1%; Pred. No. 37;  
 RESULT 1360  
 ID ADH41492 standard; DNA; 3345 BP.  
 DE Novel human nucleic acid NOV3p.  
 PN WO2003102159-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Query Match 3.2%; Score 43.6; DB 12; Length 3345;  
 Best Local Similarity 49.1%; Pred. No. 37;  
 RESULT 1361  
 ID ABL32329 standard; DNA; 5742 BP.  
 DE Human immune system associated gene SEQ ID NO: 302.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 5742;  
 Best Local Similarity 42.8%; Pred. No. 40;  
 RESULT 1362  
 ID AAS61080 standard; DNA; 6092 BP.  
 DE Human gene regulation-associated gene oligonucleotide #35.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 6092;  
 Best Local Similarity 45.5%; Pred. No. 41;  
 RESULT 1363  
 ID ABL4326 standard; DNA; 5583 BP.  
 DE Human polynucleotide associated with DNA replication SEQ ID NO 26.  
 PN WO200177377-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 6583;  
 Best Local Similarity 44.1%; Pred. No. 41;  
 RESULT 1364  
 ID ABL32791 standard; DNA; 6636 BP.  
 DE Human immune system associated gene SEQ ID NO: 764.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.

PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 6636;  
 Best Local Similarity 42.6%; Pred. No. 41;  
 RESULT 1365  
 ID ABL32739 standard; DNA; 6759 BP.  
 DE Human immune system associated gene SEQ ID NO: 712.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 6759;  
 Best Local Similarity 50.9%; Pred. No. 41;  
 RESULT 1366  
 ID ABL33929 standard; DNA; 6801 BP.  
 DE Human immune system associated gene SEQ ID NO: 1902.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 6801;  
 Best Local Similarity 49.0%; Pred. No. 41;  
 RESULT 1367  
 ID ABL92291 standard; DNA; 6801 BP.  
 DE Chemically treated DNA repair gene fragment complementary to#50.  
 PN WO200181622-A2.  
 PD 01-NOV-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 6801;  
 Best Local Similarity 49.0%; Pred. No. 41;  
 RESULT 1368  
 ID ABL49362 standard; DNA; 6801 BP.  
 DE Human polynucleotide associated with DNA replication SEQ ID NO 62.  
 PN WO200177377-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 6801;  
 Best Local Similarity 49.0%; Pred. No. 41;  
 RESULT 1369  
 ID ABL32979 standard; DNA; 6963 BP.  
 DE Human immune system associated gene SEQ ID NO: 952.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 6963;  
 Best Local Similarity 44.7%; Pred. No. 41;  
 RESULT 1370  
 ID ABL32982 standard; DNA; 7143 BP.  
 DE Human immune system associated gene SEQ ID NO: 955.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 7143;  
 Best Local Similarity 61.4%; Pred. No. 42;  
 RESULT 1371  
 ID AAQ55138 standard; DNA; 8654 BP.  
 DE Staphylococcus epidermidis probe SE-22.  
 PN WO9401583-A1.  
 PD 20-JAN-1994.  
 PA (FUSO ) FUSO PHARM IND LTD.  
 Query Match 3.2%; Score 43.6; DB 2; Length 8654;  
 Best Local Similarity 46.9%; Pred. No. 43;  
 RESULT 1372  
 ID ABZ77353 standard; DNA; 8654 BP.  
 DE Nucleotide sequence designated SE-22.  
 PN WO2002101037-A1.  
 PD 19-DEC-2002.  
 PA (FUSO ) FUSO PHARM IND LTD.  
 Query Match 3.2%; Score 43.6; DB 8; Length 8654;  
 Best Local Similarity 46.9%; Pred. No. 43;  
 RESULT 1373  
 ID AAL51841 standard; DNA; 8654 BP.  
 DE Staphylococcus epidermidis microbe identification-related DNA sequence 1.  
 PN WO200299133-A1.  
 PD 12-DEC-2002.  
 PA (FUSO ) FUSO PHARM IND LTD.

PA (OHNO/) OHNO T.  
 Query Match 3.2%; Score 43.6; DB 10; Length 8654;  
 Best Local Similarity 46.9%; Pred. No. 43;  
 RESULT 1374  
 ID ABL32910 standard; DNA; 8946 BP.  
 DE Human immune system associated gene SEQ ID NO: 883.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 8946;  
 Best Local Similarity 55.2%; Pred. No. 43;  
 RESULT 1375  
 ID ABL32656 standard; DNA; 9832 BP.  
 DE Human immune system associated gene SEQ ID NO: 629.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 9832;  
 Best Local Similarity 45.8%; Pred. No. 44;  
 RESULT 1376  
 ID ABL33545 standard; DNA; 10328 BP.  
 DE Human immune system associated gene SEQ ID NO: 1518.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 10328;  
 Best Local Similarity 57.2%; Pred. No. 44;  
 RESULT 1377  
 ID ABL32605 standard; DNA; 11155 BP.  
 DE Human immune system associated gene SEQ ID NO: 578.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 11155;  
 Best Local Similarity 44.6%; Pred. No. 45;  
 RESULT 1378  
 ID ABL32343 standard; DNA; 11534 BP.  
 DE Human immune system associated gene SEQ ID NO: 316.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 11534;  
 Best Local Similarity 45.4%; Pred. No. 45;  
 RESULT 1379  
 ID ABL34071 standard; DNA; 13503 BP.  
 DE Human immune system associated gene SEQ ID NO: 2044.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 13503;  
 Best Local Similarity 46.6%; Pred. No. 46;  
 RESULT 1380  
 ID ABL70543 standard; DNA; 15649 BP.  
 DE Chemically treated cell signalling DNA sequence#217.  
 PN WO200202807-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 15649;  
 Best Local Similarity 45.7%; Pred. No. 47;  
 RESULT 1381  
 ID ABL79985 standard; DNA; 16633 BP.  
 DE Human chemically modified disease associated gene SEQ ID NO 2.  
 PN WO200200927-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.6; DB 6; Length 16633;  
 Best Local Similarity 42.2%; Pred. No. 47;  
 RESULT 1382  
 ID AA230355 standard; DNA; 19966 BP.  
 DE Nucleotide sequence of the eps operon of S. thermophilus Sfi39.  
 PN WO9954475-A2.  
 PD 28-OCT-1999.  
 PA (NEST ) SOC PROD NESTLE SA.

Query Match 3.2%; Score 43.6; DB 3; Length 19966;  
 Best Local Similarity 44.9%; Pred. No. 49;  
 RESULT 1383  
 ID AA245258 standard; DNA; 19966 BP.  
 DE DNA encoding enzymes involved in exopolysaccharide biosynthesis.  
 PN WO9962316-A2.  
 PD 09-DEC-1999.  
 PA (NEST ) SOC PROD NESTLE SA.  
 Query Match 3.2%; Score 43.6; DB 3; Length 19966;  
 Best Local Similarity 44.9%; Pred. No. 49;  
 RESULT 1384  
 ID ABD33520 standard; DNA; 34722 BP.  
 DE Human cancer-associated (CA) gene HD07-102.  
 PN WO2004058146-A2.  
 PD 15-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Query Match 3.2%; Score 43.6; DB 13; Length 34722;  
 Best Local Similarity 44.4%; Pred. No. 53;  
 RESULT 1385  
 ID ACC79619 standard; DNA; 71843 BP.  
 DE Zebrafish protein kinase C lambda related genomic DNA SEQ ID NO:3.  
 PN WO2003023048-A2.  
 PD 20-MAR-2003.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Query Match 3.2%; Score 43.6; DB 8; Length 71843;  
 Best Local Similarity 33.7%; Pred. No. 59;  
 RESULT 1386  
 ID ABX47508 standard; CDNA; 277 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #12673.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 3.2%; Score 43.4; DB 8; Length 277;  
 Best Local Similarity 56.7%; Pred. No. 28;  
 RESULT 1387  
 ID ABX45291 standard; CDNA; 439 BP.  
 DE Bovine EST associated with lactation/muscle/fat deposition #10456.  
 PN US2002137139-A1.  
 PD 26-SEP-2002.  
 PA (BYAT/) BYATT J C.  
 PA (MATH/) MATHIALAGAN N.  
 PA (TAON/) TAO N.  
 PA (WARR/) WARREN W C.  
 Query Match 3.2%; Score 43.4; DB 8; Length 439;  
 Best Local Similarity 60.7%; Pred. No. 30;  
 RESULT 1388  
 ID ADT96917 standard; CDNA; 440 BP.  
 DE Colon cancer associated human cDNA sequence #2424.  
 PN US2003087818-A1.  
 PD 08-MAY-2003.  
 PA (CORI-) CORIXA CORP.  
 Query Match 3.2%; Score 43.4; DB 11; Length 440;  
 Best Local Similarity 51.7%; Pred. No. 30;  
 RESULT 1389  
 ID ADR61743 standard; CDNA; 649 BP.  
 DE Cotton cDNA sequence, SEQ ID 2524.  
 PN US2004181830-A1.  
 PD 16-SEP-2004.  
 PA (KOVA/) KOVALIC D K.  
 PA (ZHOU/) ZHOU Y.  
 PA (CAOY/) CAO Y.  
 Query Match 3.2%; Score 43.4; DB 13; Length 649;  
 Best Local Similarity 49.3%; Pred. No. 32;  
 RESULT 1390  
 ID AAF72814 standard; DNA; 776 BP.  
 DE Secreted protein gene #16.  
 PN WO200107459-A1.  
 PD 01-FEB-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 3.2%; Score 43.4; DB 4; Length 776;

Best Local Similarity 62.4%; Pred. No. 33;  
RESULT 1391  
ID ABL34290 standard; DNA; 1701 BP.  
DE Human immune system associated gene SEQ ID NO: 2263.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 1701;  
Best Local Similarity 43.7%; Pred. No. 37;  
RESULT 1392  
ID AAA16635 standard; cDNA; 1759 BP.  
DE Human secreted protein clone rd610\_1 nucleotide sequence SEQ ID NO:35.  
PN WO200009552-A1.  
PD 24-FEB-2000.  
PA (GEM) GENETICS INST INC.  
Query Match 3.2%; Score 43.4; DB 3; Length 1759;  
Best Local Similarity 51.4%; Pred. No. 37;  
RESULT 1393  
ID AAC77031 standard; cDNA; 2060 BP.  
DE Human ORFX ORF2586 polynucleotide sequence SEQ ID NO:5171.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 3.2%; Score 43.4; DB 3; Length 2060;  
Best Local Similarity 47.3%; Pred. No. 38;  
RESULT 1394  
ID AAH54753 standard; DNA; 3167 BP.  
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4117.  
PN WO200134809-A2.  
PD 17-MAY-2001.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 3.2%; Score 43.4; DB 4; Length 3167;  
Best Local Similarity 46.3%; Pred. No. 40;  
RESULT 1395  
ID AAH54912 standard; DNA; 3241 BP.  
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:4276.  
PN WO200134809-A2.  
PD 17-MAY-2001.  
PA (GLAX) GLAXO GROUP LTD.  
Query Match 3.2%; Score 43.4; DB 4; Length 3241;  
Best Local Similarity 46.3%; Pred. No. 41;  
RESULT 1396  
ID ABX71421 standard; cDNA; 3353 BP.  
DE Human testes-derived cDNA from clone DKFZphes3\_7j38.  
PN WO200112659-A2.  
PD 22-FEB-2001.  
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.  
Query Match 3.2%; Score 43.4; DB 5; Length 3353;  
Best Local Similarity 55.7%; Pred. No. 41;  
RESULT 1397  
ID ADQ24431 standard; DNA; 3373 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7251.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 3.2%; Score 43.4; DB 12; Length 3373;  
Best Local Similarity 47.3%; Pred. No. 41;  
RESULT 1398  
ID AAS46376 standard; DNA; 5278 BP.  
DE Tumour suppressor gene derived chemically modified sequence #98.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 4; Length 5278;  
Best Local Similarity 44.9%; Pred. No. 44;  
RESULT 1399  
ID ABL32823 standard; DNA; 5278 BP.  
DE Human immune system associated gene SEQ ID NO: 796.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 5278;  
Best Local Similarity 44.9%; Pred. No. 44;

RESULT 1400  
ID ABL33790 standard; DNA; 5324 BP.  
DE Human immune system associated gene SEQ ID NO: 1763.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 5324;  
Best Local Similarity 44.2%; Pred. No. 44;  
RESULT 1401  
ID AAQ11710 standard; DNA; 5852 BP.  
DE Dictyostellium plasmid Ddp2 containing Rep gene.  
PN WO9106644-A.  
PD 16-MAY-1991.  
PA (UYMA-) UNIV MACQUARIE.  
Query Match 3.2%; Score 43.4; DB 2; Length 5852;  
Best Local Similarity 46.7%; Pred. No. 44;  
RESULT 1402  
ID ABL33826 standard; DNA; 6204 BP.  
DE Human immune system associated gene SEQ ID NO: 1799.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 6204;  
Best Local Similarity 45.5%; Pred. No. 45;  
RESULT 1403  
ID ABL33873 standard; DNA; 6270 BP.  
DE Human immune system associated gene SEQ ID NO: 1846.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 6270;  
Best Local Similarity 48.6%; Pred. No. 45;  
RESULT 1404  
ID ABL32155 standard; DNA; 6681 BP.  
DE Human immune system associated gene SEQ ID NO: 128.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 6681;  
Best Local Similarity 46.8%; Pred. No. 45;  
RESULT 1405  
ID ABL54304 standard; DNA; 6681 BP.  
DE Chemically treated apoptosis gene complementary to gene #2.  
PN WO200177164-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 6681;  
Best Local Similarity 46.8%; Pred. No. 45;  
RESULT 1406  
ID ABL33487 standard; DNA; 6831 BP.  
DE Human immune system associated gene SEQ ID NO: 1460.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 6831;  
Best Local Similarity 47.3%; Pred. No. 45;  
RESULT 1407  
ID AAS45496 standard; DNA; 7038 BP.  
DE Chemically pretreated genomic DNA associated with cell cycle #101.  
PN WO200168911-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 4; Length 7038;  
Best Local Similarity 47.0%; Pred. No. 46;  
RESULT 1408  
ID ABL34097 standard; DNA; 7038 BP.  
DE Human immune system associated gene SEQ ID NO: 2070.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 7038;  
Best Local Similarity 47.0%; Pred. No. 46;  
RESULT 1409

ID ABX28426 standard; DNA; 7038 BP.  
 DE DNA transcription associated complementary genomic DNA #150.  
 PN WO200192565-A2.  
 PD 06-DEC-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.4; DB 6; Length 7038;  
 Best Local Similarity 47.0%; Pred. No. 46;  
 RESULT 1410  
 ID ABL32483 standard; DNA; 7134 BP.  
 DE Human immune system associated gene SEQ ID NO: 456.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.4; DB 6; Length 7134;  
 Best Local Similarity 44.0%; Pred. No. 46;  
 RESULT 1411  
 ID ABL32746 standard; DNA; 7384 BP.  
 DE Human immune system associated gene SEQ ID NO: 719.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.4; DB 6; Length 7384;  
 Best Local Similarity 51.0%; Pred. No. 46;  
 RESULT 1412  
 ID ABK39955 standard; DNA; 8076 BP.  
 DE Human chemically pretreated gene sequence #18 strand 2.  
 PN WO200202806-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.4; DB 6; Length 8076;  
 Best Local Similarity 43.8%; Pred. No. 47;  
 RESULT 1413  
 ID ABK39957 standard; DNA; 8136 BP.  
 DE Human chemically pretreated gene sequence #19 strand 2.  
 PN WO200202806-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.4; DB 6; Length 8136;  
 Best Local Similarity 43.8%; Pred. No. 47;  
 RESULT 1414  
 ID ABL32555 standard; DNA; 8136 BP.  
 DE Human immune system associated gene SEQ ID NO: 528.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.4; DB 6; Length 8136;  
 Best Local Similarity 43.8%; Pred. No. 47;  
 RESULT 1415  
 ID AAS46801 standard; DNA; 8237 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #527.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.4; DB 4; Length 8237;  
 Best Local Similarity 43.5%; Pred. No. 47;  
 RESULT 1416  
 ID AAO55138 standard; DNA; 8654 BP.  
 DE Staphylococcus epidermidis probe SE-22.  
 PN WO9401583-A1.  
 PD 20-JAN-1994.  
 PA (FUSO) FUSO PHARM IND LTD.  
 Query Match 3.2%; Score 43.4; DB 2; Length 8654;  
 Best Local Similarity 44.6%; Pred. No. 47;  
 RESULT 1417  
 ID ABZ77353 standard; DNA; 8654 BP.  
 DE Nucleotide sequence designated SE-22.  
 PN WO2002101037-A1.  
 PD 19-DEC-2002.  
 PA (FUSO) FUSO PHARM IND LTD.  
 Query Match 3.2%; Score 43.4; DB 8; Length 8654;  
 Best Local Similarity 44.6%; Pred. No. 47;  
 RESULT 1418  
 ID AAL51841 standard; DNA; 8654 BP.

DE Staphylococcus epidermidis microbe identification-related DNA sequence 1.  
 PN WO200299133-A1.  
 PD 12-DEC-2002.  
 PA (FUSO) FUSO PHARM IND LTD.  
 Query Match 3.2%; Score 43.4; DB 10; Length 8654;  
 Best Local Similarity 44.6%; Pred. No. 47;  
 RESULT 1419  
 ID ABL33512 standard; DNA; 11092 BP.  
 DE Human immune system associated gene SEQ ID NO: 1485.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.4; DB 6; Length 11092;  
 Best Local Similarity 53.9%; Pred. No. 49;  
 RESULT 1420  
 ID ABK28331 standard; DNA; 11745 BP.  
 DE DNA transcription associated genomic DNA #103.  
 PN WO200192565-A2.  
 PD 06-DEC-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.4; DB 6; Length 11745;  
 Best Local Similarity 42.0%; Pred. No. 49;  
 RESULT 1421  
 ID ABL33749 standard; DNA; 11805 BP.  
 DE Human immune system associated gene SEQ ID NO: 1722.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43.4; DB 6; Length 11805;  
 Best Local Similarity 47.0%; Pred. No. 49;  
 RESULT 1422  
 ID AAL37611 standard; DNA; 12003 BP.  
 DE Human musculoskeletal system related polynucleotide SEQ ID NO 3976.  
 PN WO200155367-A1.  
 PD 02-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 3.2%; Score 43.4; DB 4; Length 12003;  
 Best Local Similarity 45.1%; Pred. No. 49;  
 RESULT 1423  
 ID ABX60599 standard; cDNA; 12003 BP.  
 DE cDNA encoding novel human musculoskeletal system antigen #2943.  
 PN US2002147140-A1.  
 PD 10-OCT-2002.  
 PA (ROSE/) ROSEN C A.  
 PA (RUBE/) RUBEN S M.  
 PA (BARA/) BARASH S C.  
 Query Match 3.2%; Score 43.4; DB 8; Length 12003;  
 Best Local Similarity 45.1%; Pred. No. 49;  
 RESULT 1424  
 ID ADJ31349 standard; DNA; 12003 BP.  
 DE Human musculoskeletal system-associated genomic DNA - SEQ ID 3976.  
 PN US2004009488-A1.  
 PD 15-JAN-2004.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Query Match 3.2%; Score 43.4; DB 12; Length 12003;  
 Best Local Similarity 45.1%; Pred. No. 49;  
 RESULT 1425  
 ID ADN41630 standard; DNA; 12003 BP.  
 DE Novel human secreted protein polynucleotide seqid 752.  
 PN US2004044191-A1.  
 PD 04-MAR-2004.  
 PA (FISC/) FISCHER C L.  
 PA (ROSE/) ROSEN C A.  
 PA (SOPP/) SOPPET D R.  
 PA (RUBE/) RUBEN S M.  
 PA (KYAW/) KYAW H.  
 PA (LIYY/) LI Y.  
 PA (ZENG/) ZENG Z.  
 PA (LAFI/) LAFLEUR D W.  
 PA (MOOR/) MOORE P A.  
 PA (SHIY/) SHI Y.  
 PA (OLSE/) OLSEN H.

PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E. 3.2%; Score 43.4; DB 12; Length 12003;  
Query Match 45.1%; Pred. No. 49;  
Best Local Similarity  
RESULT 1426  
ID ABK40062 standard; DNA; 13784 BP.  
DE Human chemically pretreated gene sequence #72 strand 2.  
PN WO200202806-A2.  
PD 10-JAN-2002  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 13784;  
Best Local Similarity 45.0%; Pred. No. 50;  
RESULT 1427  
ID ABL32525 standard; DNA; 15861 BP.  
DE Human immune system associated gene SEQ ID NO: 498.  
PN WO200200928-A2.  
PD 03-JAN-2002  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 15861;  
Best Local Similarity 46.6%; Pred. No. 52;  
RESULT 1428  
ID AAS46771 standard; DNA; 17280 BP.  
DE Tumour suppressor gene derived chemically modified sequence #495.  
PN WO200168912-A2.  
PD 20-SEP-2001  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 4; Length 17280;  
Best Local Similarity 44.2%; Pred. No. 52;  
RESULT 1429  
ID ABL33365 standard; DNA; 17893 BP.  
DE Human immune system associated gene SEQ ID NO: 1338.  
PN WO200200928-A2.  
PD 03-JAN-2002  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 17893;  
Best Local Similarity 43.5%; Pred. No. 52;  
RESULT 1430  
ID ABV99730 standard; cDNA; 30350 BP.  
DE Human Ras-like protein encoding cDNA.  
Query Match 3.2%; Score 43.4; DB 8; Length 30350;  
Best Local Similarity 45.1%; Pred. No. 57;  
RESULT 1431  
ID ABQ67005 standard; DNA; 33053 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 35.  
PN WO200246454-A2.  
PD 13-JUN-2002  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.4; DB 6; Length 33053;  
Best Local Similarity 43.6%; Pred. No. 58;  
RESULT 1432  
ID AAL48890 standard; DNA; 53332 BP.  
DE Human Pftaire family kinase gene.  
PN WO200261060-A2.  
PD 08-AUG-2002  
PA (PEKE ) PE CORP NY.  
Query Match 3.2%; Score 43.4; DB 6; Length 53332;  
Best Local Similarity 48.8%; Pred. No. 62;  
RESULT 1433  
ID ADL13931 standard; DNA; 180385 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #463.  
PN WO2003054166-A2.  
PD 03-JUL-2003  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 3.2%; Score 43.4; DB 10; Length 180385;  
Best Local Similarity 45.9%; Pred. No. 74;  
RESULT 1434  
ID ABD32548 standard; DNA; 310268 BP.  
DE Human cancer-associated genomic DNA HD14-033.  
PN WO2004074320-A2.  
PD 02-SEP-2004  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 3.2%; Score 43.4; DB 13; Length 310268;  
Best Local Similarity 49.1%; Pred. No. 81;

RESULT 1435  
ID ACN53869 standard; cDNA; 355 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-B10, SEQ:8650.  
PN US2004123340-A1.  
PD 24-JUN-2004  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 3.2%; Score 43.2; DB 13; Length 355;  
Best Local Similarity 63.5%; Pred. No. 32;  
RESULT 1436  
ID ADI69402 standard; DNA; 528 BP.  
DE Human ovarian cancer DNA marker #2144.  
PN WO200170979-A2.  
PD 27-SEP-2001  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.2%; Score 43.2; DB 5; Length 528;  
Best Local Similarity 56.0%; Pred. No. 34;  
RESULT 1437  
ID ADI75744 standard; DNA; 528 BP.  
DE Human ovarian cancer DNA marker #8486.  
PN WO200170979-A2.  
PD 27-SEP-2001  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.2%; Score 43.2; DB 5; Length 528;  
Best Local Similarity 56.0%; Pred. No. 34;  
RESULT 1438  
ID ACN45220 standard; cDNA; 574 BP.  
DE Cotton primed seed EST Clone ID: LIB3825-002-Q1-N6-A11, SEQ:1.  
PN US2004123340-A1.  
PD 24-JUN-2004  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 3.2%; Score 43.2; DB 13; Length 574;  
Best Local Similarity 63.5%; Pred. No. 34;  
RESULT 1439  
ID ACN52180 standard; cDNA; 599 BP.  
DE Cotton androecium tissue EST Clone ID: LIB3828-012-Q1-N6-B8, SEQ:6961.  
PN US2004123340-A1.  
PD 24-JUN-2004  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FING/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
Query Match 3.2%; Score 43.2; DB 13; Length 599;  
Best Local Similarity 63.5%; Pred. No. 35;  
RESULT 1440  
ID ADR01532 standard; DNA; 782 BP.  
DE A. gossypii genomic DNA PAG1208RP.  
PN US6239264-B1.  
PD 29-MAY-2001  
PA (SYNG-) SYNGENTA PARTICIPATIONS AG.  
Query Match 3.2%; Score 43.2; DB 2; Length 782;  
Best Local Similarity 47.6%; Pred. No. 36;  
RESULT 1441  
ID AAF82249 standard; cDNA; 1220 BP.  
DE Cyclamen dihydroflavono1-4-reductase nucleotide sequence.  
PN JP2001037485-A.  
PD 13-FEB-2001  
PA (HOKK ) HOKKO CHEM IND CO LTD.  
Query Match 3.2%; Score 43.2; DB 4; Length 1220;  
Best Local Similarity 68.2%; Pred. No. 38;  
RESULT 1442  
ID AAN60472 standard; DNA; 4590 BP.  
DE Sequence encoding the ring-infected Erythrocyte Surface Antigen (RESA).  
PN WO8601802-A.  
PD 27-MAR-1986.  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
Query Match 3.2%; Score 43.2; DB 1; Length 4590;  
Best Local Similarity 44.7%; Pred. No. 47;

RESULT 1443  
ID ADS89551 standard; DNA; 5286 BP.  
DE Oligonucleotide of the invention SEQ ID NO:567.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 13; Length 5286;  
Best Local Similarity 46.2%; Pred. No. 48;  
RESULT 1444  
ID ADS89277 standard; DNA; 5286 BP.  
DE Oligonucleotide of the invention SEQ ID NO:293.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 13; Length 5286;  
Best Local Similarity 46.2%; Pred. No. 48;  
RESULT 1445  
ID ABL33676 standard; DNA; 5379 BP.  
DE Human immune system associated gene SEQ ID NO: 1649.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 5379;  
Best Local Similarity 50.5%; Pred. No. 48;  
RESULT 1446  
ID ABL34576 standard; DNA; 5379 BP.  
DE Human metastasis associated gene SEQ ID NO: 129.  
PN WO200177376-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 5379;  
Best Local Similarity 50.5%; Pred. No. 48;  
RESULT 1447  
ID ABL70369 standard; DNA; 5379 BP.  
DE Chemically treated cell signalling DNA sequence#130.  
PN WO200202867-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 5379;  
Best Local Similarity 50.5%; Pred. No. 48;  
RESULT 1448  
ID ADS99837 standard; DNA; 5379 BP.  
DE Bsalphite treated human gene associated with metastasis #65.  
PN US2003148327-A1.  
PD 07-AUG-2003.  
PA (OLEK/) OLEK A.  
PA (PIEP/) PIEPENBROCK C.  
PA (BERL/) BERLIN K.  
Query Match 3.2%; Score 43.2; DB 7; Length 5379;  
Best Local Similarity 50.5%; Pred. No. 48;  
RESULT 1449  
ID ABL32101 standard; DNA; 5728 BP.  
DE Human immune system associated gene SEQ ID NO: 74.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 5728;  
Best Local Similarity 46.4%; Pred. No. 49;  
RESULT 1450  
ID ABL32891 standard; DNA; 6131 BP.  
DE Human immune system associated gene SEQ ID NO: 864.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 6131;  
Best Local Similarity 43.2%; Pred. No. 49;  
RESULT 1451  
ID ABL33010 standard; DNA; 6171 BP.  
DE Human immune system associated gene SEQ ID NO: 983.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 6171;  
Best Local Similarity 45.7%; Pred. No. 53;  
Best Local Similarity 44.3%; Pred. No. 49;  
RESULT 1452  
ID ABL32960 standard; DNA; 6255 BP.  
DE Human immune system associated gene SEQ ID NO: 933.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 6255;  
Best Local Similarity 48.1%; Pred. No. 49;  
RESULT 1453  
ID ADQ24856 standard; DNA; 6816 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7676.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 3.2%; Score 43.2; DB 12; Length 6816;  
Best Local Similarity 36.4%; Pred. No. 50;  
RESULT 1454  
ID ABL34145 standard; DNA; 7076 BP.  
DE Human immune system associated gene SEQ ID NO: 2118.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 7076;  
Best Local Similarity 45.7%; Pred. No. 50;  
RESULT 1455  
ID ABL32401 standard; DNA; 7167 BP.  
DE Human immune system associated gene SEQ ID NO: 374.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 7167;  
Best Local Similarity 42.3%; Pred. No. 50;  
RESULT 1456  
ID ABL32028 standard; DNA; 7351 BP.  
DE Human immune system associated gene SEQ ID NO: 1.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 7351;  
Best Local Similarity 46.1%; Pred. No. 50;  
RESULT 1457  
ID ABL34152 standard; DNA; 9255 BP.  
DE Human immune system associated gene SEQ ID NO: 2125.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 9255;  
Best Local Similarity 47.6%; Pred. No. 52;  
RESULT 1458  
ID AAS63354 standard; DNA; 9265 BP.  
DE Chemically pretreated metabolism associated gene #49.  
PN WO200176451-A2.  
PD 18-OCT-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 9265;  
Best Local Similarity 47.6%; Pred. No. 52;  
RESULT 1459  
ID ABL33689 standard; DNA; 9646 BP.  
DE Human immune system associated gene SEQ ID NO: 1662.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 9646;  
Best Local Similarity 46.2%; Pred. No. 52;  
RESULT 1460  
ID AEN80083 standard; DNA; 10250 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 100.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 10250;  
Best Local Similarity 45.7%; Pred. No. 53;

RESULT 1461  
ID ABL34135 standard; DNA; 10886 BP.  
DE Human immune system associated gene SEQ ID NO: 2108.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 10886;  
Best Local Similarity 43.2%; Pred. No. 53;  
RESULT 1462  
ID AAS46471 standard; DNA; 12269 BP.  
DE Tumour suppressor gene derived chemically modified sequence #193.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 4; Length 12269;  
Best Local Similarity 48.1%; Pred. No. 54;  
RESULT 1463  
ID ABL33410 standard; DNA; 12269 BP.  
DE Human immune system associated gene SEQ ID NO: 1383.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 6; Length 12269;  
Best Local Similarity 48.1%; Pred. No. 54;  
RESULT 1464  
ID ABL56202 standard; DNA; 50000 BP.  
DE AnePV genome fragment#4.  
PN WO200212526-A2.  
PD 14-FEB-2002.  
PA (UVFL) UNIV FLORIDA.  
Query Match 3.2%; Score 43.2; DB 6; Length 50000;  
Best Local Similarity 43.6%; Pred. No. 67;  
RESULT 1465  
ID AAS46794 standard; DNA; 56153 BP.  
DE Tumour suppressor gene derived chemically modified sequence #520.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43.2; DB 4; Length 56153;  
Best Local Similarity 44.7%; Pred. No. 68;  
RESULT 1466  
Query Match 3.2%; Score 43.2; DB 2; Length 110000;  
Best Local Similarity 45.8%; Pred. No. 76;  
RESULT 1467  
ID ACN44998 standard; DNA; 122614 BP.  
DE Human genomic sequence hCG29191.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Query Match 3.2%; Score 43.2; DB 11; Length 122614;  
Best Local Similarity 46.0%; Pred. No. 77;  
RESULT 1468  
ID ADO47190 standard; DNA; 200000 BP.  
DE DNA sequence of a human immunoglobulin heavy chain variable region.  
PN WO2004029249-A1.  
PD 08-APR-2004.  
PA (CENT-) CENTENARY INST CANCER MEDICINE & CELL BI.  
Query Match 3.2%; Score 43.2; DB 12; Length 200000;  
Best Local Similarity 58.6%; Pred. No. 83;  
RESULT 1469  
ID AAL76073 standard; DNA; 51 BP.  
DE Human silent SNP containing nucleic acid SEQ:3014.  
PN WO200140521-A2.  
PD 07-JUN-2001.  
PA (CURA-) CURAGEN CORP.  
Query Match 3.2%; Score 43; DB 4; Length 51;  
Best Local Similarity 90.2%; Pred. No. 26;  
RESULT 1470  
ID ADI73348 standard; DNA; 291 BP.  
DE Human ovarian cancer DNA marker #6090.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 3.2%; Score 43; DB 5; Length 291;  
Best Local Similarity 48.8%; Pred. No. 34;  
RESULT 1471  
ID ADL38479 standard; DNA; 291 BP.  
DE Human ovarian cancer DNA marker #12369.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.2%; Score 43; DB 5; Length 291;  
Best Local Similarity 48.8%; Pred. No. 34;  
RESULT 1472  
ID AAI91325 standard; cDNA; 412 BP.  
DE Human polynucleotide SEQ ID NO 11385.  
PN WO200164835-A2.  
PD 07-SEP-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 3.2%; Score 43; DB 4; Length 412;  
Best Local Similarity 69.9%; Pred. No. 36;  
RESULT 1473  
ID ADL43533 standard; DNA; 492 BP.  
DE Human ovarian cancer DNA marker #17423.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.2%; Score 43; DB 5; Length 492;  
Best Local Similarity 54.8%; Pred. No. 37;  
RESULT 1474  
ID ABV46528 standard; cDNA; 563 BP.  
DE Human prostate expression marker cDNA 46519.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.2%; Score 43; DB 5; Length 563;  
Best Local Similarity 62.0%; Pred. No. 38;  
RESULT 1475  
ID ADL37093 standard; DNA; 714 BP.  
DE Human ovarian cancer DNA marker #10983.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.2%; Score 43; DB 5; Length 714;  
Best Local Similarity 50.0%; Pred. No. 39;  
RESULT 1476  
ID ADI71942 standard; DNA; 714 BP.  
DE Human ovarian cancer DNA marker #4684.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Query Match 3.2%; Score 43; DB 5; Length 714;  
Best Local Similarity 50.0%; Pred. No. 39;  
RESULT 1477  
ID AAN93084 standard; cDNA; 857 BP.  
DE Lambda gt 11 pl(13T) contg. cDNA encoding Der p I antigen.  
PN WO8810297-A.  
PD 29-DEC-1988.  
PA (PRIN-) PRINCESS MARGARET CHILD.  
PA (LUDW-) LUDWIG INST CANCER RES.  
PA (HALL-) HALL W & E INST MED RES.  
Query Match 3.2%; Score 43; DB 1; Length 857;  
Best Local Similarity 60.8%; Pred. No. 40;  
RESULT 1478  
ID ADO25281 standard; DNA; 1129 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 8101.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 3.2%; Score 43; DB 12; Length 1129;  
Best Local Similarity 64.6%; Pred. No. 42;  
RESULT 1479  
ID AAZ99724 standard; cDNA; 4137 BP.  
DE cDNA encoding human cardiovascular system associated protein kinase-1.  
PN WO200014212-A1.  
PD 16-MAR-2000.



PA (MILL-) MILLENNIUM PHARM INC.  
 Query Match 3.2%; Score 43; DB 3; Length 4137;  
 Best Local Similarity 45.7%; Pred. No. 51;  
 RESULT 1480  
 ID ADC51563 standard; DNA; 4176 BP.  
 DE Schizosaccharomyces pombe alpha-glucosidase coding sequence.  
 PN JP2003088365-A.  
 PD 25-MAR-2003.  
 PA (NTSO) NIPPON SHOKUHN KAKO KK.  
 Query Match 3.2%; Score 43; DB 10; Length 4176;  
 Best Local Similarity 73.3%; Pred. No. 51;  
 RESULT 1481  
 ID ABL32636 standard; DNA; 5308 BP.  
 DE Human immune system associated gene SEQ ID NO: 609.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 5308;  
 Best Local Similarity 45.1%; Pred. No. 53;  
 RESULT 1482  
 ID ABK31164 standard; DNA; 6133 BP.  
 DE Signal transduction associated gene modified DNA #4.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 6133;  
 Best Local Similarity 47.3%; Pred. No. 54;  
 RESULT 1483  
 ID ABL70503 standard; DNA; 6133 BP.  
 DE Chemically treated cell signalling DNA sequence#197.  
 PN WO200202807-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 6133;  
 Best Local Similarity 47.3%; Pred. No. 54;  
 RESULT 1484  
 ID AAS61051 standard; DNA; 6133 BP.  
 DE Human gene regulation-associated gene oligonucleotide #6.  
 PN WO200177375-A2.  
 PD 18-OCT-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 6133;  
 Best Local Similarity 47.3%; Pred. No. 54;  
 RESULT 1485  
 ID ABN79986 standard; DNA; 6133 BP.  
 DE Human chemically modified disease associated gene SEQ ID NO 3.  
 PN WO200200927-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 6133;  
 Best Local Similarity 47.3%; Pred. No. 54;  
 RESULT 1486  
 ID ABL32485 standard; DNA; 6244 BP.  
 DE Human immune system associated gene SEQ ID NO: 458.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 6244;  
 Best Local Similarity 44.7%; Pred. No. 54;  
 RESULT 1487  
 ID AAS46644 standard; DNA; 6261 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #366.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 4; Length 6261;  
 Best Local Similarity 45.8%; Pred. No. 54;  
 RESULT 1488  
 ID ABK31161 standard; DNA; 6261 BP.  
 DE Signal transduction associated gene modified complementary DNA #2.  
 PN WO200200926-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.

Query Match 3.2%; Score 43; DB 6; Length 6261;  
 Best Local Similarity 45.8%; Pred. No. 54;  
 RESULT 1489  
 ID ABL32566 standard; DNA; 6907 BP.  
 DE Human immune system associated gene SEQ ID NO: 539.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 6907;  
 Best Local Similarity 46.1%; Pred. No. 55;  
 RESULT 1490  
 ID ABK34029 standard; DNA; 8056 BP.  
 DE Human DNA for staging of Astrocytomas #59.  
 PN WO200202808-A2.  
 PD 10-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 8056;  
 Best Local Similarity 45.2%; Pred. No. 56;  
 RESULT 1491  
 ID ABZ09933 standard; DNA; 8056 BP.  
 DE Human 5' and/or regulatory region of CMYCex3 DNA SEQ ID NO:73.  
 PN WO200277272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 8; Length 8056;  
 Best Local Similarity 45.2%; Pred. No. 56;  
 RESULT 1492  
 ID ABZ10099 standard; DNA; 8056 BP.  
 DE Haematopoietic cell proliferation disorder related DNA sequence #239.  
 PN WO200277272-A2.  
 PD 03-OCT-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 8; Length 8056;  
 Best Local Similarity 45.2%; Pred. No. 56;  
 RESULT 1493  
 ID ABL92313 standard; DNA; 8079 BP.  
 DE Chemically treated DNA repair gene fragment complementary to#61.  
 PN WO200181622-A2.  
 PD 01-NOV-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 8079;  
 Best Local Similarity 73.3%; Pred. No. 56;  
 RESULT 1494  
 ID ABL32203 standard; DNA; 8246 BP.  
 DE Human immune system associated gene SEQ ID NO: 176.  
 PN WO200200928-A2.  
 PD 03-JAN-2002.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 8246;  
 Best Local Similarity 46.0%; Pred. No. 56;  
 RESULT 1495  
 ID ABL16590 standard; DNA; 8786 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1243.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE) PE CORP NY.  
 Query Match 3.2%; Score 43; DB 4; Length 8786;  
 Best Local Similarity 46.7%; Pred. No. 57;  
 RESULT 1496  
 ID AAS46805 standard; DNA; 10996 BP.  
 DE Tumour suppressor gene derived chemically modified sequence #531.  
 PN WO200168912-A2.  
 PD 20-SEP-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 4; Length 10996;  
 Best Local Similarity 45.2%; Pred. No. 59;  
 RESULT 1497  
 ID ABK28465 standard; DNA; 10996 BP.  
 DE DNA transcription associated genomic DNA #170.  
 PN WO200192565-A2.  
 PD 06-DEC-2001.  
 PA (EPIG-) EPIGENOMICS AG.  
 Query Match 3.2%; Score 43; DB 6; Length 10996;

Best Local Similarity 45.2%; Pred. No. 59;  
RESULT 1498  
ID ABK39930 standard; DNA; 12069 BP.  
DE Human chemically pretreated gene sequence #6 strand 1.  
PN WO200202806-A2.  
PD 10-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43; DB 6; Length 12069;  
Best Local Similarity 46.7%; Pred. No. 60;  
RESULT 1499  
ID ADS89426 standard; DNA; 12610 BP.  
DE Oligonucleotide of the invention SEQ ID NO:442.  
PN WO2004035803-A2.  
PD 29-APR-2004.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43; DB 13; Length 12610;  
Best Local Similarity 55.8%; Pred. No. 60;  
RESULT 1500  
ID ABL32583 standard; DNA; 13376 BP.  
DE Human immune system associated gene SEQ ID NO: 556.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Query Match 3.2%; Score 43; DB 6; Length 13376;  
Best Local Similarity 47.5%; Pred. No. 61;

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OM nucleic - nucleic search, using sw model

Run on: September 4, 2005, 02:25:37 ; Search time 4201 Seconds  
(without alignments)  
12195.788 Million cell updates/sec

Title: US-09-989-724-386  
Perfect score: 1346  
Sequence: 1 gaagaatgtgtgctgct.....aaaaaaaaaaaaaaaa 1346

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hlc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	791.2	58.8	870	4	BI760941
2	751.2	55.8	978	4	BI762437
3	746.8	55.5	779	4	BG217185
4	743.6	55.2	782	5	BU689227
5	736.6	54.7	826	4	BG194741
6	732	54.4	788	4	BG211841
7	729	54.2	801	4	BG2118203
8	715.4	53.2	750	6	CA312017
9	706.8	52.5	780	4	BG429174
10	704.4	52.3	754	4	BG181765
11	695.2	51.6	792	4	BG400845
12	675.4	50.2	791	4	BG400319
13	665.8	49.5	1081	4	BM811234
14	661.6	49.2	855	4	BG427247
15	657	48.8	669	9	AY399636
16	649.4	48.2	866	4	BG428618
17	648.2	48.2	804	4	BG429705
18	641.2	47.6	792	4	BG209271
19	639.4	47.5	850	4	BG430955
20	637	47.3	782	4	BG433974
21	636.8	47.3	688	4	BG776793
22	633	47.0	668	4	BG400436
23	631.4	46.9	736	4	BG399402
24	628.4	46.7	888	4	BG400513

98	466.8	34.7	848	6	CA493268	AGENCOURT	171	352.8	26.2	463	1	AA275670	VC33C12.F
99	466.8	34.7	901	2	BF786687	602111448	172	352.2	26.2	925	2	BF784692	602111325
100	463.6	34.2	744	4	EG566957	602589463	173	347.8	25.3	566	2	AA475605	un68n06.Y
101	461	34.2	868	6	CA481303	AGENCOURT	174	340.4	25.3	482	1	AA273463	VC37D10.F
102	456.6	33.9	730	6	CD241570	AGENCOURT	175	334	24.8	644	7	CB627074	mJ31a04.Y
103	455	33.8	455	2	AW779364	hm80f05.X	176	326.4	24.2	436	6	CB163923	K-EST0224
104	455	33.8	742	6	CB133561	K-EST0184	177	326.2	24.2	696	1	AJ660081	AJ660081
105	454.8	33.8	479	4	BG969794	602838708	C 178	323.4	24.0	360	4	BG182824	RST1685.A
106	453.4	33.7	501	5	EX106610	EX106610	179	322.4	24.0	474	1	AI931440	u168d11.Y
107	453.2	33.7	592	7	CG625448	mJ09D01.Y	180	318.6	23.7	457	5	BY006328	BY006328
108	453	33.7	628	4	BG428990	602501903	181	317	23.6	405	5	AA109637	mm01f02.F
109	449	33.4	808	8	BF780136	602103808	182	316.6	23.5	532	9	CG532959	OST117705
110	448.2	33.3	456	1	AI433883	t117f03.X	183	315.6	23.4	427	2	BB847292	BB847292
111	448	33.3	824	6	CA492547	AGENCOURT	184	315	23.4	437	2	BB844940	BB844940
112	446	33.1	812	7	CK474508	AGENCOURT	C 185	308	22.9	413	2	BB847970	BB847970
113	444.6	33.0	846	2	BF780978	602106606	C 186	308	22.9	697	7	CO683419	DG11-169e
114	444.4	33.0	446	1	AI253234	AGENCOURT	187	307.8	22.9	416	4	BB848103	BB848103
115	443.4	32.9	738	6	CB953900	QZ39C10.X	188	303.8	22.6	716	4	BG400370	602464583
116	439	32.6	659	6	BY741654	BY741654	189	303.6	22.6	410	1	AA066328	mm14D08.F
117	438	32.5	439	1	AI613056	ty68R02.X	190	303	22.5	408	2	BB848163	BB848163
118	437.8	32.5	863	2	BF211834	601813181	191	298.2	22.2	361	4	EG181204	RST129.AC
119	435.4	32.3	445	1	AI478325	tm39G03.X	192	293.8	21.8	416	2	BB846622	BB846622
120	432.2	32.1	581	2	AW106515	um29a07.Y	193	291.8	21.7	386	1	AA109535	mm01G04.F
121	431.8	32.0	620	7	CK624653	mJ23f12.Y	C 194	289.4	21.5	688	7	CO681115	DG11-1251
122	431	32.0	830	4	BG401091	602465157	195	288.6	21.4	479	5	BP769681	BP769681
123	428.6	31.8	807	4	BI099731	602884596	196	287.6	21.4	392	2	AW260024	um82C07.Y
124	426	31.6	436	1	AI650909	wz20a10.X	197	287.4	21.4	437	2	BB844950	BB844950
125	425.6	31.6	440	1	AI524824	t177h07.X	198	287	21.3	412	5	BY006356	BY006356
126	425	31.6	426	2	BE465778	hw22h10.X	199	286.8	21.3	427	2	BB848288	BB848288
127	425	31.6	448	1	AI671437	wC30C08.X	200	284.2	21.1	429	5	BY006674	BY006674
128	424	31.5	446	6	CK133508	K-EST0184	C 201	282.8	21.0	293	1	AI470468	tJ44C08.X
129	423.8	31.5	430	2	AW299600	x852D09.X	202	282.8	21.0	338	6	CA494798	AGENCOURT
130	420.4	31.2	422	2	BF431418	naa44d08.F	203	282	21.0	509	9	CG611484	OST296516
131	414.2	30.8	554	1	AI788483	uk57907.Y	204	281.4	20.9	506	9	CG668483	OST464441
132	411.4	30.6	534	4	BM022547	i461g10.Y	205	278.6	20.7	426	2	BB847279	BB847279
133	410.8	30.5	571	1	AI315913	uJ27f01.Y	C 206	278.2	20.5	677	7	CO679660	DG11-104g
134	409	30.4	704	6	CB955090	AGENCOURT	C 207	276.4	20.5	375	2	BB843933	BB843933
135	408.8	30.4	547	1	AI789468	uk99e12.Y	208	275.6	20.5	421	2	BB848169	BB848169
136	407.4	30.3	948	7	CF582583	AGENCOURT	209	275.6	20.5	492	1	AA065156	zm50a10.F
137	406	30.2	892	6	CA468414	AGENCOURT	210	274.8	20.4	428	2	AW259271	um89h04.Y
138	405	30.1	547	4	BI965141	i434a06.Y	211	274	20.4	372	2	BB843467	BB843467
139	405	30.1	569	4	BI966990	i427a07.Y	C 212	274	20.4	459	2	AW244613	BR-END09H
140	404	29.9	546	1	AI789448	uk99d02.Y	213	270.8	20.1	640	4	BM439885	pgT1n.pk0
141	402.4	29.9	539	2	AW012244	uJ18g07.Y	C 214	270.4	20.1	903	7	CF582582	AGENCOURT
142	394.6	29.3	508	2	BF550608	UI-R-C1-X	C 215	267	19.8	667	7	CO693790	DG11-67n1
143	393.6	29.2	511	7	CK624505	mJ22a01.Y	216	266.2	19.8	369	2	BB843868	BB843868
144	393.4	29.2	499	1	AG681737	AJ681737	217	266	19.8	370	2	BB843459	BB843459
145	392.8	29.2	586	4	BI345729	374635.MA	218	265.4	19.7	407	6	CD217554	pgT1n.pk0
146	392.4	29.2	582	5	BP370260	BP370260	219	264.2	19.6	698	6	CD217554	pgT1n.pk0
147	392	29.1	574	2	AW045074	um17d10.Y	220	263	19.5	458	2	BB846267	BB846267
148	391	29.0	891	6	CA469320	AGENCOURT	221	262.8	19.5	290	6	CB137087	K-EST0189
149	390	29.0	525	1	AI882207	uJ13g03.Y	C 222	260.6	19.4	610	7	CO696699	DG32-100j
150	389.8	29.0	505	1	AI746613	u101d01.Y	223	259.8	19.3	430	5	BY006046	BY006046
151	388.6	28.9	794	6	CB955392	AGENCOURT	C 224	257.4	19.1	281	1	AI473091	tJ56a03.X
152	387.6	28.8	513	1	AA445683	f62h07.F	225	255	18.9	375	2	BB843929	BB843929
153	386.8	28.7	804	4	BG431368	602499982	226	255	18.9	450	1	AJ655099	AJ655099
154	385.4	28.6	519	1	AI747322	u105a06.Y	C 227	254.2	18.9	608	7	CO683836	DG11-175g
155	384.2	28.5	428	1	AI431850	t125h12.X	228	254	18.8	455	2	BB845438	BB845438
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158	376.4	28.0	763	5	BX926439	BX926439	231	249.6	18.5	418	2	BB848084	BB848084
159	374.2	27.8	541	1	AA11483	z08a05.F	C 232	249	18.5	602	9	CE845885	tJgr-q8e-
160	373.8	27.8	485	2	AW106894	um34h05.Y	C 233	248.6	18.5	606	7	CO693615	DG11-6511
161	373.4	27.7	881	6	CA468090	AGENCOURT	C 234	248	18.4	610	7	CO685560	DG11-201F
162	368.8	27.4	504	1	CF682987	AJ682987	235	245.2	18.2	340	2	BB843625	BB843625
163	368.6	27.4	779	7	CK778629	965794.MA	236	245	18.2	366	2	BB847608	BB847608
164	368.4	27.4	547	6	CB222923	1JEJ17E10	237	244.8	18.2	307	4	BG185958	RST4913.A
165	366.4	27.2	536	1	AI663506	uk3f11.Y	238	244.6	18.2	378	5	BY086677	BY086677
166	361.8	26.9	533	1	AI663460	uk33h03.Y	C 239	244.4	18.2	613	7	CO694612	DG11-74j1
167	361.6	26.9	778	7	CR451583	CR451583	240	243.8	18.1	693	2	BF031348	601559115
168	361	26.8	499	1	AI882240	u156b05.Y	241	243.4	18.1	248	1	AA345162	EST51144
169	353.8	26.3	489	2	AW259149	um89b04.Y	242	242	18.0	372	2	BB843455	BB843455
170	352.8	26.2	452	1	AA289223	vc93f01.F	C 243	239.8	17.8	652	5	BP769682	BP769682

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BE115317 UI-R-CA0-

390	128	9.5	852	7	CK237456	CK237456	AGENCYCOURT	463	94.8	7.0	480	6	CA9565795	CA9565795	CCLX05a19
391	127.8	9.5	703	5	BU376588	BU376588	603809540	464	93.2	6.9	423	6	CD284299	CD284299	G39172.71
392	127.4	9.5	410	2	BB739012	BB739012	BB739012	465	92.6	6.9	293	2	BB745854	BB745854	BB745854
393	127.4	9.5	810	2	CK239284	CK239284	AGENCYCOURT	466	92.4	6.9	773	6	CB308042	CB308042	AGENCYCOURT
394	127.4	9.5	909	6	CA975643	CA975643	AGENCYCOURT	467	90.6	6.7	1154	4	BM460886	BM460886	AGENCYCOURT
395	127	9.4	377	2	BB738099	BB738099	BB738099	468	90.4	6.7	308	2	BB435895	BB435895	BB435895
396	126.8	9.4	784	7	CF348736	CF348736	AGENCYCOURT	469	90.4	6.7	359	1	AV004150	AV004150	AV004150
397	126.8	9.4	787	7	CN512318	CN512318	AGENCYCOURT	470	90.2	6.7	330	5	BY368561	BY368561	BY368561
398	126.8	9.4	860	7	CK016244	CK016244	AGENCYCOURT	471	90.2	6.7	369	5	BY398655	BY398655	BY398655
399	126.2	9.4	1035	1	AL551235	AL551235	AGENCYCOURT	472	89.8	6.7	689	5	BB788867	BB788867	BB788867
C 400	126	9.4	242	4	BI403931	BI403931	MI-P-CPI-1	473	89	6.6	304	2	BB499397	BB499397	BB499397
401	125.8	9.3	804	6	CD758550	CD758550	AGENCYCOURT	474	89	6.6	772	5	BB499397	BB499397	BB499397
402	125.8	9.3	818	6	CD759140	CD759140	AGENCYCOURT	475	89	6.6	772	5	BB499397	BB499397	BB499397
403	125.8	9.3	836	7	CK236662	CK236662	AGENCYCOURT	476	88.2	6.6	794	5	BB499397	BB499397	BB499397
404	125.6	9.3	386	1	AV001269	AV001269	AGENCYCOURT	477	87.6	6.5	552	5	BB499397	BB499397	BB499397
405	125.4	9.3	389	2	BB737963	BB737963	AGENCYCOURT	478	87.6	6.5	674	7	CK948392	CK948392	CK948392
406	125.4	9.3	332	2	BB737949	BB737949	AGENCYCOURT	479	86.8	6.4	837	6	CA473716	CA473716	AGENCYCOURT
407	125	9.3	1690	3	CR599955	CR599955	full-1-leag	480	86.4	6.4	732	5	BB499397	BB499397	BB499397
408	125	9.3	3337	3	BC032938	BC032938	Homo sapi	481	86.4	6.4	863	7	CF663100	CF663100	CCLX07a30
409	125	9.3	3339	3	EC048144	EC048144	Homo sapi	482	86.4	6.4	863	7	CF663100	CF663100	CCLX07a30
410	124.8	9.3	302	9	CG668540	CG668540	OST464486	483	86.2	6.4	314	2	BB502721	BB502721	BB502721
411	124.6	9.3	762	5	CK304380	CK304380	AGENCYCOURT	484	85.2	6.3	310	2	BB436562	BB436562	BB436562
412	124.2	9.2	767	7	CK239480	CK239480	AGENCYCOURT	485	84	6.2	294	2	BB498684	BB498684	BB498684
413	124.2	9.2	773	7	CK239430	CK239430	AGENCYCOURT	486	82.8	6.2	1101	9	CNS008EVL	CNS008EVL	AL069706 Drosophila
414	124.2	9.2	888	6	CA787423	CA787423	AGENCYCOURT	487	82.8	6.2	778	4	BI831019	BI831019	BI831019
415	124.2	9.2	965	6	CA473387	CA473387	AGENCYCOURT	488	82.2	6.1	688	6	BY708410	BY708410	BY708410
416	124	9.2	376	1	AV002739	AV002739	AGENCYCOURT	489	81.8	6.1	483	2	BF938662	BF938662	BF938662
417	124	9.2	337	5	BY368461	BY368461	AGENCYCOURT	490	81.2	6.0	418	2	BB687602	BB687602	BB687602
418	123.8	9.2	381	2	BB739767	BB739767	AGENCYCOURT	491	81.2	6.0	832	6	CB197355	CB197355	AGENCYCOURT
419	123.4	9.2	448	2	BB748146	BB748146	AGENCYCOURT	492	80.6	6.0	204	2	BB741525	BB741525	BB741525
420	122.8	9.1	370	1	AV000544	AV000544	AGENCYCOURT	493	80.4	6.0	322	2	BB146668	BB146668	BB146668
421	122.6	9.1	816	7	CK236057	CK236057	AGENCYCOURT	494	80	5.9	189	2	BB747903	BB747903	BB747903
422	122.6	9.1	836	7	CK238801	CK238801	AGENCYCOURT	495	80	5.9	282	2	BB434595	BB434595	BB434595
423	121.4	9.0	430	2	BB472993	BB472993	AGENCYCOURT	C 496	79.4	5.9	574	1	AI116021	AI116021	ue25h10.x
424	120.6	9.0	360	1	AA066112	AA066112	ml66605.r	497	78.4	5.8	201	1	AA207583	AA207583	mv81a11.r
C 425	120	8.9	599	1	AI108820	AI108820	EST237111	498	78	5.8	293	2	BB435508	BB435508	BB435508
C 426	120	8.9	631	1	AI105157	AI105157	EST214446	C 499	77.4	5.8	1101	9	CNS0039G	CNS0039G	AL063921 Drosophila
C 427	118	8.8	854	6	CA474850	CA474850	AGENCYCOURT	C 500	77.2	5.7	512	2	BB748027	BB748027	BB748027
C 428	117.6	8.7	804	1	AI058885	AI058885	UI-R-Cl-k	C 501	77	5.7	283	2	BB054531	BB054531	BB054531
C 429	117	8.7	862	6	CA471692	CA471692	AGENCYCOURT	C 502	77	5.7	1156	6	CD508270	CD508270	CD508270
C 430	116.8	8.7	459	1	AI233636	AI233636	EST230324	503	76.8	5.7	266	1	AV003912	AV003912	AV003912
431	116.6	8.7	891	6	CA472074	CA472074	AGENCYCOURT	504	76.8	5.7	269	2	BB497254	BB497254	BB497254
C 432	115.8	8.6	600	1	AA891752	AA891752	EST195555	505	76.8	5.7	1092	9	CNS020K7	CNS020K7	AL175696 Tetraodon
C 433	115.4	8.6	829	6	CA496216	CA496216	AGENCYCOURT	506	76.6	5.7	679	5	BY319688	BY319688	BY319688
C 434	115	8.5	395	2	AW320077	AW320077	unl4603.x	507	76.4	5.7	637	7	CNS984278	CNS984278	CNS984278
C 435	114.6	8.5	423	2	BB743814	BB743814	AGENCYCOURT	C 508	75.4	5.6	392	2	BF334479	BF334479	BF334479
C 436	114.6	8.5	459	1	AI105375	AI105375	EST214664	C 509	75.2	5.6	1101	9	CNS008EVL	CNS008EVL	AL069706 Drosophila
437	114.2	8.5	723	5	BX862922	BX862922	AGENCYCOURT	510	74.4	5.5	192	1	AV004210	AV004210	AV004210
C 438	114.2	8.5	1013	7	CO581670	CO581670	ILLUMIGEN	511	74.4	5.5	311	2	BB500810	BB500810	BB500810
C 439	111.4	8.3	435	1	AA076449	AA076449	AGENCYCOURT	512	74.4	5.5	337	2	BB497528	BB497528	BB497528
440	111	8.2	659	6	CA364229	CA364229	639103 NC	513	74.4	5.5	944	6	CB180137	CB180137	CB180137
441	109.8	8.2	1603	3	AK008530	AK008530	Mus muscu	514	72.8	5.4	680	5	BB319687	BB319687	BB319687
442	107.2	8.0	620	5	BU472823	BU472823	603761782	515	72.6	5.4	241	1	AV003248	AV003248	AV003248
443	106.6	7.9	370	2	BB741610	BB741610	AGENCYCOURT	516	72	5.3	241	1	BB010750	BB010750	BB010750
C 444	106.6	7.9	492	2	AW260204	AW260204	um74f04.x	517	72	5.3	1101	9	CNS008057	CNS008057	AL069440 Drosophila
445	106.4	7.9	590	4	BI884757	BI884757	f068f09.y	518	71.6	5.3	290	2	BB009853	BB009853	BB009853
446	105.6	7.8	426	2	BB561901	BB561901	BB561901	519	71.6	5.3	296	2	BB005788	BB005788	BB005788
C 447	105.4	7.8	265	2	BB561901	BB561901	BB561901	C 520	71.6	5.3	306	6	CA043283	CA043283	CA043283
448	105	7.8	388	1	AI648938	AI648938	uk33b03.x	521	71.6	5.3	669	6	CD810900	CD810900	CD810900
449	104.8	7.8	685	6	CA965680	CA965680	CCLX05a15	C 522	71.4	5.3	699	6	BB435424	BB435424	BB435424
450	103.4	7.7	421	1	AA273564	AA273564	VC38f10.r	C 523	71.2	5.3	269	2	BB435424	BB435424	BB435424
451	101.4	7.5	447	5	BY153686	BY153686	AGENCYCOURT	524	71	5.3	243	2	BB741599	BB741599	BB741599
452	101.2	7.5	773	6	CB559001	CB559001	AGENCYCOURT	525	70.8	5.3	277	2	BB006347	BB006347	BB006347
C 453	100.4	7.5	499	1	AI931939	AI931939	u168b06.x	526	70.8	5.3	308	2	BB361016	BB361016	BB361016
454	100.2	7.4	246	2	BB561792	BB561792	AGENCYCOURT	527	70.6	5.2	305	2	BB433431	BB433431	BB433431
455	99.8	7.4	381	5	BY153900	BY153900	BB5153900	528	70.4	5.2	789	7	CNS975696	CNS975696	CNS975696
456	98.6	7.3	316	2	BB434065	BB434065	BB434065	529	70.4	5.2	867	7	CNS975873	CNS975873	CNS975873
457	96.8	7.2	584	5	BP371391	BP371391	AGENCYCOURT	530	70	5.2	273	2	BB010292	BB010292	BB010292
458	96.6	7.2	301	2	BB436492	BB436492	AGENCYCOURT	531	69.2	5.1	545	2	BE684228	BE684228	BE684228
459	96.6	7.2	787	5	EX911789	EX911789	AGENCYCOURT	C 532	69.2	5.1	649	1	AA893216	AA893216	AA893216
460	96	7.1	765	5	EX878953	EX878953	AGENCYCOURT	C 533	68.4	5.1	303	1	AV235006	AV235006	AV235006
461	96	7.1	777	5	EX867294	EX867294	AGENCYCOURT	534	68.4	5.1	718	5	BU262937	BU262937	BU262937
462	95.6	7.1	694	7	CK957623	CK957623	4097741 B	C 535	68.2	5.1	1024	9	CNS0203D0	CNS0203D0	Tetraodon

536	67.8	5.0	1190	9	CNS020N7	AL206908 Tetraodon	c 609	57.4	4.3	660	9	CNS070NJ	AL620449 T3 end of
537	67.6	5.0	710	5	BX912444	BY912444 BX912444	c 610	57.4	4.3	811	1	AL514901	AL514901
538	67.4	5.0	207	5	BY368458	BY368458 BY368458	c 611	57.4	4.3	1003	9	CL472292	CL472292 SAIL_175
539	67	5.0	567	5	EX086253	EX086253 EX086253	c 612	57.4	4.3	1225	8	CC238324	CC238324 CH261-192
540	67	5.0	759	9	CNS060XV	AL411257 T7 end of	c 613	57.4	4.3	1225	9	CNS0161D	AL106171 Drosophil
541	66.8	5.0	233	2	BR051098	BR051098 BB051098	c 614	57.4	4.3	1227	9	AG430010	AG430010 Mus muscu
542	66.8	5.0	274	2	BR529929	BR529929 BB529929	c 615	57.4	4.3	1242	9	CL068807	CL068807 CH216-115
543	66.6	4.9	289	4	BG200773	BG200773 RS202223	c 616	57.2	4.2	932	9	CL479576	CL479576 SAIL_308
c 544	66.6	4.9	1101	9	CNS003BD	AL064091 Drosophil	c 617	57.2	4.2	1626	7	CF238805	CF238805 AGENCOURT
c 545	66.4	4.9	928	9	CNS00DKY	AL071865 Drosophil	c 618	57	4.2	873	9	CNS024M5	AL180950 Tetraodon
546	65.8	4.9	738	5	EX884918	EX884918 BX884918	c 619	56.8	4.2	663	8	BH990661	BH990661 oen99c01
c 547	65.8	4.9	1101	9	CNS00EO7	AL069440 Drosophil	c 620	56.8	4.2	697	9	CNS04707	AL278224 Tetraodon
c 548	65.6	4.9	426	1	AL035384	AL035384 uc90d12.x	c 621	56.8	4.2	742	8	BH673165	BH673165 BOMHA94TR
c 549	65.6	4.9	651	9	CR121547	CR121547 Reverse s	c 622	56.8	4.2	1101	9	CNS00FYG	AL071206 Drosophil
550	65.2	4.8	277	2	BB434322	BB434322 BB434322	c 623	56.8	4.2	1101	9	CNS0151X	AL104895 Drosophil
c 551	65	4.8	230	1	AA893296	AA893296 EST197099	c 624	56.8	4.2	1225	9	CNS0161D	AL106171 Drosophil
552	65	4.8	452	4	BG428060	BG428060 602501471	c 625	56.8	4.2	1229	3	CR731677	CR731677 Tetraodon
553	64.4	4.8	1124	9	CNS073BM	AL427304 clone BA0	c 626	56.8	4.2	2300	3	CR734152	CR734152 Tetraodon
554	64.2	4.8	928	9	CNS00DKY	AL071865 Drosophil	c 627	56.6	4.2	569	8	BH480068	BH480068 BOHRO17TF
c 555	64.2	4.8	1043	9	CNS0145P	AL103735 Drosophil	c 628	56.6	4.2	843	9	CNS00CS1	AL059666 Drosophil
c 556	63.8	4.7	1391	9	CG754863	CG754863 P050-2-G0	c 629	56.6	4.2	1021	9	AL104032	AL104032 Drosophil
557	63.2	4.7	945	9	CNS04D0K	AL285149 Tetraodon	c 630	56.6	4.2	1101	9	CNS001FB	AL060732 Drosophil
c 558	63.2	4.7	1169	9	CNS06KHQ	AL402900 T3 end of	c 631	56.4	4.2	970	6	CB208406	CB208406 AGENCOURT
559	62.6	4.7	991	9	CL139092	CL139092 ISB1-1110	c 632	56.4	4.2	1101	9	CNS003B4	AL064082 Drosophil
c 560	62	4.6	838	9	AG489918	AG489918 Mus muscu	c 633	56.4	4.2	1190	9	CNS020N7	AL206908 Tetraodon
c 561	62	4.6	938	9	CNS006TU	AL065906 Drosophil	c 634	56.4	4.2	1805	9	CL080711	CL080711 CH216-159
c 562	62	4.6	1191	9	CL104745	CL104745 ISB1-4311	c 635	56.2	4.2	527	1	A1476983	A1476983 fb58b12.Y
c 563	62	4.6	2081	9	AG280593	AG280593 Mus muscu	c 636	56.2	4.2	1025	9	CNS014J2	AL104216 Drosophil
c 564	61.8	4.6	1101	9	CNS012TP	AL102007 Drosophil	c 637	56.2	4.2	1094	9	CNS012F2	AL101513 Drosophil
c 565	61.6	4.6	1431	9	AG365607	AG365607 Mus muscu	c 638	56.2	4.2	1101	9	CNS0039G	AL063921 Drosophil
c 566	61.6	4.6	1896	9	CG753083	CG753083 P048-1-C0	c 639	56.2	4.2	1101	9	CNS003BB	AL064089 Drosophil
c 567	61.4	4.6	1101	9	CNS00KAE	AL077628 Drosophil	c 640	56.2	4.2	1101	9	CNS00106X	AL098595 Drosophil
c 568	61	4.5	1007	9	CNS00JOV	AL076752 Drosophil	c 641	56	4.2	969	9	CL492468	CL492468 SAIL_567
c 569	61	4.5	1101	9	CNS00BEO	AL069493 Drosophil	c 642	56	4.2	1101	9	CNS00EQL	AL069526 Drosophil
c 570	60.8	4.5	639	9	CNS038CX	AL232458 Tetraodon	c 643	56	4.2	1187	8	B11102	B11102 F19C22-T7 I
c 571	60.6	4.5	618	6	CB502807	CB502807 ssalme50	c 644	56	4.2	1348	9	CG749499	CG749499 P043-4-A0
c 572	60.6	4.5	1101	9	CNS00BEO	AL069493 Drosophil	c 645	55.8	4.1	836	9	CNS01100	AL098642 Drosophil
c 573	60.6	4.5	1101	9	CNS00220	AL097152 Drosophil	c 646	55.8	4.1	845	8	AQ745537	AQ745537 HS_2272_A
c 574	60.6	4.5	1118	9	CL147481	CL147481 ISB1-234H	c 647	55.8	4.1	994	9	CNS04NOJ	AL298972 Tetraodon
575	60.4	4.5	1592	9	CG750135	CG750135 P044-3-D0	c 648	55.8	4.1	1184	9	CNS04P4P	AL300850 Tetraodon
576	60.2	4.5	753	9	AG610797	AG610797 Mus muscu	c 649	55.8	4.1	1896	3	CR722884	CR722884 Tetraodon
c 577	60.2	4.5	1202	9	CL477268	CL477268 SAIL_26_E	c 650	55.8	4.1	1896	9	CG753083	CG753083 P048-1-C0
c 578	60.2	4.5	1489	9	AG350139	AG350139 Mus muscu	c 651	55.6	4.1	943	9	CL145947	CL145947 ISB1-1461
c 579	60	4.5	937	7	CK415737	CK415737 AUF 1ppit	c 652	55.6	4.1	968	9	CNS00KOS	AL078247 Drosophil
c 580	60	4.5	1084	9	CNS071NH	AL425139 clone BA0	c 653	55.6	4.1	979	9	CNS0161W	AL101690 Drosophil
581	60	4.5	1101	9	CNS008X3	AL052544 Drosophil	c 654	55.6	4.1	1101	9	CNS00BEU	AL056987 Drosophil
c 582	59.8	4.4	600	6	CB504196	CB504196 ssalplnb5	c 655	55.6	4.1	1111	7	CF764200	CF764200 CES004349
c 583	59.8	4.4	776	9	CB561073	CB561073 tigr_988-	c 656	55.6	4.1	1176	9	CNS03R83	AL256908 Tetraodon
c 584	59.8	4.4	892	9	CW020046	CW020046 ZMMBLC001	c 657	55.6	4.1	1210	3	CR721108	CR721108 Tetraodon
c 585	59.8	4.4	1027	9	CNS02T50	AL1212733 Tetraodon	c 658	55.4	4.1	674	7	CV117970	CV117970 AGENCOURT
c 586	59.8	4.4	1101	9	CNS014XJ	AL104737 Drosophil	c 659	55.4	4.1	987	9	CNS014PQ	AL104456 Drosophil
c 587	59.8	4.4	1268	9	AG347098	AG347098 Mus muscu	c 660	55.4	4.1	1010	6	CD171719	CD171719 AGENCOURT
c 588	59.6	4.4	615	6	CA041633	CA041633 ssalme00	c 661	55.4	4.1	1118	5	BX462896	BX462896 BX462896
c 589	59.6	4.4	1101	9	CNS003BD	AL064091 Drosophil	c 662	55.4	4.1	1164	8	CC218891	CC218891 CH261-14M
c 590	59.4	4.4	1146	9	CNS021G2	AL176843 Tetraodon	c 663	55.2	4.1	905	9	CNS00KHX	AL077798 Drosophil
591	59.2	4.4	322	7	CK676494	CK676494 ZF101-P00	c 664	55.2	4.1	927	8	AZ046250	AZ046250 nbab0091D
c 592	59.2	4.4	590	7	CNS84985	CNS84985 USDA-FP_1	c 665	55.2	4.1	987	9	CNS014PQ	AL104456 Drosophil
593	59.2	4.4	1101	9	CNS0180R	AL108741 Drosophil	c 666	55.2	4.1	1011	6	CA787481	CA787481 AGENCOURT
c 594	59.2	4.4	1542	9	AG386981	AG386981 Mus muscu	c 667	55.2	4.1	1101	9	CNS0042W	AL055440 Drosophil
c 595	59	4.4	309	2	BB436540	BB436540 BB436540	c 668	55.2	4.1	1141	9	CNS07206	AL425596 clone BA0
c 596	58.8	4.4	1101	9	CNS00BEO	AL057419 Drosophil	c 669	55.2	4.1	1146	9	CNS021G2	AL178843 Tetraodon
c 597	58.8	4.4	1101	9	CNS016L1	AL106896 Drosophil	c 670	55.2	4.1	1202	9	AG338379	AG338379 Mus muscu
c 598	58.8	4.4	1260	9	AG430117	AG430117 Mus muscu	c 671	55.2	4.1	1530	9	AG382019	AG382019 Mus muscu
c 599	58.8	4.4	1326	9	AG387192	AG387192 Mus muscu	c 672	55.2	4.1	2077	3	CF667281	CF667281 Tetraodon
c 600	58.8	4.4	1624	9	CL466243	CL466243 SAIL_1253	c 673	55	4.1	553	7	CF769995	CF769995 DSBF1_5_C
c 601	58.6	4.4	895	9	CNS08F8V	AL398821 T7 end of	c 674	55	4.1	1101	9	CNS003BB	AL064089 Drosophil
c 602	58.4	4.3	1780	9	AG320553	AG320553 Mus muscu	c 675	55	4.1	1118	5	BX462896	BX462896 BX462896
c 603	58.2	4.3	609	9	CNS025K2	AL182171 Tetraodon	c 676	55	4.1	1291	9	AG430338	AG430338 Mus muscu
c 604	58	4.3	844	8	A2528979	A2528979 ENTCP05TF	c 677	55	4.1	1398	9	CL022024	CL022024 CH216-13B
c 605	58	4.3	1092	9	CNS020K7	AL175696 Tetraodon	c 678	55	4.1	1402	9	AG382069	AG382069 Mus muscu
c 606	57.8	4.3	1229	3	CF731677	CF731677 Tetraodon	c 679	55	4.1	1471	9	AG390851	AG390851 Mus muscu
c 607	57.6	4.3	1201	9	CNS0167M	AL106396 Drosophil	c 680	54.8	4.1	704	9	CL151012	CL151012 104_333_1
c 608	57.4	4.3	660	8	BH183498	BH183498 023_L_07-	c 681	54.8	4.1	843	9	CNS00CS1	AL059666 Drosophil

682	54.8	4.1	1042	9	CL461494	SAIL_1148	C 755	53	3.9	964	9	CNS07B8R	AL441457	T7 end of
683	54.8	4.1	1101	9	CNS00FYC	Drosophil	C 756	53	3.9	994	9	CNS04NOJ	AL298972	Tetradon
684	54.8	4.1	1299	9	AG360787	Mus muscu	C 757	53	3.9	1085	9	CNS0124K	AL101102	Drosophil
685	54.8	4.1	1354	9	CG744717	P037-2-F0	C 758	53	3.9	1254	9	AG349719	AG349719	Mus muscu
686	54.8	4.1	1355	9	AG346348	Mus muscu	C 759	53	3.9	1614	9	AG365768	AG365768	Mus muscu
687	54.8	4.1	1456	9	AG3382339	Mus muscu	C 760	52.8	3.9	493	9	CG804135	CG804135	1118048A0
688	54.6	4.1	725	8	BH180166	016_I_02-	C 761	52.8	3.9	710	8	BZ052236	BZ052236	jnr69q02.
689	54.6	4.1	798	9	CG795035	ZMMBB5032	C 762	52.8	3.9	713	8	AQ576566	AQ576566	mxnb0089K
690	54.6	4.1	901	9	AG494506	Mus muscu	C 763	52.8	3.9	804	9	AG519931	AG519931	Mus muscu
691	54.6	4.1	945	9	CNS04D0K	Tetradon	C 764	52.8	3.9	992	9	CL068931	CL068931	CH216-115
692	54.6	4.1	948	9	CNS0159T	Drosophil	C 765	52.8	3.9	1177	9	AG365683	AG365683	Mus muscu
693	54.6	4.1	1029	9	CNS01ZGM	AL105179	C 766	52.8	3.9	1309	2	BE420736	BE420736	HW002.A0
694	54.6	4.1	1101	9	CNS0021J	Tetradon	C 767	52.8	3.9	1388	5	BQ279227	BQ279227	AGENCOURT
695	54.6	4.1	1332	9	AG429508	Drosophil	C 768	52.6	3.9	468	5	BU767578	BU767578	SJEATP03
696	54.4	4.0	559	5	BU496707	Mus muscu	C 769	52.6	3.9	637	9	CNS036CC	AL29845	Tetradon
697	54.4	4.0	708	7	CK676883	PfESToabS	C 770	52.6	3.9	945	8	BH158204	BH158204	ENTST43TF
698	54.4	4.0	736	8	BZ474913	BOOA091TR	C 771	52.6	3.9	964	9	CNS006N9	AL065781	Drosophil
699	54.4	4.0	866	8	AZ675767	ENTID09TF	C 772	52.6	3.9	1002	8	BZ695524	BZ695524	SP_Ba006
700	54.4	4.0	947	9	CL112501	ISB1-57D2	C 773	52.6	3.9	1101	9	CNS003DQ	AL064580	Drosophil
701	54.4	4.0	1086	9	CNS00YXK	AL096962	C 774	52.6	3.9	1101	9	CNS0161I	AL106896	Drosophil
702	54.2	4.0	876	9	CNS009G1	AL033529	C 775	52.6	3.9	1131	9	CNS034FO	AL227373	Tetradon
703	54.2	4.0	1101	9	CNS000B8	AL063632	C 776	52.6	3.9	1139	8	AQ897537	AQ897537	HS_3153_A
704	54.2	4.0	1324	9	AG376784	Mus muscu	C 777	52.6	3.9	1160	9	AG396428	AG396428	Mus muscu
705	54.2	4.0	1607	9	AG390717	Mus muscu	C 778	52.6	3.9	1186	9	CL469642	CL469642	CH213-243
706	54	4.0	391	2	BB748359	BB748359	C 779	52.6	3.9	1246	9	AG341400	AG341400	Mus muscu
707	54	4.0	421	1	BJ748996	BJ748996	C 780	52.6	3.9	1279	9	AG347333	AG347333	Mus muscu
708	54	4.0	584	1	AJ442092	AJ442092	C 781	52.6	3.9	1594	9	CL067787	CL067787	CH216-112
709	54	4.0	731	8	BH937351	BH937351	C 782	52.6	3.9	1745	9	AG338221	AG338221	Mus muscu
710	54	4.0	886	8	BH177277	08_L_22-	C 783	52.4	3.9	278	1	AA480295	AA480295	ne32d11.s
711	54	4.0	886	9	CNS07JUX	T3 end of	C 784	52.4	3.9	670	9	AG103636	AG103636	Pan trogl
712	54	4.0	1101	9	CNS00B3U	AL056389	C 785	52.4	3.9	867	9	CNS075BG	AL429890	clone BA0
713	54	4.0	1168	9	CL078758	Drosophil	C 786	52.4	3.9	895	8	AZ692422	AZ692422	ENTML1TR
714	54	4.0	1210	9	CG749728	P044-1-C0	C 787	52.4	3.9	937	7	CK415737	CK415737	AUF_Ippic
715	54	4.0	1283	9	CG749728	CL641341	C 788	52.4	3.9	1001	9	CNS01400	AL103554	Drosophil
716	54	4.0	1352	9	AG381852	CL641341	C 789	52.4	3.9	1030	9	CL489693	CL489693	SAIL_528
717	54	4.0	1352	9	AG381852	CL641341	C 790	52.4	3.9	1202	8	CC362481	CC362481	CH261-167
718	53.8	4.0	500	1	AU086866	AU086866	C 791	52.4	3.9	1216	9	AG519648	AG519648	Mus muscu
719	53.8	4.0	836	9	CNS01100	AL099642	C 792	52.4	3.9	1271	9	AG360730	AG360730	Mus muscu
720	53.8	4.0	1032	9	CNS0201P	AL206746	C 793	52.4	3.9	1289	9	AG347097	AG347097	Mus muscu
721	53.8	4.0	2157	9	CL081966	AL081966	C 794	52.4	3.9	1313	7	CK997149	CK997149	1p15c02.b
722	53.8	4.0	2621	9	AG311235	Mus muscu	C 795	52.4	3.9	1554	9	AG390786	AG390786	Mus muscu
723	53.6	4.0	822	7	CK416977	CK416977	C 796	52.4	3.9	1780	9	AG320553	AG320553	Mus muscu
724	53.6	4.0	910	9	CNS0112R	AL099741	C 797	52.4	3.9	2131	5	BU497685	BU497685	PfESToab8
725	53.6	4.0	924	9	CNS0206S	AL208909	C 798	52.2	3.9	308	5	BU497685	BU497685	PfESToab8
726	53.6	4.0	933	7	CK413862	CK413862	C 799	52.2	3.9	323	4	BG894029	BG894029	kl17bl0.y
727	53.6	4.0	1101	9	CNS0039R	AL063932	C 800	52.2	3.9	661	9	CNS02QVJ	AL209800	Tetradon
728	53.6	4.0	1101	9	CNS000EQ	AL069526	C 801	52.2	3.9	672	4	BM164124	BM164124	EST56647
729	53.6	4.0	1101	9	CNS00KAE	AL077628	C 802	52.2	3.9	700	8	BH951634	BH951634	odilb10.
730	53.6	4.0	1113	7	CF994845	CF994845	C 803	52.2	3.9	737	9	BX149919	BX149919	Danio rer
731	53.6	4.0	1132	8	BZ695089	BZ695089	C 804	52.2	3.9	559	5	BP510931	BP510931	Tetradon
732	53.6	4.0	1201	9	CNS016E1	BQ576839	C 805	52.2	3.9	648	5	BU124645	BU124645	603147949
733	53.6	4.0	1227	9	AG430010	AG430010	C 806	52.2	3.9	661	9	CNS02QVJ	AL209800	Tetradon
734	53.4	4.0	699	8	BH958596	BH958596	C 807	52.2	3.9	672	4	BM164124	BM164124	EST56647
735	53.4	4.0	828	8	AQ739398	AQ739398	C 808	52.2	3.9	700	8	BH951634	BH951634	odilb10.
736	53.4	4.0	878	9	AG595634	AG595634	C 809	52.2	3.9	737	9	BX149919	BX149919	Danio rer
737	53.4	4.0	1210	9	AG390601	AG390601	C 810	52.2	3.9	842	9	CNS00ACO	AL055007	Drosophil
738	53.4	4.0	1300	4	BM468018	BM468018	C 811	52.2	3.9	878	7	CO389521	CO389521	AGENCOURT
739	53.4	4.0	1315	3	CG657214	CG657214	C 812	52.2	3.9	945	6	CD580439	CD580439	EST_PSF01
740	53.4	4.0	1364	9	AG375796	AG375796	C 813	52.2	3.9	950	9	CNS00599	CL090599	ISB1-18B1
741	53.4	4.0	1444	9	AG330892	AG330892	C 814	52.2	3.9	996	9	CNS000FUH	AL071063	Drosophil
742	53.4	4.0	1539	9	AG340947	AG340947	C 815	52.2	3.9	1240	9	AG365596	AG365596	Mus muscu
743	53.2	4.0	342	5	BQ576839	BQ576839	C 816	52	3.9	1378	9	AG350209	AG350209	Mus muscu
744	53.2	4.0	542	8	AG307428	AG307428	C 817	52	3.9	622	7	CV181140	CV181140	tsi73q07
745	53.2	4.0	715	6	CD494891	CD494891	C 818	52	3.9	764	7	CF289381	CF289381	AGENCOURT
746	53.2	4.0	816	9	CL855754	CL855754	C 819	52	3.9	817	9	CL491655	CL491655	SAIL_559
747	53.2	4.0	876	9	CNS009G1	AL053529	C 820	52	3.9	949	7	CK424488	CK424488	AUF_IpSto
748	53.2	4.0	959	9	CNS017OR	AL108309	C 821	52	3.9	1017	9	CL101048	CL101048	ISB1-36O4
749	53.2	4.0	988	9	CL087333	CL087333	C 822	52	3.9	1067	6	CD386564	CD386564	AGENCOURT
750	53.2	4.0	1013	9	CNS06RPQ	AL422260	C 823	52	3.9	1101	9	CNS00FMC	AL107092	Drosophil
751	53.2	4.0	1043	9	CNS0145P	AL103735	C 824	52	3.9	1200	9	CNS016CO	AL106578	Drosophil
752	53.2	4.0	1095	9	CNS016E8	AL106634	C 825	52	3.9	1331	9	AG311246	AG311246	Mus muscu
753	53	3.9	230	6	CA969172	CA969172	C 826	52	3.9	1626	7	CF238805	CF238805	AGENCOURT
754	53	3.9	904	9	CL096484	ISB1-28B4	C 827	51.8	3.8	1758	9	CL509408	CL509408	SAIL_811
										464	4	BI813953	BI813953	PfESToaaI







c1120	49	3.6	1101	9	CNS00801	AL057419 Drosophil	1193	48.4	3.6	179	4	BJ334175	BJ334175
1121	49	3.6	1101	9	CNS000T7	AL075293 Drosophil	1194	48.4	3.6	179	4	BJ334928	BJ334928
1122	49	3.6	1101	9	CNS000KB5	AL077453 Drosophil	1195	48.4	3.6	179	4	BJ338148	BJ338148
c1123	49	3.6	1172	3	CR734084	CR734084 Tetraodon	1196	48.4	3.6	180	4	BJ330530	BJ330530
1124	49	3.6	1184	3	CR665955	CR665955 Tetraodon	1197	48.4	3.6	180	4	BJ337662	BJ337662
c1125	49	3.6	1199	9	AG288433	AG288433 Mus muscu	1198	48.4	3.6	181	4	BJ336687	BJ336687
c1126	49	3.6	1237	9	AG390980	AG390980 Mus muscu	1199	48.4	3.6	182	4	BJ335858	BJ335858
1127	49	3.6	1292	4	BM463105	BM463105 AGENCOURT	1200	48.4	3.6	203	4	BJ371047	BJ371047
c1128	49	3.6	1704	4	BG170937	BG170937 602323914	1201	48.4	3.6	210	4	BJ332837	BJ332837
1129	48.8	3.6	431	9	CL879140	CL879140 abf36b06	1202	48.4	3.6	210	4	BJ337381	BJ337381
c1130	48.8	3.6	450	8	BM275484	BM275484 pFESToaas	1203	48.4	3.6	211	4	BJ333851	BJ333851
1131	48.8	3.6	550	8	BZ369762	BZ369762 id10d11.g	1204	48.4	3.6	212	4	BJ334886	BJ334886
c1132	48.8	3.6	567	6	CR616361	CR616361 AMGNNUC:U	1205	48.4	3.6	242	7	CF319709	CF319709
1133	48.8	3.6	607	7	CV490737	CV490737 AGENCOURT	1206	48.4	3.6	262	7	CV184748	CV184748
c1134	48.8	3.6	615	7	CN755256	CN755256 ID0AAA15B	1207	48.4	3.6	316	5	BP765680	BP765680
c1135	48.8	3.6	650	6	CD594427	CD594427 RK091A2F0	1208	48.4	3.6	345	5	BU497054	BU497054
1136	48.8	3.6	693	1	AV682300	AV682300 AV682300	1209	48.4	3.6	433	9	EX137793	EX137793
c1137	48.8	3.6	713	7	CV042107	CV042107 ta156d03	1210	48.4	3.6	435	9	BM274551	BM274551
1138	48.8	3.6	722	9	CW009855	CW009855 ZMBLa001	1211	48.4	3.6	489	4	BM274551	BM274551
c1139	48.8	3.6	734	8	BZ457345	BZ457345 B0NCQ35TF	1212	48.4	3.6	500	1	AU087306	AU087306
1140	48.8	3.6	765	8	BZ058576	BZ058576 lky34a07	1213	48.4	3.6	529	5	BQ265038	BQ265038
1141	48.8	3.6	771	8	BM482529	BM482529 B0HAG58TF	1214	48.4	3.6	599	9	CNS008XP	CNS008XP
c1142	48.8	3.6	772	8	BZ040564	BZ040564 lka43a04	1215	48.4	3.6	620	8	BH594715	BH594715
c1143	48.8	3.6	781	9	BM145762	BM145762 Danio rer	1216	48.4	3.6	652	9	CNS03HOU	CNS03HOU
1144	48.8	3.6	800	9	AG590972	AG590972 Mus muscu	1217	48.4	3.6	680	9	EX155076	EX155076
1145	48.8	3.6	805	1	AJ537921	AJ537921 AJ537921	1218	48.4	3.6	708	7	CN763389	CN763389
1146	48.8	3.6	824	6	CA195303	CA195303 SCEZSB109	1219	48.4	3.6	762	4	BM160418	BM160418
c1147	48.8	3.6	837	9	AG524361	AG524361 Mus muscu	1220	48.4	3.6	770	7	CK471256	CK471256
1148	48.8	3.6	909	9	CNS0606T	AL415467 T3 end of	1221	48.4	3.6	778	7	CO388288	CO388288
1149	48.8	3.6	928	8	AZ549545	AZ549545 ENTDS54TF	1222	48.4	3.6	869	9	CL478380	CL478380
c1150	48.8	3.6	940	9	CNS020GSH	AL196730 Tetraodon	1223	48.4	3.6	906	9	AG555384	AG555384
c1151	48.8	3.6	941	7	CF933040	CF933040 TrEST-B39	1224	48.4	3.6	908	9	CNS04KS8	CNS04KS8
1152	48.8	3.6	1012	9	CL044464	CL044464 CH216-61F	1225	48.4	3.6	939	6	BY720774	BY720774
c1153	48.8	3.6	1019	9	CNS006DU	AL065139 Drosophil	1226	48.4	3.6	965	9	CNS0075X	CNS0075X
1154	48.8	3.6	1101	9	CNS017KE	AL108152 Drosophil	1227	48.4	3.6	965	9	CL505797	CL505797
c1155	48.8	3.6	1123	6	CR325190	CR325190 AGENCOURT	1228	48.4	3.6	1037	9	AG520556	AG520556
1156	48.8	3.6	1160	9	AG289903	AG289903 Mus muscu	1229	48.4	3.6	1052	9	AG520832	AG520832
c1157	48.8	3.6	1335	9	CL646802	CL646802 CH213-123	1230	48.4	3.6	1055	5	BQ876453	BQ876453
1158	48.8	3.6	1381	9	AG321457	AG321457 Mus muscu	1231	48.4	3.6	1081	9	AG075009	AG075009
1159	48.8	3.6	2077	3	CR667281	CR667281 Tetraodon	1232	48.4	3.6	1123	9	CL078696	CL078696
1160	48.8	3.6	2142	3	CR730230	CR730230 Tetraodon	1233	48.4	3.6	1152	9	CL499024	CL499024
c1161	48.6	3.6	197	7	CR439668	CR439668 CR439668	1234	48.4	3.6	1201	8	BZ695091	BZ695091
1162	48.6	3.6	211	4	BJ337607	BJ337607 BJ337607	1235	48.4	3.6	1204	9	AG377050	AG377050
1163	48.6	3.6	365	9	DR22713S	AL744394 Danio rer	1236	48.4	3.6	1251	9	AG377050	AG377050
c1164	48.6	3.6	400	8	BH126293	BH126293 BARC-Sat	1237	48.4	3.6	1563	8	CG206942	CG206942
1165	48.6	3.6	422	8	BH126293	BH126293 BARC-Sat	1238	48.4	3.6	1563	8	CG206942	CG206942
1166	48.6	3.6	500	5	EX738522	EX738522 BX736522	1239	48.2	3.6	365	2	AW013848	AW013848
c1167	48.6	3.6	539	7	CO722076	CO722076 T9ESTzyq2	1240	48.2	3.6	500	1	AU088313	AU088313
1168	48.6	3.6	564	9	AG258155	AG258155 Lotus cor	1241	48.2	3.6	531	7	CK743616	CK743616
1169	48.6	3.6	577	7	CN477441	CN477441 rx37f08.Y	1242	48.2	3.6	625	7	CN757372	CN757372
1170	48.6	3.6	639	9	CNS017QD	AL108367 Drosophil	1243	48.2	3.6	649	8	BH687718	BH687718
c1171	48.6	3.6	657	7	CF411374	CF411374 CR411374	1244	48.2	3.6	656	8	BH343603	BH343603
1172	48.6	3.6	756	7	CF514133	CF514133 CR411374	1245	48.2	3.6	682	8	BZ002699	BZ002699
c1173	48.6	3.6	798	5	BX729254	BX729254 BX729254	1246	48.2	3.6	717	9	AG291454	AG291454
1174	48.6	3.6	806	8	BZ394525	BZ394525 E1NB13TF	1247	48.2	3.6	721	8	BH921333	BH921333
c1175	48.6	3.6	817	8	BZ388550	BZ388550 E1NCQ55TF	1248	48.2	3.6	734	7	CK410841	CK410841
1176	48.6	3.6	910	9	CNS01G8P	AL142826 Anopheles	1249	48.2	3.6	744	8	AQ050079	AQ050079
1177	48.6	3.6	960	5	BX458080	BX458080 BX458080	1250	48.2	3.6	773	8	BH186746	BH186746
1178	48.6	3.6	987	9	CL077094	CL077094 CH216-143	1251	48.2	3.6	773	8	CNS07RSM	CNS07RSM
c1179	48.6	3.6	991	9	CL139092	CL139092 ISB1-1110	1252	48.2	3.6	783	5	BX773950	BX773950
1180	48.6	3.6	1014	6	CD048535	CD048535 AGENCOURT	1253	48.2	3.6	783	5	CR568215	CR568215
c1181	48.6	3.6	1101	9	CNS00QGM	AL071284 Drosophil	1254	48.2	3.6	791	9	AG581577	AG581577
1182	48.6	3.6	1101	9	CNS00LVZ	AL078819 Drosophil	1255	48.2	3.6	810	8	BH480090	BH480090
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DEFINITION mRNA sequence.
ACCESSION BI762437.1 GI:15754015
VERSION BI762437
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 978)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
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## COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLML1472 row: g column: 08  
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## FEATURES

## source

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Gruber (Invitrogen). Research Genetics tracking code  
023. Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 55.8%; Score 751.2; DB 4; Length 978;  
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Matches 863; Conservative 0; Mismatches 53; Indels 13; Gaps 7;  
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ACCESSION BG217185  
VERSION BG217185.1 GI:13743206  
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1 (bases 1 to 779)  
Harrington,J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,  
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Offenbacher, J., Danzig, J. and Ducar, M.  
Creation of genome-wide protein expression libraries using random  
activation of gene expression  
Nat. Biotechnol. 19 (5), 440-445 (2001)  
21227151  
11329013  
Contact: Scott J. Cain  
Athersys, Inc.  
3201 Carnegie Ave, Cleveland, OH 44115, USA  
Tel: 216 431 9900  
Fax: 216 361 9596  
Email: scai@atersys.com  
High quality sequence stop: 547.  
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method was used, these sequence tags are not necessarily  
expressed in HT1080 under normal circumstances."

## FEATURES

source

## ORIGIN

Query Match 55.5%; Score 746.8; DB 4; Length 779;

Best Local Similarity 99.0%; Pred. No. 5e-154;  
Matches 762; Conservative 0; Mismatches 7; Indels 1; Gaps 1;  
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Qy 277 TCAAAAATCACACCCCTTCTGCTGTGGTGGTCAATCAGCCATAGAATAGCAAGAAC 336  
Db 70 TCAAAAATCACACCCCTTCTGCTGTGGTGGTCAATCAGCCATAGAATAGCAAGAAC 129  
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Qy 337 CGATCAACATGCTCTTCTTAAATGACCAACTCTGGAATTTTAAAAATCCCTTCC 396  
Db 130 CGATCAACATGCTCTTCTTAAATGACCAACTCTGGAATTTTAAAAATCCCTTCC 189  
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Qy 397 ACATTTGCACACCCATGGACCCATCTGTGCCATCTGGATTTATTTTGGTGTGATA 456  
Db 190 ACATTTGCACACCCATGGACCCATCTGTGCCATCTGGATTTATTTTGGTGTGATA 249  
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Db 310 AGAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGTAAAGTGTGAAACATGATC 369  
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Qy 577 ACAATTTGAAATGGCATCCCTCTGATCCCTGGACATGAAGGG-GGGCATATTTAATGAT 635  
Db 370 ACAATTTGAAATGGCATCCCTCTGATCCCTGGACATGAAGGGGGCATATTTAATGAT 429  
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Qy 636 GCCTTCATGACAGAGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTGTTGCTGCTTCC 695  
Db 430 GCCTTCATGACAGAGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTGTTGCTGCTTCC 489  
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Qy 696 CAAGAAATTAACATTTGTTCTGTGACTGTGACATCCTGAAATACCAAGAGCAGA 755  
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Qy 936 ATTGATTTAAGCATTTTGAATAAATAGATCAGGCATATGATATATTTTTC 985  
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RESULT 4  
BU689227/c  
LOCUS BU689227 782 bp mRNA linear EST 07-OCT-2002  
DEFINITION UI-CF-EC1-adw-i-18-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone  
UI-CF-EC1-adw-i-18-0-UI 3', mRNA sequence.  
ACCESSION BU689227  
VERSION BU689227.1 GI:23546785  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 782)  
Bonaldo, M.F., Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
Genome Res. 6 (9), 791-806 (1996)  
JOURNAL









MEDLINE  
PUBMED  
COMMENT

97044477  
8889548  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
Seq primer: M13 FORWARD  
POLYA-Yes.

Location/Qualifiers  
1. .750  
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/note="Organ: Lung; Vector: pVT73-Pac (Pharmacia) with a  
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UI-CF-FNO is a subtracted cDNA library derived from two  
normalized Human lung epithelial cell libraries (EN1 and  
DUI) The library was subtracted according to according to  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. For additional information, contact:  
bento-soares@uiowa.edu  
bento-soares@uiowa.edu  
TAG\_TISSUE=Human Lung Epithelial Cell Lines untreated LPS  
6hr to LPS 24h  
TAG\_LIB=UI-CF-FNO  
TAG\_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 53.2%; Score 715.4; DB 6; Length 750;  
Best Local Similarity 98.8%; Pred. No. 4.2e-147;  
Matches 741; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

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Qy 657 AGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTT 716  
Db 690 AGGCTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCTCAAGAAATTAACATTTGTT 631  
Qy 717 CTGTGTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTGTTCCACAT 776  
Db 630 CTGTGTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTGTTCCACAT 571  
Qy 777 TCTTCTTTTGAATAAATTTTGAATGTGCTTGAAGTGAAGCAATCAATATACCCAC 836  
Db 570 TCTTCTTTTGAATAAATTTTGAATGTGCTTGAAGTGAAGCAATCAATATACCCAC 511  
Qy 837 CAACACCACTGAATCATAGCTATTACGACTCAAAATATTCTAAATATTTTCTGAC 896  
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Qy 1256 CCATTTCTACAATTTGTAAAGTCCCAATCTGTCTAACTTAAATAAGTAAATAATCATCTC 1315  
Db 90 CCATTTCTACAATTTGTAAAGTCCCAATCTGTCTAACTTAAATAAGTAAATAATCATCTC 31  
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RESULT 9  
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LOCUS 602498032F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4612062 5',  
DEFINITION mRNA sequence.  
ACCESSION BG429174  
VERSION BG429174.1 GI:133335680  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 780)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LML)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LML at:  
http://image.llnl.gov  
Plate: L1CM1359 row: 0 column: 07  
High quality sequence stop: 718.

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3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGCGGCGGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.65  
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones  
and was constructed by Clontech Laboratories (Palo Alto,  
CA). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match 52.5%; Score 706.8; DB 4; Length 780;

Best Local Similarity 97.4%; Pred. No. 3.3e-145; Matches 750; Conservative 0; Mismatches 17; Indels 3; Gaps 3;			
Qy	36	TGCCATTATGCTGAACTCTGTCAACACGAGTGCAGAAAATGCTTTTAAAGTGAAGCTTAG	95
Db	1	TGCCATTATGCTGAACTCTGTCAACACGAGTGCAGAAAATGCTTTTAAAGTGAAGCTTAG	60
Qy	96	TATCAGAACAGCTCTGGGAGATAAGCATATGCTGGGATACCAATGAAGAAATACCTCTT	155
Db	61	TATCAGAACAGCTCTGGGAGATAAGCATATGCTGGGATACCAATGAAGAAATACCTCTT	120
Qy	156	CAAAGCGATGCTAGCTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAAATTC	215
Db	121	CAAAGCGATGCTAGCTTCTCCATGAGAAAAGTTCCCAACAGAGAAGCAACAGAAAATTC	180
Qy	216	CCATGCTCTACTTTGCAATGTAAACCCAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCC	275
Db	181	CCATGCTCTACTTTGCAATGTAAACCCAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCC	240
Qy	276	TTCAAAAAATCACACCTTCTGCTGTGTAGGTGCAATCAGCCATGAAGTAAGCAAGAA	335
Db	241	TTCAAAAAATCACACCTTCTGCTGTGTAGGTGCAATCAGCCATGAAGTAAGCAAGAA	300
Qy	336	CCGATCAACAATGCCCTTCTTCTAAATGACCAACTCTGGAATTTTAAAAATCCCTTC	395
Db	301	CCGATCAACAATGCCCTTCTTCTAAATGACCAACTCTGGAATTTTAAAAATCCCTTC	360
Qy	396	CACATTGACACCCCATGACCCATCTGTGCCATCTGGATTATTATATTGGTGTGAT	455
Db	361	CACATTGACACCCCATGACCCATCTGTGCCATCTGGATTATTATATTGGTGTGAT	420
Qy	456	ATTTTGCATCATATAGTTGCAATTTGCACTACTGATTTTATCAGGGATCTGGCAAGTAG	515
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Qy	516	AAGAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAGAACATGAT	575
Db	481	AAGAAGAACAAAGAACCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAGAACATGAT	540
Qy	576	CACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGG-GGGCATATTAATGA	634
Db	541	CACAATTGAAAATGGCATCCCTCTGATCCCTGGACATGAAGGAGGGCATATTAATGA	600
Qy	635	TGCTTTCATGACAGAGATGAGGGCTC-ACCTCTCTGAAAGGCTGTGTTCTGCTTC	693
Db	601	TGCTTTCATGACAGAGATGAGAGGCTCAACCCCTCTCTGAAGGGCTGTGTTCTGCTTT	660
Qy	694	CTCAAGAAATTAACATTTGTTCTGT-GTGACTGTGACATCCTGAAATACCAAGAGC	752
Db	661	CTCAGGAAATTAACATTTGTTCTGTGTGTGACTTGTGACATCTGAAATACCAAGAGC	720
Qy	753	AGATCATATATTTGTTTACCAATCTCTTTTGTAAATAAATTTGAATG	802
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BG181765			
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DEFINITION			
ACCESSION			
VERSION			
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Homo sapiens (human)			
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 754)			
Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R.,			
Cain, S., Leventhal, C., Thornton, M., Ramachandran, R.,			
Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,			
Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,			
Offenbacher, J., Danzig, J. and Ducar, M.			

Creation of genome-wide protein expression libraries using random activation of gene expression Nat. Biotechnol. 19 (5), 440-445 (2001)			
2127151			
PUBMED			
COMMENT			
Contact: Scott J. Cain			
Athersys, Inc.			
3201 Carnegie Ave., Cleveland, OH 44115, USA			
Tel: 216 431 9900			
Fax: 216 361 9596			
Email: scain@atersys.com			
High quality sequence stop: 548.			
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ORIGIN			
Query Match 52.3%; Score 704.4; DB 4; Length 754;			
Best Local Similarity 97.7%; Pred. No. 1.1e-144;			
Matches 725; Conservative 0; Mismatches 16; Indels 1; Gaps 1;			
Qy	217	CATGTCCTACTTTGCAATGTAAACCCAGAGGGTATCATTTCTGGTTTGTGGTTACAGACCT	276
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Db	131	CGGATCAACAATGCCCTTCTTTCTAAAGATCAAACTCTGGAATTTTAAAAATCCCTTC	190
Qy	397	ACACTTGCACACCCATGACCCATCTGCCCCATCTGGCCATCTGGATTATTATTTGGTGTGA	456
Db	191	ACACTTGCACACCCATGACCCATCTGCCCCATCTGGCCATCTGGATTATTATATTGGTGTGA	250
Qy	457	TTTGTGATCATCATAGTTGCAATTGCACTACTCATTTTATCAGGGATCTGGCAACGTAGA	516
Db	251	TTTGTGATCATCATAGTTGCAATTGCACTACTCATTTTATCAGGGATCTGGCAACGTAGA	310
Qy	517	AGAAAGAACAAAGAACCAATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAGAACATGATC	576
Db	311	AGAAAGAACAAAGAACCAATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAGAACATGATC	370
Qy	577	ACAATGAAAATGGCATCCCTCTGATCCCTGGACATGAAGG-GGGCATATTATATGAT	635
Db	371	TCAATTGAATAATGGCATCCCTCTGATCCCTGGACATGAAGGGGGCATATTATATGAT	430
Qy	636	GCCTTCATCAGAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTGTTCTGTCTTCCT	695
Db	431	GCCTTCATCAGAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGTGTTCTGTCTTCCT	490
Qy	696	CAAGAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCTCTGAAATACCAAGAGCAGA	755
Db	491	CAAAAAATTAACATTTGTTTCTGTGTGACTGCTGAGCATCTCTGAAATACCAAGAGCAGA	550
Qy	756	TCATATATTTTCTTTCACCATCTCTTTTGTAAATAAATTTGAATGTCTTGAAGTGA	815
Db	551	TCATATATTTTGTTCACCATCTCTTCTTTTGTAAATAAATTTGAATGTCTTGAAGTGA	610
Qy	816	AAAGCAATCAATTAATATACCCCAACCACTGAAATCATGAAGCTATTTCAGCACTCAAAAT	875

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Db 671 ATTCATAAATATTTTCTGACAGTATAGTGATATAAATGTGTGTCATGTGTGATTTGTAGTT 730
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Db 731 ATTGATTTAAGCATTTTAGAAA 752

RESULT 11
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LOCUS 602464068F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4592296 5',
DEFINITION mRNA sequence.
ACCESSION BG400845
VERSION BG400845.1 GI:13294293
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 792)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM1330 row: g column: 17
High quality sequence stop: 784.
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/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
SfiI (ggccgctcgcc); Site_2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGCGAGCGCGCAGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 51.6%; Score 695.2; DB 4; Length 792;
Best Local Similarity 98.0%; Pred. No. 1.2e-142;
Matches 747; Conservative 0; Mismatches 8; Indels 7; Gaps 4;

Qy 1 GAAAGATGTTGTGGCTGCTCTTTTCTGTGACTGCGCATTCATGCTGAACCTGTGCAA 60
Db 26 GAAAGATGTTGTGGCTGCTCTTTTCTGTGACTGCGCATTCATGCTGAACCTGTGCAA 85
Qy 61 CCAGGTGAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db 86 CCAGGTGAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 145
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Db 146 GCATATCGCTGGGATACCAATGAGAAATACCTCTTCAAGCGATGGTAGCTTTCCTCATG 205
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Qy 181 AGAAAAGTTCCTCAACAGAGAAAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAAACC 240
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Qy 301 GTTGAGGTGCAATCAGGCATTAAGAAATGAACAGAAACCGGATCAACAATGCTTCTTTCTA 360
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ACCESSION BG400319
VERSION BG400319.1 GI:13293767
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 791)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1CM1331 row: c column: 08
High quality sequence stop: 711.
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SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CAGGCCATTATGGC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCCGAGCGCGGCATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."

ORIGIN
Query Match 50.2%; Score 675.4; DB 4; Length 791;
Best Local Similarity 97.7%; Pred. No. 2.8e-138;
Matches 749; Conservative 0; Mismatches 11; Indels 7; Gaps 6;

QY 1 GAAAGAAATGTTGGCTGCTCTTTTTCGTGACTGCGCATTCATGCTGAACCTCTGTCAA 60
DB 25 GAAAGAAATGTTGGCTGCTCTTTTTCGTGACTGCGCATTCATGCTGAACCTCTGTCAA 84
QY 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
DB 85 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 144
QY 121 GCATATGCTCTGGGATCCAAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180
DB 145 GCATATGCTCTGGGATCCAAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 204
QY 181 AGAAAGTTCCTCAACAGAGAACCAACAGAAATTCCTGCTCTACTTTCGAATGTAACC 240
DB 205 AGAAAGTTCCTCAACAGAGAACCAACAGAAATTCCTGCTCTACTTTCGAATGTAACC 264
QY 241 CAGAGGTATCATCTCTGGTTGGTTGTACAGACCTTTCAAAATACACACCTTCTCTGCT 300
DB 265 CAGAGGTATCATCTCTGGTTGGTTGTACAGACCTTTCAAAATACACACCTTCTCTGCT 324
QY 301 GTTGAGGTGAATCAGCCATGAAGATGAACAGAACCGGATCAACAAATGCTTTCTTCTA 360
DB 325 GTTGAGGTGAATCAGCCATGAAGATGAACAGAACCGGATCAACAAATGCTTTCTTCTA 384
QY 361 AATGACCAACTCTGGAATTTTAAATCCCTTCCACACTTCGACCCATGGACCCA 420
DB 385 AATGACCAACTCTGGAATTTTAAATCCCTTCCACACTTCGACCCATGGACCCA 444
QY 421 TCTGTGCCATCTGGATATTATATT-TTGGTGATATT-TTGGATCATCATAGTTGCAAT 479
DB 445 TCTGTGCCATCTGGATATTATATT-TTGGTGATATT-TTGGATCATCATAGTTGCAAT 504
QY 480 TGCATCTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAACCAAGAACCATCTGA 539
DB 505 TGCATCTGAT-TTTATCAGGATCTGGCAACGTAGAAGAAAGAACCAAGAACCATCTGA 563
QY 540 AGTGGATGACGCTGAAGATGAAGTGTGAAGACATGATCAATTTGAAGATGGCATCCCTC 599
DB 564 AGTGGATGACGCTGAAGATGAAGTGTGAAGACATGATCAATTTGAAGATGGCATCCCTC 623
QY 600 TGATCCCTTGGACATGAAGG-GGGCATATTAA-TGATGCTTTCATGACAGAGATGAGA 657
DB 624 TGATCCCTTGGACATGAAGGAGGCGATATTAGTATGCTTTCATGACAGAGATGAGA 683
QY 658 GGCTACCCCTCTCTGAAGGGCTGTTGTCTGCTTCC--TCAAGAAATTAACATTTGTT 715
DB 684 GGCTCAACCTCTCTGAAGGGCTGTTGTCTGCTTCCGTCAGAGAAATTAACATTTGTT 743
QY 716 TCTGTGACTGCTGA-GCATCTGAAATACCAAGAGCAGATCATAT 761
DB 744 ACTGTGTGATTGTGAGGCTCTGAAATTTCCAAGAGCAGATCATAT 790
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RESULT 13  
BM811234  
LOCUS  
DEFINITION  
AGENCOURT\_6489717 NIH\_MGC\_125 Homo sapiens cDNA clone IMAGE:5723829  
5', mRNA sequence.  
BM811234  
VERSION  
BM811234.1 GI:19128057  
EST.  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 1081)  
NIH-MGC <http://mgs.nci.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
UNPUBLISHED (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Invitrogen  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM12712 row: b column: 22  
High quality sequence stop: 721.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5723829"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_125"  
/note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;  
Site\_1: BcoRV (destroyed); Site\_2: NotI; RNA source pool  
of three ovaries, from females ranging in age from 38 to  
49 yo. Library is oligo-dT primed and directionally cloned  
(BcoRV site is destroyed upon cloning). Average insert  
size 2.1 kb, insert size range 1-3.5 kb. Library is  
normalized and enriched for full-length clones and was  
constructed by C. Gruber (Invitrogen). Research Genetics  
tracking code 036."

ORIGIN  
Query Match 49.5%; Score 665.8; DB 4; Length 1081;  
Best Local Similarity 96.2%; Pred. No. 3.8e-136;  
Matches 715; Conservative 0; Mismatches 22; Indels 6; Gaps 3;  
QY 61 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120  
DB 165 CCAGGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 224  
QY 121 GCATATGCTCTGGGATCCAAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 180  
DB 225 GCATATGCTCTGGGATCCAAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATG 284  
QY 181 AGAAAGTTCCTCAACAGAGAACCAACAGAAATTTCCCATGTCTTACTTTTGCATGTAACC 240  
DB 285 AGAAAGTTCCTCAACAGAGAACCAACAGAAATTTCCCATGTCTTACTTTGCAATGTAACC 344  
QY 241 CAGAGGTATCATCTCTGGTTTGTGGTTTACAGACCTTCAAAAATACACACCTTCTCTGCT 300  
DB 345 CAGAGGTATCATCTCTGGTTTGTGGTTTACAGACCTTCAAAAATACACACCTTCTCTGCT 404  
QY 301 GTTGAGTGCATTCAGCCATGAAGATGAAGAACCGGATCAACAAATGCTTCTTCTTA 360  
DB 405 GTTGAGTGCATTCAGCCATGAAGATGAAGAACCGGATCAACAAATGCTTCTTCTTA 464  
QY 361 AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTCGACCCATGGACCCA 420  
DB 465 AATGACCAAACTCTGGAATTTTAAATAATCCCTTCCACACTTCGACCCATGGACCCA 524

QY 421 TCTGTGCCCATCTGGATTATTAATTTGGTGTGATATTTTGGATCATCATATAGTTGCAATT 480  
Db |||||  
QY 481 GCACCTACTGATTTTATCAGGGATCTGGCAACGTAGAACAGAAAGAACCAAGACCATCTCGAA 540  
Db |||||  
QY 541 GTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAATGGCATCCCTCT 600  
Db |||||  
QY 601 GATCCCTGGACATGAAGGG-GGGCATATTAATGATGCTTCATGACAGAGATGAGAGG 659  
Db |||||  
QY 660 CTCACCCC--TCTCTGAAGGGCTGTGTTCTGCTTCCTCAAGAAATTAACATTTGTTTC 717  
Db |||||  
QY 718 TGTGTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGT---CAC 774  
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QY 775 ATTCTCTTTTGTATAAATTTT 797  
Db |||||

RESULT 14  
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LOCUS 602494304F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4608048 5',  
DEFINITION mRNA sequence.  
ACCESSION BG427247 GI:13333753  
VERSION BG427247.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 855)  
NIH-MGC <http://mhc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCMI349 row: h column: 01  
High quality sequence stop: 735.  
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/clones="IMAGE:4608048"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_75"  
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site.1:  
SfiI (ggccattatggcc); Site.2: SfiI (ggccattatggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGCGCATTTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGGGCGGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.65  
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones

FEATURES  
source  
1. .855  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clones="IMAGE:4608048"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NIH\_MGC\_75"  
/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site.1:  
SfiI (ggccattatggcc); Site.2: SfiI (ggccattatggcc); 5' and  
3' adaptors were used in cloning as follows: 5' adaptor  
sequence: 5'-CAGCGCATTTATGGCC-3' and 3' adaptor sequence:  
5'-ATTCTAGAGCCGAGGGCGGACATG-dt(30)BN-3' (where B = A,  
C, or G and N = A, C, G, or T). Average insert size 1.65  
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts  
by PCR. This library was enriched for full-length clones

and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

Query Match 49.2%; Score 661.6; DB 4; Length 855;  
Best Local Similarity 95.2%; Pred. No. 3.1e-135; Indels 10; Gaps 8;  
Matches 769; Conservative 0; Mismatches 29;

QY 1 GAAAGAAATGTTGTGGCTGCTCTTTTCTGTGTGATGCCATTTCTATGCTGAACTCTGTCAA 60  
Db |||||  
QY 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120  
Db |||||  
QY 87 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 146  
Db |||||  
QY 121 GCATATCCCTGGGATACCAATGAAGTACTCTTCAAAGCGATGATGCTTTCTCCATG 180  
Db |||||  
QY 147 GCATATCCCTGGGATACCAATGAAGTACTCTTCAAAGCGATGATGCTTTCTCCATG 206  
Db |||||  
QY 181 AGAAAGTTCCTCAACAGAGAACCAAGAAATTTCCCATGTCCTTACATTTGCAATGTAAACC 240  
Db |||||  
QY 207 AGAAAGTTCCTCAACAGAGAACCAAGAAATTTCCCATGTCCTTACATTTGCAATGTAAACC 266  
Db |||||  
QY 241 CAGAGGTATCATTTCTGGTTGTGGTTACAGACCTTTCAAAAAATCAACCCCTTCCTGCT 300  
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QY 267 CAGAGGTATCATTTCTGGTTGTGGTTACAGACCTTTCAAAAAATCAACCCCTTCCTGCT 326  
Db |||||  
QY 301 GTTGAGGTGCAATCAGCCATAAGATGAACAGAACCGGATCAACATGCTTTCTTCTA 360  
Db |||||  
QY 327 GTTGAGGTGCAATCAGCCATAAGATGAACAGAACCGGATCAACATGCTTTCTTCTA 386  
Db |||||  
QY 361 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCAACCATCGACCCA 420  
Db |||||  
QY 387 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCAACCATCGACCCA 446  
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QY 421 TCTGTGCCCATCTGGATTATTAATTTGGTGTGATATTTTGCATCATATAGTTGCAATT 480  
Db |||||  
QY 447 TCTGTGCCCATCTGGATTATTAATTTGGTGTGATATTTTGCATCATATAGTTGCAATT 506  
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QY 481 GCACCTACTGATTTTATCAGGGATCTGGCAACGTAGAACAGAAAGAAC-NAAGAACCATCTGA 539  
Db |||||  
QY 507 GCACCTACTGATTTTATCAGGGATCTGGCAACGTAGAACAGAAAGAACCAAGAACCATCTGA 566  
Db |||||  
QY 540 AGTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTTGAAATGGCATCCCTC 599  
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QY 567 AGTGGATGACGCTGAAGAT-AGTGTGAAACATGATCACAATTTGAAATGGCATCCCTC 625  
Db |||||  
QY 600 TGATCCCTGGACATGAAGGG-GGGCATATTAATGATGCTTTCATGAC-AGAGGATGAGA 657  
Db |||||  
QY 626 TGATCCCTGGACATGAAGGGGGGCATATTAATGATGCTTTCATGACAGAGGATGAGA 685  
Db |||||  
QY 658 GGCTCA-CCCTCTCTGAAGGGCTGTGTTCTGCTTCCCTCAAGAAATTAACATTTGTTT 716  
Db |||||  
QY 686 GGCTCAACCCCTCTCTGAAGGGCTGTGTTCTGCTTCCCTCAAGAAATTA-ACAATGTT 742  
Db |||||  
QY 717 CTGTGTGACTGCTGAGCATCTCGAATATCCCAAGAGGAGATCATATATTTTGTTCACCAT 776  
Db |||||  
QY 743 CTGTGTGACTG-TGAGCATCTTTAAAAAACCAAGAGC-GATTATATATTTGTTTCCCATCT 800  
Db |||||  
QY 777 TCTTCTTTTGTAAATAAATTTTGAATGTG 804  
Db |||||  
QY 801 TCTTGTAAATACTTTTGATGTGCTAAAGTG 828  
Db |||||

RESULT 15  
AY399636  
LOCUS AY399636  
DEFINITION Homo sapiens HCM0290 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY399636  
VERSION AY399636.1  
KEYWORDS GSS. GI:39755625





GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2005, 03:35:57 ; Search time 267 Seconds  
(without alignments)  
8248.796 Million cell updates/sec

Title: US-09-989-724-386  
Perfect score: 1346  
Sequence: 1 gaagaatgtgtgctgct.....aaaaaaaaaaaaaaaaaaaa 1346

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued Patents NA.\*

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- 2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*
- 5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq.\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	799.4	59.4	848	3	US-09-247-155-27
4	799.4	59.4	848	4	US-09-663-600A-27
5	799.4	59.4	848	4	US-09-621-976-5
6	799.4	59.4	848	4	US-09-513-999C-5
7	799.4	59.4	848	4	US-09-471-276-5
8	125	9.3	2415	3	US-08-989-299-3
9	125	9.3	2415	4	US-09-407-427-3
10	125	9.3	3388	4	US-09-949-016-5413
11	125	9.3	3396	3	US-08-989-299-1
12	125	9.3	3396	4	US-10-158-847-141
13	125	9.3	3396	4	US-09-407-427-1
14	117	8.7	2920	4	US-10-158-847-137
15	77.4	5.8	43986	4	US-09-949-016-17155
16	69.4	5.2	2350	3	US-09-280-116-40
17	54	4.0	11288	3	US-08-646-301A-1
18	54	4.0	11288	3	US-08-481-968A-4
19	54	4.0	11288	3	US-08-154-712B-4
20	54	4.0	15056	4	US-09-474-699-10
21	54	4.0	15056	4	US-09-814-351-14
22	54	4.0	15056	4	US-09-814-351-14
23	53.8	4.0	1141	4	US-09-806-708B-22
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26	51.8	3.8	50383	4	US-09-949-016-17600
27	51.6	3.8	168575	3	US-09-426-290-1
28	51.2	3.8	187169	4	US-09-949-016-12776
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30	50.8	3.8	30820	4	US-09-949-016-15940
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37	49.6	3.7	601	4	US-09-949-016-145868
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49	48.8	3.6	231129	4	US-09-806-708B-22
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73	48	3.6	601	4	US-09-949-016-146407
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88	47.4	3.5	134987	4	US-09-949-016-15350
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90	47.4	3.5	134987	4	US-09-949-016-15508
91	47.2	3.5	1055	4	US-09-949-016-15509
92	47.2	3.5	8757	4	US-09-806-708B-23
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94	47.2	3.5	298336	4	US-09-949-016-17067
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96	46.8	3.5	601	4	US-09-949-016-168053
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98	46.8	3.5	601	4	US-09-949-016-168055
99	46.8	3.5	141560	4	US-09-949-016-168056
100	46.8	3.5	231129	4	US-09-949-016-16476
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c 252	42.4	3.2	23790	4	US-09-949-016-14212	Sequence 14212, A	325	40.8	3.0	136029	4	US-09-949-016-14731	Sequence 14731, A
c 253	42.4	3.2	57507	4	US-09-949-016-15019	Sequence 15019, A	c 326	40.8	3.0	640681	4	US-09-730-988-1	Sequence 1, Appli
c 254	42.4	3.2	304533	4	US-09-949-016-15371	Sequence 15371, A	327	40.6	3.0	370	3	US-09-376-113-1	Sequence 1, Appli
c 255	42.4	3.2	304533	4	US-09-949-016-15372	Sequence 15372, A	328	40.6	3.0	958	2	US-08-757-046A-5	Sequence 5, Appli
c 256	42.2	3.1	597	4	US-09-248-796A-7629	Sequence 7629, Ap	329	40.6	3.0	958	3	US-09-447-208-5	Sequence 5, Appli
c 257	42.2	3.1	601	4	US-09-949-016-18854	Sequence 18854, A	330	40.6	3.0	958	3	US-09-135-988-5	Sequence 5, Appli
c 258	42.2	3.1	601	4	US-09-949-016-56719	Sequence 56719, A	331	40.6	3.0	958	3	US-09-277-716-5	Sequence 5, Appli
c 259	42.2	3.1	612	4	US-09-902-540-1357	Sequence 1357, Ap	332	40.6	3.0	958	3	US-08-597-274A-5	Sequence 5, Appli
260	42	3.1	2058	2	US-08-749-391-1	Sequence 1, Appli	333	40.6	3.0	958	3	US-08-908-909-5	Sequence 5, Appli
261	42	3.1	2058	3	US-09-390-200-1	Sequence 1, Appli	334	40.6	3.0	958	3	US-09-609-161B-5	Sequence 5, Appli
c 262	42	3.1	360470	4	US-09-949-016-13173	Sequence 13173, A	335	40.6	3.0	958	3	US-08-990-103-5	Sequence 5, Appli
c 263	42	3.1	1664976	4	US-08-916-421B-1	Sequence 1, Appli	336	40.6	3.0	958	4	US-09-746-485A-5	Sequence 5, Appli
c 264	42	3.1	1664976	4	US-09-692-570-1	Sequence 1, Appli	337	40.6	3.0	958	4	US-10-126-139-5	Sequence 5, Appli
265	41.8	3.1	601	4	US-09-949-016-191305	Sequence 191305, A	338	40.6	3.0	958	4	US-10-126-798-5	Sequence 5, Appli
266	41.8	3.1	881	4	US-08-956-171E-518	Sequence 518, App	339	40.6	3.0	958	4	US-10-126-777-5	Sequence 5, Appli
267	41.8	3.1	881	4	US-08-781-986A-518	Sequence 518, App	340	40.6	3.0	2304	4	US-08-956-171B-432	Sequence 432, App
268	41.8	3.1	2038	4	US-09-885-723-6	Sequence 6, Appli	341	40.6	3.0	2304	4	US-08-781-986A-432	Sequence 432, App
269	41.8	3.1	19438	4	US-09-949-016-12699	Sequence 12699, A	342	40.6	3.0	2360	3	US-08-836-567-9	Sequence 9, Appli
c 270	41.8	3.1	121970	4	US-09-949-016-17216	Sequence 17216, A	343	40.6	3.0	2360	4	US-09-606-304-9	Sequence 9, Appli
c 271	41.8	3.1	124110	4	US-09-949-016-13353	Sequence 13353, A	c 344	40.6	3.0	12313	4	US-09-949-016-13248	Sequence 13248, A
272	41.6	3.1	406	4	US-09-829-481-3	Sequence 3, Appli	345	40.6	3.0	111235	4	US-09-949-016-15328	Sequence 15328, A
273	41.6	3.1	561	4	US-09-601-198-172	Sequence 172, App	c 346	40.4	3.0	601	4	US-09-949-016-196365	Sequence 196365, A
c 274	41.6	3.1	601	4	US-09-949-016-179398	Sequence 179398, A	c 347	40.4	3.0	601	4	US-09-949-016-196366	Sequence 196366, A
c 275	41.6	3.1	601	4	US-09-949-016-179399	Sequence 179399, A	c 348	40.4	3.0	601	4	US-09-949-016-196367	Sequence 196367, A
c 276	41.6	3.1	832	4	US-08-621-976-2813	Sequence 2813, Ap	349	40.4	3.0	17612	4	US-09-949-016-15081	Sequence 15081, A
c 277	41.6	3.1	29927	4	US-09-949-016-11814	Sequence 11814, A	350	40.4	3.0	42381	4	US-09-949-016-12012	Sequence 12012, A
c 278	41.6	3.1	29927	4	US-09-949-016-17474	Sequence 17474, A	351	40.4	3.0	134890	4	US-09-949-016-15602	Sequence 15602, A
c 279	41.6	3.1	29927	4	US-09-949-016-17475	Sequence 17475, A	c 352	40.4	3.0	258775	4	US-09-949-016-16435	Sequence 16435, A
c 280	41.6	3.1	37802	4	US-09-949-016-12639	Sequence 12639, A	c 353	40.2	3.0	601	4	US-09-949-016-109751	Sequence 109751, A
281	41.6	3.1	136917	4	US-09-949-016-16369	Sequence 16369, A	354	40.2	3.0	601	4	US-09-949-016-153149	Sequence 153149, A
c 282	41.4	3.1	1039	4	US-09-902-540-1280	Sequence 1280, Ap	355	40.2	3.0	616	2	US-08-630-822A-93	Sequence 93, Appl
283	41.4	3.1	1039	4	US-09-323-427-1	Sequence 1, Appli	356	40.2	3.0	616	2	US-09-005-069-93	Sequence 93, Appl
c 284	41.4	3.1	1779	3	US-09-323-427-1	Sequence 1, Appli	357	40.2	3.0	616	3	US-09-171-156A-42	Sequence 42, Appl
c 285	41.4	3.1	1779	3	US-09-323-427-2	Sequence 2, Appli	358	40.2	3.0	616	4	US-09-004-730A-42	Sequence 42, Appl
c 286	41.4	3.1	1779	3	US-09-812-642-1	Sequence 1, Appli	359	40.2	3.0	616	4	US-08-981-799A-42	Sequence 42, Appl
c 287	41.4	3.1	1779	3	US-09-812-642-2	Sequence 2, Appli	360	40.2	3.0	1518	4	US-09-614-912-191	Sequence 191, App
c 288	41.4	3.1	1779	4	US-10-054-562A-1	Sequence 1, Appli	c 361	40.2	3.0	36242	4	US-09-949-016-12996	Sequence 12996, A
c 289	41.4	3.1	1779	4	US-10-054-562A-2	Sequence 2, Appli	c 362	40.2	3.0	36242	4	US-09-949-016-12997	Sequence 12997, A
c 290	41.4	3.1	2276	4	US-09-090-672B-6	Sequence 6, Appli	c 363	40.2	3.0	36242	4	US-09-949-016-12998	Sequence 12998, A
c 291	41.4	3.1	124110	4	US-09-949-016-13353	Sequence 13353, A	c 364	40.2	3.0	36242	4	US-09-949-016-12999	Sequence 12999, A
c 292	41.4	3.1	225127	4	US-09-949-016-16480	Sequence 16480, A	c 365	40.2	3.0	36242	4	US-09-949-016-13000	Sequence 13000, A
c 293	41.4	3.1	304533	4	US-09-949-016-15371	Sequence 15371, A	c 366	40.2	3.0	44353	4	US-09-949-016-15302	Sequence 15302, A
c 294	41.4	3.1	304533	4	US-09-949-016-15372	Sequence 15372, A	c 367	40.2	3.0	101128	4	US-09-949-016-14233	Sequence 14233, A
c 295	41.4	3.1	317366	4	US-09-949-016-16001	Sequence 16001, A	c 368	40.2	3.0	134434	4	US-09-949-016-17362	Sequence 17362, A
c 296	41.2	3.1	1897	1	US-09-184-632-1	Sequence 1, Appli	c 369	40.2	3.0	145320	4	US-09-949-016-15858	Sequence 15858, A
c 297	41.2	3.1	97376	4	US-09-949-016-16093	Sequence 16093, A	c 370	40	3.0	436	3	US-09-439-313-353	Sequence 353, App
c 298	41	3.0	601	4	US-09-949-016-18853	Sequence 18853, A	c 371	40	3.0	436	3	US-09-352-616A-353	Sequence 353, App
c 299	41	3.0	601	4	US-09-949-016-37135	Sequence 37135, A	c 372	40	3.0	436	4	US-09-636-215-353	Sequence 353, App
c 300	41	3.0	601	4	US-09-949-016-56718	Sequence 56718, A	c 373	40	3.0	436	4	US-09-685-166A-353	Sequence 353, App
c 301	41	3.0	601	4	US-09-949-016-161112	Sequence 161112, A	c 374	40	3.0	436	4	US-09-679-426-353	Sequence 353, App
c 302	41	3.0	41798	4	US-09-949-016-16058	Sequence 16058, A	c 375	40	3.0	436	4	US-09-759-143-353	Sequence 353, App
c 303	41	3.0	107800	4	US-09-949-016-13118	Sequence 13118, A	c 376	40	3.0	436	4	US-09-651-236-353	Sequence 353, App
c 304	41	3.0	116425	4	US-09-949-016-11809	Sequence 11809, A	c 377	40	3.0	601	4	US-09-949-016-75657	Sequence 75657, A
c 305	41	3.0	139049	4	US-09-949-016-17030	Sequence 17030, A	c 378	40	3.0	1274	4	US-09-523-899A-1	Sequence 1, Appli
c 306	41	3.0	211049	4	US-09-949-016-15770	Sequence 15770, A	c 379	40	3.0	2112	4	US-09-248-796A-5361	Sequence 5361, Ap
c 307	41	3.0	319608	4	US-09-539-333D-1	Sequence 1, Appli	c 380	40	3.0	14871	4	US-09-949-016-13013	Sequence 13013, A
c 308	41	3.0	319608	4	US-09-679-409-1	Sequence 1, Appli	c 381	40	3.0	51259	3	US-08-781-891-209	Sequence 209, App
c 309	40.8	3.0	601	4	US-09-949-016-54021	Sequence 54021, A	c 382	40	3.0	51259	4	US-09-618-166-209	Sequence 209, App
c 310	40.8	3.0	601	4	US-09-949-016-54022	Sequence 54022, A	c 383	40	3.0	65415	4	US-09-949-016-16669	Sequence 16669, A
c 311	40.8	3.0	601	4	US-09-949-016-54023	Sequence 54023, A	c 384	40	3.0	95255	4	US-09-949-016-17067	Sequence 17067, A
c 312	40.8	3.0	601	4	US-09-949-016-54024	Sequence 54024, A	c 385	40	3.0	120213	4	US-09-949-016-13304	Sequence 13304, A
c 313	40.8	3.0	601	4	US-09-949-016-108655	Sequence 108655, A	c 386	40	3.0	120217	4	US-09-949-016-12260	Sequence 12260, A
c 314	40.8	3.0	601	4	US-09-949-016-108656	Sequence 108656, A	c 387	40	3.0	129415	4	US-09-949-016-16997	Sequence 16997, A
c 315	40.8	3.0	601	4	US-09-949-016-108657	Sequence 108657, A	c 388	40	3.0	155617	4	US-09-949-016-16191	Sequence 16191, A
c 316	40.8	3.0	601	4	US-09-949-016-108658	Sequence 108658, A	c 389	40	3.0	263693	4	US-09-949-016-12386	Sequence 12386, A
c 317	40.8	3.0	789	6	5219739-8	Patent No. 5219739	c 390	40	3.0	263694	4	US-09-949-016-16915	Sequence 16915, A
c 318	40.8	3.0	789	6	5219739-8	Patent No. 5219739	c 391	39.8	3.0	601	4	US-09-949-016-77299	Sequence 7299, A
c 319	40.8	3.0	1461	3	US-08-722-126A-4	Sequence 4, Appli	c 392	39.8	3.0	601	4	US-09-949-016-199095	Sequence 199095, A

393	39.8	3.0	1719	4	US-09-949-016-667	Sequence 667, Appl	466	39.4	2.9	29327	4	US-09-949-016-11814	Sequence 11814, A
394	39.8	3.0	2527	4	US-09-244-805-29	Sequence 29, Appl	467	39.4	2.9	29327	4	US-09-949-016-17474	Sequence 17474, A
395	39.8	3.0	2751	4	US-09-970-767-14784	Sequence 14784, A	468	39.4	2.9	29327	4	US-09-949-016-17475	Sequence 17475, A
396	39.8	3.0	2860	4	US-09-991-458A-1	Sequence 1, Appl	469	39.4	2.9	37802	4	US-09-949-016-12639	Sequence 12639, A
397	39.8	3.0	6124	3	US-08-213-419B-3	Sequence 3, Appl	C 470	39.4	2.9	57392	4	US-09-949-016-12070	Sequence 12070, A
398	39.8	3.0	6265	3	US-09-129-112-3	Sequence 3, Appl	C 471	39.4	2.9	57402	4	US-09-949-016-13293	Sequence 13293, A
399	39.8	3.0	46823	4	US-09-949-016-12723	Sequence 12723, A	472	39.4	2.9	60465	4	US-09-949-016-15995	Sequence 15995, A
400	39.8	3.0	46940	4	US-09-949-016-16252	Sequence 16252, A	473	39.4	2.9	124480	4	US-09-949-016-15921	Sequence 15921, A
401	39.8	3.0	78649	4	US-09-949-016-14619	Sequence 14619, A	C 474	39.4	2.9	314798	4	US-09-949-016-13539	Sequence 13539, A
402	39.8	3.0	78649	4	US-09-949-016-14620	Sequence 14620, A	C 475	39.4	2.9	580073	4	US-08-545-528D-1	Sequence 1, Appl
403	39.8	3.0	78649	4	US-09-949-016-16227	Sequence 16227, A	C 476	39.2	2.9	458	1	US-08-524-757-1	Sequence 1, Appl
404	39.8	3.0	78649	4	US-09-949-016-16228	Sequence 16228, A	477	39.2	2.9	601	4	US-09-949-016-54020	Sequence 54020, A
405	39.8	3.0	157644	4	US-09-949-016-16179	Sequence 16179, A	478	39.2	2.9	601	4	US-09-949-016-108654	Sequence 108654, A
406	39.8	3.0	157644	4	US-09-949-016-16180	Sequence 16180, A	479	39.2	2.9	1146	3	US-09-452-239-3	Sequence 3, Appl
407	39.8	3.0	225127	4	US-09-949-016-16480	Sequence 16480, A	480	39.2	2.9	1286	4	US-09-489-847-124	Sequence 124, Appl
408	39.8	3.0	360470	4	US-09-949-016-13173	Sequence 13173, A	481	39.2	2.9	1342	4	US-09-489-847-89	Sequence 89, Appl
409	39.6	2.9	601	4	US-09-949-016-36969	Sequence 36969, A	482	39.2	2.9	1622	4	US-08-956-171B-732	Sequence 732, Appl
410	39.6	2.9	601	4	US-09-949-016-93907	Sequence 93907, A	483	39.2	2.9	1622	4	US-08-781-986A-732	Sequence 732, Appl
411	39.6	2.9	601	4	US-09-949-016-138144	Sequence 138144, A	484	39.2	2.9	2020	4	US-09-716-129-29	Sequence 29, Appl
412	39.6	2.9	601	4	US-09-949-016-138145	Sequence 138145, A	485	39.2	2.9	2514	4	US-09-004-056-1	Sequence 1, Appl
413	39.6	2.9	682	4	US-09-614-912-17	Sequence 17, Appl	C 486	39.2	2.9	6124	3	US-08-213-419B-3	Sequence 3, Appl
414	39.6	2.9	7050	4	US-09-976-594-683	Sequence 683, Appl	C 487	39.2	2.9	53722	4	US-09-949-016-12077	Sequence 12077, A
415	39.6	2.9	20674	3	US-09-641-638-651	Sequence 651, Appl	C 488	39.2	2.9	96922	4	US-09-949-016-17061	Sequence 17061, A
416	39.6	2.9	20674	4	US-10-170-097-651	Sequence 651, Appl	489	39.2	2.9	114139	4	US-09-949-016-16536	Sequence 16536, A
417	39.6	2.9	27783	4	US-09-949-016-16736	Sequence 16736, A	490	39.2	2.9	227750	4	US-09-949-016-17175	Sequence 17175, A
418	39.6	2.9	54576	4	US-09-949-016-15954	Sequence 15954, A	491	39	2.9	239	4	US-09-621-976-16632	Sequence 16632, A
419	39.6	2.9	54576	4	US-09-949-016-15955	Sequence 15955, A	492	39	2.9	536	1	US-08-329-704-1	Sequence 1, Appl
420	39.6	2.9	112705	4	US-09-949-016-15630	Sequence 15630, A	493	39	2.9	536	2	US-08-472-604-1	Sequence 1, Appl
421	39.6	2.9	164061	4	US-09-949-016-17422	Sequence 17422, A	494	39	2.9	536	3	US-08-486-117-1	Sequence 1, Appl
422	39.6	2.9	393753	4	US-09-949-016-14573	Sequence 14573, A	495	39	2.9	536	3	US-08-477-537-1	Sequence 1, Appl
423	39.6	2.9	393753	4	US-09-949-016-14574	Sequence 14574, A	C 496	39	2.9	582	4	US-09-949-016-61868	Sequence 61868, A
424	39.6	2.9	818128	4	US-09-949-016-14546	Sequence 14546, A	497	39	2.9	601	4	US-09-949-016-37133	Sequence 37133, A
425	39.6	2.9	818128	4	US-09-949-016-14547	Sequence 14547, A	498	39	2.9	601	4	US-09-949-016-37134	Sequence 37134, A
426	39.6	2.9	818128	4	US-09-949-016-14548	Sequence 14548, A	C 499	39	2.9	601	4	US-09-949-016-77371	Sequence 77371, A
427	39.6	2.9	818128	4	US-09-949-016-14549	Sequence 14549, A	C 500	39	2.9	601	4	US-09-949-016-86306	Sequence 86306, A
428	39.6	2.9	818128	4	US-09-949-016-14550	Sequence 14550, A	C 501	39	2.9	601	4	US-09-949-016-86307	Sequence 86307, A
429	39.6	2.9	818128	4	US-09-949-016-14551	Sequence 14551, A	C 502	39	2.9	601	4	US-09-949-016-87162	Sequence 87162, A
430	39.6	2.9	818128	4	US-09-949-016-14552	Sequence 14552, A	C 503	39	2.9	601	4	US-09-949-016-109750	Sequence 109750, A
431	39.6	2.9	818128	4	US-09-949-016-14553	Sequence 14553, A	C 504	39	2.9	601	4	US-09-949-016-144794	Sequence 144794, A
432	39.6	2.9	818128	4	US-09-949-016-14554	Sequence 14554, A	C 505	39	2.9	601	4	US-09-949-016-161110	Sequence 161110, A
433	39.6	2.9	818128	4	US-09-949-016-14555	Sequence 14555, A	C 506	39	2.9	601	4	US-09-949-016-161111	Sequence 161111, A
434	39.6	2.9	818128	4	US-09-949-016-14556	Sequence 14556, A	507	39	2.9	792	4	US-09-244-111-3	Sequence 3, Appl
435	39.6	2.9	818128	4	US-09-949-016-14557	Sequence 14557, A	C 508	39	2.9	1296	5	PCF-US94-12912-3	Sequence 3, Appl
436	39.6	2.9	818128	4	US-09-949-016-14558	Sequence 14558, A	C 509	39	2.9	1478	1	US-08-090-523-27	Sequence 27, Appl
437	39.6	2.9	818128	4	US-09-949-016-14559	Sequence 14559, A	C 510	39	2.9	1478	1	US-08-398-621-27	Sequence 27, Appl
438	39.6	2.9	818128	4	US-09-949-016-14560	Sequence 14560, A	C 511	39	2.9	1478	1	US-08-406-857-1	Sequence 3, Appl
439	39.6	2.9	818128	4	US-09-949-016-14561	Sequence 14561, A	C 512	39	2.9	1478	1	US-08-596-024-3	Sequence 3, Appl
440	39.6	2.9	818128	4	US-09-949-016-14562	Sequence 14562, A	C 513	39	2.9	1478	3	US-09-020-818-3	Sequence 3, Appl
441	39.6	2.9	818128	4	US-09-949-016-14564	Sequence 14564, A	C 514	39	2.9	1478	3	US-08-907-740-3	Sequence 3, Appl
442	39.6	2.9	818128	4	US-09-949-016-14565	Sequence 14565, A	C 515	39	2.9	1478	4	US-09-797-467-3	Sequence 3, Appl
443	39.6	2.9	818128	4	US-09-949-016-14566	Sequence 14566, A	C 516	39	2.9	1478	4	US-08-399-023-27	Sequence 27, Appl
444	39.6	2.9	818128	4	US-09-949-016-14567	Sequence 14567, A	C 517	39	2.9	1478	5	PCF-US94-07072-1	Sequence 1, Appl
445	39.4	2.9	396	4	US-09-640-173-10	Sequence 10, Appl	C 518	39	2.9	1651	3	US-09-311-021-93	Sequence 93, Appl
446	39.4	2.9	396	4	US-09-713-550-10	Sequence 10, Appl	C 519	39	2.9	1579	3	US-09-465-558-49	Sequence 49, Appl
447	39.4	2.9	396	4	US-09-825-294-10	Sequence 10, Appl	C 520	39	2.9	3781	3	US-08-688-988-5	Sequence 5, Appl
448	39.4	2.9	396	4	US-09-970-966-10	Sequence 10, Appl	C 521	39	2.9	5021	4	US-09-949-016-786	Sequence 786, Appl
449	39.4	2.9	601	4	US-09-949-016-168196	Sequence 168196, A	C 522	39	2.9	14176	1	US-08-307-499-1	Sequence 1, Appl
450	39.4	2.9	660	1	US-07-991-867B-32	Sequence 32, Appl	C 523	39	2.9	14176	1	US-08-307-499-14	Sequence 14, Appl
451	39.4	2.9	660	1	US-08-107-755A-32	Sequence 32, Appl	C 524	39	2.9	14176	3	US-09-299-268-1	Sequence 1, Appl
452	39.4	2.9	660	2	US-08-544-332-32	Sequence 32, Appl	C 525	39	2.9	14176	3	US-09-299-268-14	Sequence 14, Appl
453	39.4	2.9	660	3	US-09-370-861A-32	Sequence 32, Appl	C 526	39	2.9	23569	4	US-09-949-016-12153	Sequence 12153, A
454	39.4	2.9	946	3	US-08-316-443A-15	Sequence 15, Appl	C 527	39	2.9	23574	4	US-09-949-016-13551	Sequence 15351, A
455	39.4	2.9	1319	2	US-08-504-459-7	Sequence 7, Appl	C 528	39	2.9	45587	4	US-09-949-016-15836	Sequence 15836, A
456	39.4	2.9	1511	1	US-07-991-867B-8	Sequence 8, Appl	C 529	39	2.9	47781	4	US-09-949-016-16492	Sequence 16492, A
457	39.4	2.9	1511	1	US-08-107-755A-8	Sequence 8, Appl	C 530	39	2.9	47781	4	US-09-949-016-16493	Sequence 16493, A
458	39.4	2.9	1511	2	US-08-544-332-8	Sequence 8, Appl	C 531	39	2.9	47781	4	US-09-949-016-16494	Sequence 16494, A
459	39.4	2.9	1511	3	US-09-370-861A-8	Sequence 8, Appl	C 532	39	2.9	83697	4	US-09-949-016-16040	Sequence 16040, A
460	39.4	2.9	1853	4	US-09-220-132-120	Sequence 120, Appl	C 533	39	2.9	86116	4	US-09-949-016-14766	Sequence 14766, A
461	39.4	2.9	2193	3	US-09-427-261-2	Sequence 2, Appl	C 534	39	2.9	140224	4	US-09-949-016-17002	Sequence 17002, A
462	39.4	2.9	2193	3	US-09-427-261-3	Sequence 3, Appl	C 535	39	2.9	140844	4	US-09-949-016-14199	Sequence 14199, A
463	39.4	2.9	4810	3	US-08-852-629-11	Sequence 11, Appl	C 536	39	2.9	154626	4	US-09-949-016-14000	Sequence 14000, A
464	39.4	2.9	4838	3	US-08-852-629-15	Sequence 15, Appl	C 537	39	2.9	285478	4	US-09-949-016-13362	Sequence 13362, A
465	39.4	2.9	29291	4	US-09-949-016-16263	Sequence 16263, A	C 538	38.8	2.9	601	4	US-09-949-016-45739	Sequence 45739, A

C 539	38.8	2.9	601	4	US-09-949-016-45740	Sequence 45740, A	612	38.2	2.8	1068	3	US-08-913-842-12	Sequence 12, Appl
540	38.8	2.9	660	1	US-07-991-867B-32	Sequence 32, Appl	c 613	38.2	2.8	1296	4	US-09-601-198-154	Sequence 154, App
541	38.8	2.9	660	1	US-08-107-755A-32	Sequence 32, Appl	614	38.2	2.8	1330	4	US-09-557-170A-26	Sequence 26, Appl
542	38.8	2.9	660	3	US-08-544-332-32	Sequence 32, Appl	615	38.2	2.8	1337	4	US-09-557-170A-24	Sequence 24, Appl
543	38.8	2.9	660	3	US-09-370-861A-32	Sequence 32, Appl	616	38.2	2.8	1441	3	US-08-821-994-63	Sequence 63, Appl
544	38.8	2.9	772	4	US-08-437-306-1	Sequence 1, Appl	617	38.2	2.8	1941	2	US-09-008-960-2	Sequence 2, Appl
545	38.8	2.9	1004	4	US-09-071-232-3	Sequence 3, Appl	618	38.2	2.8	1941	3	US-09-368-240-2	Sequence 2, Appl
C 546	38.8	2.9	1230	3	US-09-140-466-1	Sequence 1, Appl	619	38.2	2.8	1941	3	US-09-468-702-2	Sequence 2, Appl
547	38.8	2.9	1511	1	US-07-991-867B-8	Sequence 8, Appl	620	38.2	2.8	2089	4	US-09-369-247-19	Sequence 19, Appl
548	38.8	2.9	1511	1	US-08-107-755A-8	Sequence 8, Appl	621	38.2	2.8	2950	4	US-09-489-847-92	Sequence 92, Appl
549	38.8	2.9	1511	2	US-08-544-332-8	Sequence 8, Appl	622	38.2	2.8	2964	4	US-09-578-063-25	Sequence 25, Appl
550	38.8	2.9	1511	3	US-09-370-861A-8	Sequence 8, Appl	623	38.2	2.8	3001	4	US-09-539-333D-187	Sequence 187, App
551	38.8	2.9	3605	4	US-08-949-016-36	Sequence 36, Appl	624	38.2	2.8	3999	3	US-09-351-224B-9	Sequence 9, Appl
552	38.8	2.9	4810	3	US-08-852-629-11	Sequence 11, Appl	625	38.2	2.8	3999	4	US-09-677-488A-9	Sequence 9, Appl
553	38.8	2.9	4838	3	US-08-852-629-15	Sequence 15, Appl	626	38.2	2.8	3999	4	US-09-677-488B-9	Sequence 9, Appl
C 554	38.8	2.9	2435	4	US-09-949-016-13927	Sequence 13927, A	627	38.2	2.8	3999	4	US-09-882-694B-9	Sequence 9, Appl
555	38.8	2.9	13631	4	US-09-949-016-17517	Sequence 17517, A	628	38.2	2.8	4545	6	5183884-3	Patent No. 5183884
C 556	38.8	2.9	37580	4	US-09-949-016-16658	Sequence 16658, A	629	38.2	2.8	4545	6	5183884-3	Patent No. 5183884
557	38.8	2.9	45299	4	US-09-949-016-12455	Sequence 12455, A	630	38.2	2.8	4905	1	US-07-978-895-3	Sequence 3, Appl
558	38.8	2.9	45300	4	US-09-949-016-13045	Sequence 13045, A	631	38.2	2.8	4905	1	US-08-473-119-3	Sequence 3, Appl
559	38.8	2.9	94142	4	US-09-949-016-16553	Sequence 16553, A	632	38.2	2.8	4905	2	US-08-475-352-3	Sequence 3, Appl
560	38.8	2.9	143248	4	US-09-949-016-16652	Sequence 16652, A	633	38.2	2.8	4905	4	US-09-170-699-3	Sequence 3, Appl
C 561	38.8	2.9	285478	4	US-09-949-016-13362	Sequence 13362, A	634	38.2	2.8	12246	4	US-09-949-016-14950	Sequence 14950, A
C 562	38.8	2.9	678533	4	US-09-949-016-14577	Sequence 14577, A	635	38.2	2.8	12513	4	US-09-949-016-14989	Sequence 14989, A
564	38.6	2.9	601	4	US-09-949-016-14578	Sequence 14578, A	636	38.2	2.8	27059	4	US-09-949-016-13893	Sequence 13893, A
565	38.6	2.9	601	4	US-09-949-016-37132	Sequence 37132, A	c 637	38.2	2.8	37385	4	US-09-949-016-12466	Sequence 12466, A
566	38.6	2.9	601	4	US-09-949-016-161109	Sequence 161109, A	638	38.2	2.8	37388	4	US-09-949-016-16846	Sequence 16846, A
567	38.6	2.9	601	4	US-09-949-016-179398	Sequence 179398, A	639	38.2	2.8	5586	4	US-09-949-016-15129	Sequence 15129, A
568	38.6	2.9	601	4	US-09-949-016-207003	Sequence 207003, A	640	38.2	2.8	92387	4	US-09-949-016-14563	Sequence 14563, A
569	38.6	2.9	601	4	US-09-949-016-207004	Sequence 207004, A	641	38.2	2.8	107800	4	US-09-949-016-13118	Sequence 13118, A
C 570	38.6	2.9	665	2	US-08-883-795A-36	Sequence 36, Appl	642	38.2	2.8	116425	4	US-09-949-016-11809	Sequence 11809, A
571	38.6	2.9	703	3	US-09-313-300-6	Sequence 3, Appl	643	38.2	2.8	151295	4	US-09-949-016-14568	Sequence 14568, A
C 572	38.6	2.9	870	5	PCT-US95-13658-3	Sequence 3, Appl	644	38.2	2.8	151295	4	US-09-949-016-14569	Sequence 14569, A
573	38.6	2.9	1420	2	US-08-909-965C-3	Sequence 3, Appl	645	38.2	2.8	151295	4	US-09-949-016-14570	Sequence 14570, A
574	38.6	2.9	1641	1	US-08-300-903A-8	Sequence 3, Appl	646	38.2	2.8	151295	4	US-09-949-016-14571	Sequence 14571, A
575	38.6	2.9	1641	4	US-08-988-197-8	Sequence 8, Appl	647	38.2	2.8	151295	4	US-09-949-016-14572	Sequence 14572, A
576	38.6	2.9	1641	4	US-10-385-072-8	Sequence 8, Appl	648	38.2	2.8	333753	4	US-09-949-016-14573	Sequence 14573, A
577	38.6	2.9	1689	3	US-09-053-374A-4	Sequence 4, Appl	649	38.2	2.8	333753	4	US-09-949-016-14574	Sequence 14574, A
C 578	38.6	2.9	19698	4	US-09-949-016-14079	Sequence 14079, A	650	38.2	2.8	580073	4	US-08-545-528B-1	Sequence 1, Appl
C 579	38.6	2.9	32488	4	US-09-949-016-15490	Sequence 15490, A	651	38.2	2.8	818128	4	US-09-949-016-14546	Sequence 14546, A
C 580	38.6	2.9	33044	4	US-09-949-016-17613	Sequence 17613, A	652	38.2	2.8	818128	4	US-09-949-016-14547	Sequence 14547, A
C 581	38.6	2.9	43069	4	US-09-292-542A-1	Sequence 1, Appl	653	38.2	2.8	818128	4	US-09-949-016-14548	Sequence 14548, A
582	38.6	2.9	46319	4	US-09-949-016-12526	Sequence 12526, A	654	38.2	2.8	818128	4	US-09-949-016-14549	Sequence 14549, A
C 583	38.6	2.9	46323	4	US-09-949-016-13267	Sequence 13267, A	655	38.2	2.8	818128	4	US-09-949-016-14550	Sequence 14550, A
C 584	38.6	2.9	88758	4	US-09-949-016-13502	Sequence 13502, A	656	38.2	2.8	818128	4	US-09-949-016-14551	Sequence 14551, A
C 585	38.6	2.9	95318	4	US-09-949-016-11784	Sequence 11784, A	657	38.2	2.8	818128	4	US-09-949-016-14552	Sequence 14552, A
C 586	38.6	2.9	95318	4	US-09-949-016-13998	Sequence 13998, A	658	38.2	2.8	818128	4	US-09-949-016-14553	Sequence 14553, A
C 587	38.6	2.9	114139	4	US-09-949-016-16536	Sequence 16536, A	659	38.2	2.8	818128	4	US-09-949-016-14554	Sequence 14554, A
588	38.4	2.9	207	4	US-09-621-976-10240	Sequence 10240, A	660	38.2	2.8	818128	4	US-09-949-016-14555	Sequence 14555, A
C 589	38.4	2.9	277	1	US-08-244-113-18	Sequence 18, Appl	661	38.2	2.8	818128	4	US-09-949-016-14556	Sequence 14556, A
C 590	38.4	2.9	340	1	US-08-171-385-27	Sequence 27, Appl	662	38.2	2.8	818128	4	US-09-949-016-14557	Sequence 14557, A
C 591	38.4	2.9	340	3	US-08-361-441B-27	Sequence 27, Appl	663	38.2	2.8	818128	4	US-09-949-016-14558	Sequence 14558, A
C 592	38.4	2.9	601	4	US-09-949-016-62108	Sequence 62108, A	664	38.2	2.8	818128	4	US-09-949-016-14559	Sequence 14559, A
C 593	38.4	2.9	601	4	US-09-949-016-75658	Sequence 75658, A	665	38.2	2.8	818128	4	US-09-949-016-14560	Sequence 14560, A
C 594	38.4	2.9	1033	4	US-09-610-185C-3	Sequence 3, Appl	666	38.2	2.8	818128	4	US-09-949-016-14561	Sequence 14561, A
C 595	38.4	2.9	2006	4	US-09-489-847-28	Sequence 28, Appl	667	38.2	2.8	818128	4	US-09-949-016-14562	Sequence 14562, A
C 596	38.4	2.9	2020	4	US-09-270-767-31322	Sequence 31322, A	668	38.2	2.8	818128	4	US-09-949-016-14564	Sequence 14564, A
C 597	38.4	2.9	2204	4	US-09-270-767-15031	Sequence 15031, A	669	38.2	2.8	818128	4	US-09-949-016-14565	Sequence 14565, A
C 598	38.4	2.9	9447	4	US-09-949-016-14649	Sequence 14649, A	670	38.2	2.8	818128	4	US-09-949-016-14566	Sequence 14566, A
C 599	38.4	2.9	57507	4	US-09-949-016-15019	Sequence 15019, A	c 671	38.2	2.8	818128	4	US-09-949-016-14567	Sequence 14567, A
C 600	38.4	2.9	108310	4	US-09-949-016-16366	Sequence 16366, A	672	38	2.8	511	4	US-09-621-976-17658	Sequence 17658, A
C 601	38.4	2.9	152070	4	US-09-949-016-15402	Sequence 15402, A	673	38	2.8	601	4	US-09-949-016-46620	Sequence 46620, A
C 602	38.4	2.9	462589	4	US-09-949-016-12900	Sequence 12900, A	674	38	2.8	601	4	US-09-949-016-46621	Sequence 46621, A
C 603	38.4	2.9	476044	4	US-09-949-016-12412	Sequence 12412, A	c 675	38	2.8	601	4	US-09-949-016-113173	Sequence 113173, A
C 604	38.2	2.8	168	4	US-09-621-976-15316	Sequence 15316, A	676	38	2.8	601	4	US-09-949-016-113636	Sequence 113636, A
C 605	38.2	2.8	173	4	US-09-621-976-15319	Sequence 15319, A	677	38	2.8	1096	4	US-09-270-767-5590	Sequence 5590, Ap
C 606	38.2	2.8	178	4	US-09-621-976-15322	Sequence 15322, A	678	38	2.8	1096	4	US-09-270-767-20872	Sequence 20872, A
C 607	38.2	2.8	180	4	US-09-621-976-15330	Sequence 15330, A	679	38	2.8	1240	4	US-09-720-317A-5	Sequence 5, Appl
C 608	38.2	2.8	194	4	US-09-621-976-15317	Sequence 15317, A	680	38	2.8	1477	4	US-09-585-173B-7	Sequence 7, Appl
C 609	38.2	2.8	675	4	US-09-621-976-2461	Sequence 2461, Ap	681	38	2.8	1688	2	US-08-439-814-2	Sequence 2, Appl
C 610	38.2	2.8	865	4	US-09-557-170A-1	Sequence 1, Appl	682	38	2.8	1910	3	US-09-517-467B-7	Sequence 7, Appl
C 611	38.2	2.8	865	4	US-09-557-170A-12	Sequence 12, Appl	683	38	2.8	1964	3	US-09-434-613-2	Sequence 2, Appl
							684	38	2.8				



c 831	37.2	2.8	396	4	US-09-970-966-16	Sequence 16, Appl	904	37	2.7	2007	4	US-09-328-352-2460	Sequence 2460, Ap
c 832	37.2	2.8	601	4	US-09-949-016-130251	Sequence 130251,	905	37	2.7	2144	3	US-08-747-221B-57	Sequence 57, Appl
c 833	37.2	2.8	601	4	US-09-949-016-167173	Sequence 167173,	c 906	37	2.7	2144	3	US-08-747-221B-59	Sequence 59, Appl
c 834	37.2	2.8	610	4	US-09-270-767-15032	Sequence 15032, A	c 907	37	2.7	2144	3	US-09-005-051-57	Sequence 57, Appl
c 835	37.2	2.8	757	4	US-09-270-767-5589	Sequence 5589, Ap	c 908	37	2.7	2144	3	US-09-005-051-59	Sequence 59, Appl
c 836	37.2	2.8	757	4	US-09-270-767-20871	Sequence 20871, A	c 909	37	2.7	2144	4	US-09-403-942F-57	Sequence 57, Appl
c 837	37.2	2.8	817	3	US-08-885-469-1	Sequence 1, Appli	c 910	37	2.7	2144	4	US-09-403-942F-59	Sequence 59, Appl
c 838	37.2	2.8	817	3	US-09-625-918-1	Sequence 1, Appli	c 911	37	2.7	2287	4	US-09-949-016-134	Sequence 134, App
c 839	37.2	2.8	923	3	US-08-906-769-144	Sequence 144, App	c 912	37	2.7	3130	2	US-08-474-379C-62	Sequence 62, Appl
c 840	37.2	2.8	923	3	US-08-906-616-144	Sequence 144, App	c 913	37	2.7	3130	2	US-09-146-249A-62	Sequence 62, Appl
c 841	37.2	2.8	923	3	US-08-639-075A-144	Sequence 144, App	c 914	37	2.7	3130	3	US-08-206-188B-62	Sequence 62, Appl
c 842	37.2	2.8	923	3	US-09-012-431-144	Sequence 144, App	c 915	37	2.7	4595	4	US-09-023-905A-9	Sequence 9, Appli
c 843	37.2	2.8	923	3	US-09-012-692-144	Sequence 144, App	c 916	37	2.7	5798	4	US-09-377-285B-33	Sequence 33, Appl
c 844	37.2	2.8	923	3	US-08-906-613-144	Sequence 144, App	c 917	37	2.7	6152	3	US-08-973-462-1	Sequence 1, Appli
c 845	37.2	2.8	1159	3	US-09-410-464-14	Sequence 14, Appl	c 918	37	2.7	22294	4	US-09-949-016-14020	Sequence 14020, A
c 846	37.2	2.8	1279	3	US-09-277-716-31	Sequence 31, Appl	c 919	37	2.7	25199	4	US-09-949-016-13361	Sequence 13361, A
c 847	37.2	2.8	1279	3	US-09-609-161B-31	Sequence 31, Appl	c 920	37	2.7	33519	4	US-09-949-016-17165	Sequence 17165, A
c 848	37.2	2.8	1289	4	US-09-270-767-6619	Sequence 6619, Ap	c 921	37	2.7	45587	4	US-09-949-016-15836	Sequence 15836, A
c 849	37.2	2.8	1289	4	US-09-270-767-21901	Sequence 21901, A	c 922	37	2.7	56939	4	US-09-949-016-13613	Sequence 13613, A
c 850	37.2	2.8	1712	4	US-09-148-545-106	Sequence 106, App	c 923	37	2.7	66933	4	US-09-544-398B-11	Sequence 11, Appl
c 851	37.2	2.8	1753	3	US-09-149-476-56	Sequence 56, Appl	c 924	37	2.7	66933	4	US-09-543-771B-11	Sequence 11, Appl
c 852	37.2	2.8	1822	4	US-09-148-545-105	Sequence 105, App	c 925	37	2.7	72049	4	US-09-544-398B-9	Sequence 9, Appli
c 853	37.2	2.8	1939	1	US-07-715-751B-2	Sequence 2, Appli	c 926	37	2.7	72049	4	US-09-543-771B-9	Sequence 9, Appli
c 854	37.2	2.8	2202	3	US-09-388-743-1	Sequence 1, Appli	c 927	37	2.7	76281	4	US-09-949-016-12708	Sequence 12708, A
c 855	37.2	2.8	2202	4	US-10-044-543-1	Sequence 1, Appli	c 928	37	2.7	117391	4	US-09-949-016-13945	Sequence 13945, A
c 856	37.2	2.8	2680	4	US-09-614-408-7	Sequence 7, Appli	c 929	37	2.7	192302	4	US-09-949-016-15270	Sequence 15270, A
c 857	37.2	2.8	2798	3	US-09-318-448-34	Sequence 34, Appl	c 930	37	2.7	343352	4	US-09-949-016-13498	Sequence 13498, A
c 858	37.2	2.8	3355	4	US-09-949-016-57	Sequence 57, Appl	c 931	36.8	2.7	90	4	US-09-621-976-9330	Sequence 9330, Ap
c 859	37.2	2.8	3437	3	US-08-860-339-17	Sequence 17, Appl	c 932	36.8	2.7	351	4	US-09-621-976-15134	Sequence 15134, A
c 860	37.2	2.8	3437	4	US-09-573-629-17	Sequence 17, Appl	c 933	36.8	2.7	396	4	US-09-640-173-25	Sequence 25, Appl
c 861	37.2	2.8	3437	4	US-10-208-349-7	Sequence 7, Appli	c 934	36.8	2.7	396	4	US-09-713-550-25	Sequence 25, Appl
c 862	37.2	2.8	3527	2	US-08-909-965C-7	Sequence 7, Appli	c 935	36.8	2.7	396	4	US-09-713-550-33	Sequence 33, Appl
c 863	37.2	2.8	4239	4	US-09-815-048-1	Sequence 1, Appli	c 936	36.8	2.7	396	4	US-09-825-294-25	Sequence 25, Appl
c 864	37.2	2.8	7879	4	US-09-949-016-12132	Sequence 12132, A	c 937	36.8	2.7	396	4	US-09-825-294-33	Sequence 33, Appl
c 865	37.2	2.8	10136	1	US-08-353-700-2	Sequence 2, Appli	c 938	36.8	2.7	396	4	US-09-825-294-33	Sequence 33, Appl
c 866	37.2	2.8	10136	5	PCT-US95-16216-2	Sequence 2, Appli	c 939	36.8	2.7	396	4	US-09-970-966-25	Sequence 25, Appl
c 867	37.2	2.8	47555	4	US-09-949-016-16549	Sequence 16549, A	c 940	36.8	2.7	396	4	US-09-970-966-33	Sequence 33, Appl
c 868	37.2	2.8	49673	4	US-09-949-016-12598	Sequence 12598, A	c 941	36.8	2.7	531	3	US-09-399-913-37	Sequence 37, Appl
c 869	37.2	2.8	52971	4	US-09-949-016-16452	Sequence 16452, A	c 942	36.8	2.7	531	3	US-09-350-614-37	Sequence 37, Appl
c 870	37.2	2.8	88758	4	US-09-949-016-13502	Sequence 13502, A	c 943	36.8	2.7	601	4	US-09-949-016-37136	Sequence 37136, A
c 871	37.2	2.8	108310	4	US-09-949-016-16366	Sequence 16366, A	c 944	36.8	2.7	601	4	US-09-949-016-53731	Sequence 53731, A
c 872	37.2	2.8	786431	4	US-09-751-389-3	Sequence 3, Appli	c 945	36.8	2.7	601	4	US-09-949-016-161113	Sequence 161113, A
c 873	37	2.7	259	4	US-09-621-976-10203	Sequence 10203, A	c 946	36.8	2.7	601	4	US-09-949-016-185995	Sequence 185995, A
c 874	37	2.7	259	4	US-09-621-976-10297	Sequence 10297, A	c 947	36.8	2.7	601	4	US-09-949-016-185996	Sequence 185996, A
c 875	37	2.7	266	4	US-09-621-976-10269	Sequence 10269, A	c 948	36.8	2.7	979	4	US-09-770-916-3	Sequence 3, Appli
c 876	37	2.7	271	4	US-09-621-976-10193	Sequence 10193, A	c 949	36.8	2.7	1016	4	US-09-716-129-42	Sequence 42, Appl
c 877	37	2.7	279	4	US-09-621-976-10220	Sequence 10220, A	c 950	36.8	2.7	1100	3	US-07-861-458C-4	Sequence 4, Appli
c 878	37	2.7	299	4	US-09-621-976-10211	Sequence 10211, A	c 951	36.8	2.7	1230	3	US-09-387-574-5	Sequence 5, Appli
c 879	37	2.7	595	3	US-09-385-982-276	Sequence 276, App	c 952	36.8	2.7	1230	3	US-09-668-096-5	Sequence 5, Appli
c 880	37	2.7	601	4	US-09-949-016-144793	Sequence 144793,	c 953	36.8	2.7	1440	2	US-08-743-637B-174	Sequence 174, App
c 881	37	2.7	601	4	US-09-949-016-144794	Sequence 144794,	c 954	36.8	2.7	1440	2	US-08-526-840B-174	Sequence 174, App
c 882	37	2.7	822	1	US-07-644-372-1	Sequence 1, Appli	c 955	36.8	2.7	1440	4	US-09-107-532A-3398	Sequence 3398, Ap
c 883	37	2.7	832	4	US-09-621-976-2813	Sequence 2813, Ap	c 956	36.8	2.7	1440	4	US-09-134-000C-1302	Sequence 1302, Ap
c 884	37	2.7	991	3	US-08-924-747-25	Sequence 25, Appl	c 957	36.8	2.7	1466	3	US-08-984-919A-10	Sequence 10, Appl
c 885	37	2.7	991	3	US-09-247-373B-25	Sequence 25, Appl	c 958	36.8	2.7	1466	3	US-08-984-919A-12	Sequence 12, Appl
c 886	37	2.7	991	3	US-09-236-715-25	Sequence 25, Appl	c 959	36.8	2.7	1472	3	US-08-781-420-10	Sequence 10, Appl
c 887	37	2.7	1042	3	US-09-978-289-7	Sequence 7, Appli	c 960	36.8	2.7	1472	3	US-08-781-420-12	Sequence 12, Appl
c 888	37	2.7	1151	4	US-09-270-767-12633	Sequence 12633, A	c 961	36.8	2.7	1472	3	US-08-874-102-10	Sequence 10, Appl
c 889	37	2.7	1190	4	US-09-390-207-1	Sequence 1, Appli	c 962	36.8	2.7	1472	3	US-08-874-102-12	Sequence 12, Appl
c 890	37	2.7	1374	4	US-09-601-198-158	Sequence 158, App	c 963	36.8	2.7	1472	3	US-09-006-595A-10	Sequence 10, Appl
c 891	37	2.7	1465	4	US-09-573-906-1	Sequence 1, Appli	c 964	36.8	2.7	1472	3	US-09-006-595A-12	Sequence 12, Appl
c 892	37	2.7	1486	4	US-09-461-325-73	Sequence 73, Appl	c 965	36.8	2.7	1580	4	US-09-057-996-16	Sequence 16, Appl
c 893	37	2.7	1486	4	US-10-012-542-73	Sequence 73, Appl	c 966	36.8	2.7	1803	3	US-09-134-001C-799	Sequence 799, App
c 894	37	2.7	1486	4	US-10-115-123-73	Sequence 73, Appl	c 967	36.8	2.7	1875	3	US-08-984-919A-46	Sequence 46, Appl
c 895	37	2.7	1872	3	US-09-801-052-1	Sequence 1, Appli	c 968	36.8	2.7	1875	3	US-08-984-919A-48	Sequence 48, Appl
c 896	37	2.7	1872	4	US-10-020-121-1	Sequence 1, Appli	c 969	36.8	2.7	1881	3	US-08-874-102-46	Sequence 46, Appl
c 897	37	2.7	1927	4	US-09-187-999-12	Sequence 12, Appl	c 970	36.8	2.7	1881	3	US-08-874-102-48	Sequence 48, Appl
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c 899	37	2.7	1982	3	US-08-747-221B-15	Sequence 15, Appl	c 972	36.8	2.7	2047	3	US-09-414-453A-1	Sequence 1, Appli
c 900	37	2.7	1982	3	US-09-005-051-13	Sequence 13, Appl	c 973	36.8	2.7	2311	4	US-09-720-317A-19	Sequence 19, Appl
c 901	37	2.7	1982	3	US-09-005-051-15	Sequence 15, Appl	c 974	36.8	2.7	2369	4	US-09-057-996-13	Sequence 13, Appl
c 902	37	2.7	1982	4	US-09-403-942F-13	Sequence 13, Appl	c 975	36.8	2.7	3335	4	US-09-710-279-3503	Sequence 3503, Ap
c 903	37	2.7	1982	4	US-09-403-942F-15	Sequence 15, Appl	c 976	36.8	2.7	3377	6	US-09-403-942F-15	Sequence 15, Appl



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978	36.8	2.7	3465	4	US-09-710-279-4254	Sequence 4254, Ap	1051	36.6	2.7	7101	3	US-08-957-310-9	Sequence 9, Appli
979	36.8	2.7	3606	4	US-10-164-595-37	Sequence 37, Appl	1052	36.6	2.7	7101	4	US-10-011-366-9	Sequence 9, Appli
980	36.8	2.7	4685	3	US-08-948-378A-7	Sequence 7, Appli	1053	36.6	2.7	7101	4	US-09-084-517-9	Sequence 9, Appli
981	36.8	2.7	4665	3	US-09-169-425C-7	Sequence 7, Appli	1054	36.6	2.7	20674	3	US-09-641-638-651	Sequence 651, App
982	36.8	2.7	4665	3	US-09-759-960-7	Sequence 7, Appli	1055	36.6	2.7	20674	3	US-10-170-097-651	Sequence 651, App
c 983	36.8	2.7	43435	4	US-09-949-016-12909	Sequence 12909, A	c1056	36.6	2.7	50381	4	US-09-949-016-17122	Sequence 17122, A
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985	36.8	2.7	80246	3	US-08-078-294-4	Sequence 4, Appli	1058	36.6	2.7	52032	4	US-09-949-016-11789	Sequence 11789, A
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987	36.8	2.7	87648	4	US-09-949-016-13655	Sequence 13655, A	1060	36.6	2.7	69813	4	US-09-949-016-13905	Sequence 13905, A
988	36.8	2.7	93493	4	US-09-949-016-13672	Sequence 12063, A	1061	36.6	2.7	69813	4	US-09-949-016-13906	Sequence 13906, A
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c 993	36.8	2.7	107458	4	US-09-949-016-15687	Sequence 15687, A	c1066	36.6	2.7	115508	4	US-09-949-016-11800	Sequence 11800, A
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c 996	36.8	2.7	194515	4	US-09-949-016-15584	Sequence 15584, A	c1069	36.6	2.7	129658	4	US-09-949-016-17195	Sequence 17195, A
c 997	36.8	2.7	201529	4	US-08-949-016-12740	Sequence 12740, A	c1070	36.6	2.7	153866	4	US-09-949-016-16919	Sequence 16919, A
c 998	36.8	2.7	260247	4	US-09-949-016-13358	Sequence 13358, A	c1071	36.6	2.7	165841	4	US-09-949-016-16192	Sequence 16192, A
c 999	36.8	2.7	298336	4	US-09-949-016-16600	Sequence 16600, A	c1072	36.6	2.7	173992	4	US-09-949-016-13379	Sequence 13379, A
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1001	36.6	2.7	147	4	US-09-621-976-10254	Sequence 10254, Ap	c1074	36.6	2.7	319608	4	US-09-679-409-1	Sequence 1, Appli
1002	36.6	2.7	155	4	US-09-621-976-11009	Sequence 11009, A	1075	36.6	2.7	331814	4	US-09-949-016-12008	Sequence 12008, A
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c1005	36.6	2.7	601	4	US-09-949-016-31837	Sequence 31837, A	1078	36.4	2.7	165	4	US-09-621-976-8127	Sequence 8127, Ap
c1006	36.6	2.7	601	4	US-09-949-016-40022	Sequence 40022, A	1079	36.4	2.7	168	4	US-09-621-976-16870	Sequence 16870, A
c1007	36.6	2.7	601	4	US-09-949-016-66699	Sequence 66699, A	1080	36.4	2.7	179	4	US-09-621-976-16872	Sequence 16872, A
c1008	36.6	2.7	601	4	US-09-949-016-74004	Sequence 74004, A	1081	36.4	2.7	182	4	US-09-621-976-16871	Sequence 16871, A
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c1010	36.6	2.7	601	4	US-09-949-016-75960	Sequence 75960, A	1083	36.4	2.7	235	4	US-09-270-767-30375	Sequence 30375, A
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1016	36.6	2.7	725	4	US-09-270-767-14605	Sequence 14605, A	1089	36.4	2.7	558	4	US-09-736-457-554	Sequence 554, App
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c1019	36.6	2.7	1308	4	US-09-270-767-12890	Sequence 12890, A	1092	36.4	2.7	558	4	US-09-589-184-554	Sequence 554, App
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1021	36.6	2.7	1454	2	US-08-975-316-7	Sequence 7, Appli	1094	36.4	2.7	575	1	US-08-554-659-11	Sequence 11, Appli
1022	36.6	2.7	1454	3	US-09-211-710-7	Sequence 7, Appli	c1095	36.4	2.7	601	4	US-09-949-016-27085	Sequence 27085, A
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1024	36.6	2.7	1454	3	US-09-169-789-7	Sequence 7, Appli	1097	36.4	2.7	601	4	US-09-949-016-81779	Sequence 81779, A
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1124	36.4	2.7	601	4	US-09-949-016-115291	Sequence 115291,	1197	36.2	2.7	266	4	US-09-621-976-16813	Sequence 16813, A
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1126	36.4	2.7	601	4	US-09-949-016-115293	Sequence 115293,	1199	36.2	2.7	378	4	US-09-621-976-17965	Sequence 17965, A
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1128	36.4	2.7	601	4	US-09-949-016-115295	Sequence 115295,	1201	36.2	2.7	601	4	US-09-949-016-28996	Sequence 28996, A
1129	36.4	2.7	601	4	US-09-949-016-115296	Sequence 115296,	1202	36.2	2.7	601	4	US-09-949-016-28997	Sequence 28997, A
1130	36.4	2.7	601	4	US-09-949-016-126254	Sequence 126254,	1203	36.2	2.7	601	4	US-09-949-016-28998	Sequence 28998, A
1131	36.4	2.7	601	4	US-09-949-016-137684	Sequence 137684,	1204	36.2	2.7	601	4	US-09-949-016-62109	Sequence 62109, A
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1133	36.4	2.7	767	3	US-08-998-416-472	Sequence 472, App	1206	36.2	2.7	601	4	US-09-949-016-74456	Sequence 74456, A
1134	36.4	2.7	882	2	US-08-909-965C-9	Sequence 9, Appli	1207	36.2	2.7	601	4	US-09-949-016-111546	Sequence 111546,
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1136	36.4	2.7	1001	4	US-09-508-824-18	Sequence 18, Appl	1209	36.2	2.7	601	4	US-09-949-016-111840	Sequence 111840,
1137	36.4	2.7	1193	4	US-09-526-597D-5	Sequence 5, Appli	1210	36.2	2.7	601	4	US-09-949-016-111985	Sequence 111985,
1138	36.4	2.7	1236	6	5202236-4	Patent No. 5202236	1211	36.2	2.7	601	4	US-09-949-016-148284	Sequence 148284,
1139	36.4	2.7	1236	6	5202236-4	Patent No. 5202236	1212	36.2	2.7	601	4	US-09-949-016-148285	Sequence 148285,
1140	36.4	2.7	1274	3	US-08-335-844A-13	Sequence 13, Appl	1213	36.2	2.7	601	4	US-09-949-016-148286	Sequence 148286,
1141	36.4	2.7	1274	3	US-09-129-366-13	Sequence 13, Appl	1214	36.2	2.7	663	3	US-08-998-416-191	Sequence 191, App
1142	36.4	2.7	1343	4	US-09-270-767-14246	Sequence 14246, A	1215	36.2	2.7	803	4	US-09-800-729-60	Sequence 60, Appl
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1144	36.4	2.7	1386	2	US-09-252-329-1	Sequence 1, Appli	1217	36.2	2.7	1114	3	US-09-152-060-41	Sequence 41, Appl
1145	36.4	2.7	1699	3	US-09-152-060-19	Sequence 19, Appl	1218	36.2	2.7	1116	3	US-08-916-443A-16	Sequence 16, Appl
1146	36.4	2.7	1802	3	US-09-032-523-5	Sequence 5, Appli	1219	36.2	2.7	1240	1	US-08-388-756-1	Sequence 1, Appli
1147	36.4	2.7	1802	3	US-09-802-633-5	Sequence 5, Appli	1220	36.2	2.7	1240	2	US-08-748-428-1	Sequence 1, Appli
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1151	36.4	2.7	2080	4	US-10-003-392-1	Sequence 1, Appli	1224	36.2	2.7	1378	4	US-09-935-038A-4	Sequence 4, Appli
1152	36.4	2.7	2101	4	US-08-190-204-1	Sequence 1, Appli	1225	36.2	2.7	1411	3	US-08-964-127-5	Sequence 5, Appli
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1154	36.4	2.7	2218	3	US-09-165-543-31	Sequence 31, Appl	1227	36.2	2.7	1411	3	US-10-000-272-5	Sequence 5, Appli
1155	36.4	2.7	2581	2	US-09-013-634-1	Sequence 1, Appli	1228	36.2	2.7	1459	3	US-09-537-654-3	Sequence 3, Appli
1156	36.4	2.7	2646	4	US-09-673-395A-116	Sequence 116, App	1229	36.2	2.7	1582	3	US-08-545-196B-10	Sequence 10, Appl
1157	36.4	2.7	3244	3	US-09-165-543-4	Sequence 4, Appli	1230	36.2	2.7	1582	3	US-08-545-196B-12	Sequence 12, Appl
1158	36.4	2.7	3720	3	US-09-342-681C-12	Sequence 12, Appl	1231	36.2	2.7	1821	4	US-08-545-196B-59	Sequence 59, Appl
1159	36.4	2.7	3722	3	US-09-058-947A-1	Sequence 1, Appli	1232	36.2	2.7	1851	3	US-09-149-476-62	Sequence 62, Appl
1160	36.4	2.7	3981	4	US-09-799-451-250	Sequence 250, App	1233	36.2	2.7	1866	4	US-09-673-395A-24	Sequence 24, Appl
1161	36.4	2.7	4275	4	US-09-972-115A-5	Sequence 5, Appli	1234	36.2	2.7	1882	3	US-09-370-253-1	Sequence 1, Appli
1162	36.4	2.7	4297	4	US-09-972-115A-3	Sequence 3, Appli	1235	36.2	2.7	1883	4	US-09-419-679-13	Sequence 13, Appl
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1169	36.4	2.7	13335	4	US-09-949-016-14676	Sequence 14676, A	1242	36.2	2.7	4827	4	US-09-949-016-525	Sequence 525, App
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1174	36.4	2.7	88036	4	US-09-949-016-15608	Sequence 15608, A	1247	36.2	2.7	6768	1	US-08-107-755A-1	Sequence 1, Appli
1175	36.4	2.7	93920	4	US-09-949-016-15335	Sequence 15335, A	1248	36.2	2.7	8457	2	US-07-991-867B-1	Sequence 1, Appli
1176	36.4	2.7	93920	4	US-09-949-016-12431	Sequence 12431, A	1249	36.2	2.7	8457	2	US-08-544-332-1	Sequence 1, Appli
1177	36.4	2.7	93920	4	US-09-949-016-16853	Sequence 16853, A	1250	36.2	2.7	8457	3	US-09-370-861A-1	Sequence 1, Appli
1178	36.4	2.7	125192	4	US-09-949-016-14120	Sequence 14120, A	1251	36.2	2.7	8920	3	US-08-446-855A-1	Sequence 1, Appli
1179	36.4	2.7	135476	4	US-09-949-016-14896	Sequence 14896, A	1252	36.2	2.7	8920	3	US-09-150-741-1	Sequence 1, Appli
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1181	36.4	2.7	135476	4	US-09-949-016-14413	Sequence 14413, A	1254	36.2	2.7	12909	4	US-09-949-016-16689	Sequence 16689, A
1182	36.4	2.7	140925	4	US-09-949-016-11777	Sequence 11777, A	1255	36.2	2.7	15442	4	US-09-949-016-13916	Sequence 13916, A
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1185	36.4	2.7	193555	4	US-09-949-016-15553	Sequence 15553, A	1258	36.2	2.7	35355	4	US-09-949-016-14197	Sequence 14197, A
1186	36.4	2.7	193555	4	US-09-949-016-15554	Sequence 15554, A	1259	36.2	2.7	42894	4	US-09-949-016-12301	Sequence 12301, A
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c1277	36.2	2.7	222452	4	US-09-949-016-12968	Sequence 12968, A	c1350	36	2.7	58768	4	US-09-949-016-13175	Sequence 13175, A
c1278	36.2	2.7	255679	4	US-09-949-016-17189	Sequence 17189, A	c1351	36	2.7	77861	4	US-09-949-016-12770	Sequence 12770, A
c1279	36.2	2.7	300598	4	US-09-949-016-11868	Sequence 11868, A	c1352	36	2.7	77862	4	US-09-949-016-13751	Sequence 13751, A
c1280	36.2	2.7	312474	4	US-09-949-016-17434	Sequence 17434, A	c1353	36	2.7	79824	4	US-09-949-016-13919	Sequence 13919, A
c1281	36	2.7	144	1	US-08-702-344-26	Sequence 26, Appl	c1354	36	2.7	90050	3	US-09-245-041-5	Sequence 5, Appl
c1282	36	2.7	189	4	US-09-621-976-14761	Sequence 14761, A	c1355	36	2.7	90050	4	US-09-358-0558-5	Sequence 5, Appl
c1283	36	2.7	220	4	US-09-621-976-12495	Sequence 12495, A	c1356	36	2.7	90050	4	US-09-893-238-5	Sequence 5, Appl
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c1285	36	2.7	413	3	US-09-227-357-71	Sequence 71, Appl	c1358	36	2.7	112507	4	US-09-949-016-12420	Sequence 12420, A
c1286	36	2.7	441	4	US-09-270-767-11553	Sequence 11553, A	c1359	36	2.7	112507	4	US-09-949-016-12794	Sequence 12794, A
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c1293	36	2.7	601	4	US-09-949-016-163707	Sequence 163707, A	c1366	36	2.7	112508	4	US-09-949-016-16590	Sequence 16590, A
c1294	36	2.7	601	4	US-09-949-016-168298	Sequence 168298, A	c1367	36	2.7	112508	4	US-09-949-016-16590	Sequence 16590, A
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c1298	36	2.7	601	4	US-09-949-016-196367	Sequence 196367, A	c1371	35.8	2.7	147	4	US-09-621-976-10383	Sequence 10383, A
c1299	36	2.7	687	4	US-09-774-639-106	Sequence 106, Appl	c1372	35.8	2.7	244	3	US-08-750-717-8	Sequence 8, Appl
c1300	36	2.7	708	4	US-09-270-767-13081	Sequence 13081, A	c1373	35.8	2.7	596	4	US-09-311-021-163	Sequence 163, Appl
c1301	36	2.7	739	1	US-08-363-010-3	Sequence 3, Appl	c1374	35.8	2.7	601	4	US-09-949-016-28999	Sequence 28999, A
c1302	36	2.7	813	1	US-08-514-014-11	Sequence 11, Appl	c1375	35.8	2.7	601	4	US-09-949-016-54238	Sequence 54238, A
c1303	36	2.7	813	1	US-08-833-823-11	Sequence 11, Appl	c1376	35.8	2.7	601	4	US-09-949-016-54239	Sequence 54239, A
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c1305	36	2.7	813	3	US-08-685-239-1	Sequence 1, Appl	c1378	35.8	2.7	601	4	US-09-949-016-76700	Sequence 76700, A
c1306	36	2.7	1040	3	US-08-978-289-5	Sequence 5, Appl	c1379	35.8	2.7	601	4	US-09-949-016-86309	Sequence 86309, A
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c1308	36	2.7	1215	1	US-08-592-214A-1	Sequence 1, Appl	c1381	35.8	2.7	601	4	US-09-949-016-148287	Sequence 148287, A
c1309	36	2.7	1215	3	US-09-149-976-1	Sequence 1, Appl	c1382	35.8	2.7	664	4	US-09-904-615-66	Sequence 165815, A
c1310	36	2.7	1652	3	US-09-627-6508-2	Sequence 2, Appl	c1383	35.8	2.7	763	4	US-09-743-207-3	Sequence 3, Appl
c1311	36	2.7	1652	3	US-09-436-0630-2	Sequence 2, Appl	c1384	35.8	2.7	863	3	US-08-998-416-498	Sequence 498, Appl
c1312	36	2.7	1740	1	US-08-362-512A-3	Sequence 3, Appl	c1385	35.8	2.7	1215	4	US-09-710-279-1129	Sequence 1129, Appl
c1313	36	2.7	1740	3	US-08-964-939-3	Sequence 3, Appl	c1386	35.8	2.7	1215	4	US-09-244-805-7	Sequence 7, Appl
c1314	36	2.7	1740	4	US-09-854-774-3	Sequence 3, Appl	c1387	35.8	2.7	1330	4	US-09-344-882-7	Sequence 7, Appl
c1315	36	2.7	1810	4	US-09-800-729-73	Sequence 73, Appl	c1388	35.8	2.7	1539	3	US-09-364-230-29	Sequence 29, Appl
c1316	36	2.7	1811	4	US-08-706-214-1	Sequence 1, Appl	c1389	35.8	2.7	1810	4	US-09-369-247-11	Sequence 11, Appl
c1317	36	2.7	1856	1	US-08-706-214-1	Sequence 1, Appl	c1390	35.8	2.7	1848	4	US-09-323-998E-46	Sequence 46, Appl
c1318	36	2.7	1856	4	US-09-949-016-475	Sequence 475, Appl	c1391	35.8	2.7	2196	3	US-09-149-476-163	Sequence 163, Appl
c1319	36	2.7	2132	3	US-09-552-322-1	Sequence 1, Appl	c1392	35.8	2.7	2239	4	US-09-196-390-1	Sequence 1, Appl
c1320	36	2.7	2511	4	US-09-319-497-36	Sequence 36, Appl	c1393	35.8	2.7	2239	4	US-09-952-677-1	Sequence 1, Appl
c1321	36	2.7	2525	3	US-09-234-393-39	Sequence 39, Appl	c1394	35.8	2.7	2525	4	US-09-579-383-5	Sequence 5, Appl
c1322	36	2.7	2525	3	US-09-865-171-39	Sequence 39, Appl	c1395	35.8	2.7	2620	1	US-08-188-228-57	Sequence 57, Appl
c1323	36	2.7	2862	1	US-08-148-209A-1	Sequence 1, Appl	c1396	35.8	2.7	2625	1	US-08-332-643-51	Sequence 51, Appl
c1324	36	2.7	3001	4	US-09-539-3330-204	Sequence 204, Appl	c1397	35.8	2.7	2625	1	US-08-332-643-57	Sequence 57, Appl
c1325	36	2.7	3453	1	US-07-813-593-1	Sequence 1, Appl	c1398	35.8	2.7	2625	3	US-09-654-328-1	Sequence 1, Appl
c1326	36	2.7	3453	1	US-07-977-451-1	Sequence 1, Appl	c1399	35.8	2.7	3252	3	US-09-118-442-1	Sequence 1, Appl
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c1329	36	2.7	3453	1	US-07-306-397A-1	Sequence 1, Appl	c1402	35.8	2.7	3712	2	US-10-164-595-9	Sequence 9, Appl
c1330	36	2.7	3453	1	US-08-601-891-1	Sequence 1, Appl	c1403	35.8	2.7	3712	2	US-10-164-595-5	Sequence 5, Appl
c1331	36	2.7	3453	2	US-09-021-324-1	Sequence 1, Appl	c1404	35.8	2.7	3862	4	US-10-164-595-7	Sequence 7, Appl
c1332	36	2.7	3453	4	US-09-872-1368-1	Sequence 1, Appl	c1405	35.8	2.7	3937	4	US-10-164-595-3	Sequence 3, Appl
c1333	36	2.7	3453	5	PCT-US92-02750-1	Sequence 1, Appl	c1406	35.8	2.7	3985	4	US-08-869-696-1	Sequence 1, Appl
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c1335	36	2.7	3453	5	PCT-US92-09893-1	Sequence 1, Appl	c1408	35.8	2.7	7430	4	US-08-956-171E-260	Sequence 260, Appl
c1336	36	2.7	7382	4	US-09-233-857-1	Sequence 1, Appl	c1409	35.8	2.7	7430	4	US-08-781-986A-260	Sequence 260, Appl
c1337	36	2.7	8239	4	US-09-029-047C-1	Sequence 1, Appl	c1410	35.8	2.7	12311	3	US-08-750-717-1	Sequence 1, Appl
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c1430 35.6 2.6 149 4 US-09-621-976-17385 Sequence 17385, A
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c1433 35.6 2.6 261 4 US-09-621-976-18330 Sequence 18330, A
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c1453 35.6 2.6 601 4 US-09-949-016-53733 Sequence 53733, A
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c1470 35.6 2.6 723 4 US-09-270-767-4630 Sequence 4630, Ap
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c1472 35.6 2.6 731 1 US-08-451-405A-2 Sequence 2, Appli
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1498 35.6 2.6 1621 4 US-09-688-489-107 Sequence 107, App
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## ALIGNMENTS

## RESULT 1

US-09-289-349-6

; Sequence 6, Application US/09289349

; Patent No. 6277574

; GENERAL INFORMATION:

; APPLICANT: Walker, Michael, G.

; APPLICANT: Voikmuth, Wayne

; APPLICANT: Klingner, Tod, M.

; APPLICANT: Azimzai, Yalda

; APPLICANT: Yue, Henry

; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY

; FILE REFERENCE: PB-0010 US

; CURRENT APPLICATION NUMBER: US/09/289,349

; CURRENT FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PERL Program

; SEQ ID NO 6

; LENGTH: 862

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE: -

; OTHER INFORMATION: 2580580CT1

US-09-289-349-6

Query Match 62.8%; Score 845.2; DB 3; Length 862;  
Best Local Similarity 99.5%; Pred. No. 2.3e-200;  
Matches 858; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

Qy 472 GTTGCATTGCCTACTCTGATTTTATCAGGATCTGGCAACGTAGAACGACACAGAA 531

Db 1 GTTGCATTGCCTACTCTGATTTTATCAGGATCTGGCAACGTAGAACGACACAGAA 60

Qy 532 CCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTGAAATGGC 591

Db 61 CCATCTGAAGTGGATGACGCTGAAGATAAGTGTGAAACATGATCACAATTGAAATGGC 120

Qy 592 ATCCCTCTGATCCCTGGACATGAAGGG-GGGCATATTATGATGCTTCATGACAGAG 650

Db 121 ATCCCTCTGATCCCTGGACATGAAGGGGGCATATTATGATGCTTCATGACAGAG 180

Qy 651 GATGAGAGGCTCACCCCTCTCTGAGGGCTGTGTTCTGCTTCTCAAGAAATTAACAT 710

Db 181 GATGAGAGGCTCACCCCTCTCTGAGGGGCTGTGTTCTGCTTCTCAAGAAATTAACAT 240

Qy 711 TTGTTCTCTGTGCTACTCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTGTTT 770

Db 241 TTGTTCTCTGTGCTACTCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTGTTT 300

Qy 771 CACCATTTCTTTTGTGTAATAAATTTTGAATGTGCTTGAAGTGAAGCAATCAATAT 830

Db 301 CACCATTTCTTTTGTGTAATAAATTTTGAATGTGCTTGAAGTGAAGCAATCAATAT 360

Qy 831 ACCCACCACACCACTGAAATCATATGAGCTATTACGACTCAAAATATTTCTAAATATTTT 890

Db 361 ACCCACCACACCACTGAAATCATATGAGCTATTACGACTCAAAATATTTCTAAATATTTT 420

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QY 1071 TTGACAGTCACTTATATCACTCTGTATATGACCTAAAGTAAACAAAAGTGAGAAATTAAT 1130
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QY 1191 CACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCTTAATAGGACAAATTTCTATT 1250
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QY 1251 GTTGACCAATTTCTACAAATTTGTAAAAGTCCAAATCTGTGCTAACTTAATAAGTAATAATC 1310
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Db 841 ATCTCTTAAAAAATAAAAAA 862
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## RESULT 2

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US-08-905-223-27
; Sequence 27, Application US/08905223
; Patent No. 622029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duclert, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESS: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelien, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: DOUBLE
; TOPOLOGY: LINEAR
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; MOLECULE TYPE: CDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; DEVELOPMENTAL STAGE: Fetal
; TISSUE TYPE: kidney
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 10.7
; OTHER INFORMATION: seq LWLFLFLVTAIHA/EL
US-08-905-223-27
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Query Match 59.4%; Score 799.4; DB 3; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.5e-189;
Matches 809; Conservative 6; Mismatches 1; Gaps 1;

QY 1 GAAAGAAATCTTGTGGCTGCTCTTTTCTGGTGAGCTGCCATTTCATGCTGAACTCTCTGCAA 60
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Db 206 AGAAAAGTTCCCAACAGAGAAAGCAACAGAAAATTTCCCATGTCTACTTTGGCAATGTAACC 265
QY 241 CAGAGGGTATCAATCTGTGTTTGTGTTACAGACCTTCAAAAAATCACACCTTCTCTGCT 300
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RESULT 3
US-09-247-155-27
; Sequence 27, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32...73
; OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27

Query Match      59.4%; Score 799.4; DB 3; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.5e-189;
Matches 809; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

Qy 1 GAAAGAAATGTTGGCTGCTCTTTTCTGTGAGTGCATTCATCAGAACAGCTCTGGGAGATAAA 120
Db 26 GAAAGAAATGTTGGCTGCTCTTTTCTGTGAGTGCATTCATCAGAACAGCTCTGGGAGATAAA 145
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US-09-663-600A-27
; Sequence 27, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663,600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32...73
; OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

Query Match      59.4%; Score 799.4; DB 4; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.5e-189;
Matches 809; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

Qy 1 GAAAGAAATGTTGGCTGCTCTTTTCTGTGAGTGCATTCATCAGAACAGCTCTGGGAGATAAA 60
Db 26 GAAAGAAATGTTGGCTGCTCTTTTCTGTGAGTGCATTCATCAGAACAGCTCTGGGAGATAAA 85
Qy 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db 86 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 145
Qy 121 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGGATGGTAGCTTTCTCCATG 180
Db 146 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGGATGGTAGCTTTCTCCATG 205
Qy 181 AGAAAAGTTCCCAACAGAGAACCAAGAAAATTTCCCATGTCCTACTTTGCAATGTAACC 240
Db 206 AGAAAAGTTCCCAACAGAGAACCAAGAAAATTTCCCATGTCCTACTTTGCAATGTAACC 265
Qy 241 CAGAGGGTATCATTTCTGTTTGTGGTTACAGACCCCTTCAAAAATCAGACCCCTTCCTGCT 300
Db 266 CAGAGGGTATCATTTCTGTTTGTGGTTACAGACCCCTTCAAAAATCAGACCCCTTCCTGCT 325
Qy 301 GTTCAGGTGCAATCAGCCATGAAGTAAAGAACCGGATCAACAATGCTCTCTTTCTA 360
Db 326 GTTCAGGTGCAATCAGCCATGAAGTAAAGAACCGGATCAACAATGCTCTCTTTCTA 385
Qy 361 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCACCCATCGAACCA 420
Db 386 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACCCACCCATCGAACCA 445
Qy 421 TCTGTGCCCATCTCGAATTAATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480
Db 446 TCTGTGCCCATCTCGAATTAATATTTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505
Qy 481 GCATCTGATTTTATCAGGGATCTGGCAAGTGAAGAACCAAGAACCAATCTGAA 540
Db 506 GCATCTGATTTTATCAGGGATCTGGCAAGTGAAGAACCAAGAACCAATCTGAA 565
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Db 146 GCATATGCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 205  
QY 181 AGAAAGTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTACTTTCGCAATGTAACC 240  
Db 206 AGAAAGTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTACTTTCGCAATGTAACC 265  
QY 241 CAGAGGATCATCTCTGGTTTGGTTTACAGACCTTTCAAAATCACAACCCCTTCTCTGT 300  
Db 266 CAGAGGATCATCTCTGGTTTGGTTTACAGACCTTTCAAAATCACAACCCCTTCTCTGT 325  
QY 301 GTTGAGGTGCAATCAGCCATTAAGAATGAACAGAACCGGATCAACAATGCTTTCTTTCTA 360  
Db 326 GTTGAGGTGCAATCAGCCATTAAGAATGAACAGAACCGGATCAACAATGCTTTCTTTCTA 385  
QY 361 AATGACCAACTCTGGAATTTTAAATTCCTTCCACATCTTGCAACCCCATGGAACCA 420  
Db 386 AATGACCAACTCTGGAATTTTAAATTCCTTCCACATCTTGCAACCCCATGGAACCA 445  
QY 421 TCTGTGCCATCTGGATTTATTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480  
Db 446 TCTGTGCCATCTGGATTTATTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505  
QY 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAAACCAAGAACCCATCTGAA 540  
Db 506 GCACTACTGATTTTATCAGGGATCTGGCAACGTADAARAAGAAACCAAGAACCCATCTGAA 565  
QY 541 GTGGATGACGCTGAAGATAGTGAACATGATCAACAATTTGAAATGGCATCCCTCT 600  
Db 566 GTGGATGACGCTGAARATAAATGTGAACATGATCAACAATTTGAAATGGCATCCCTCT 625  
QY 601 GATCCCTTGACATGAAGG-GGGCATATTAATGATGCCCTTCATGACAGAGATGAGAG 659  
Db 626 GATCCCTTGACATGAAGGAGGGGCATATTAATGATGCCCTTCATGACAGAGATGAGAG 685  
QY 660 CTCACCCCTCTGAAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACAATTTGTTTCTG 719  
Db 686 CTCACCCCTCTGAAAGGGCTGTGTTCTGCTTCTCAARAATTAACAATTTGTTTCTG 745  
QY 720 TGTGACTGTGACATCCTGAAATACCAAGACAGATCATATATTTGTTTTCACCATCT 779  
Db 746 TGTGACTGTGACATCCTGAAATACCAAGACAGATCATATATTTGTTTTCACCATCT 805  
QY 780 TCTTTTGTATAAATTTTGAATGTGCTTGAAGTGA AAA 818  
Db 806 TCTTTTGTATAAATTTTGAATGTGCTTGA AAAAAAAAA 844

RESULT 5

US-09-621-976-5  
; Sequence 5, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 5  
; LENGTH: 848  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 32..697  
; NAME/KEY: sig\_peptide  
; LOCATION: 32..73  
; OTHER INFORMATION: Von Heijne matrix  
US-09-621-976-5

Query Match 59.4%; Score 799.4; DB 4; Length 848;  
Best Local Similarity 98.8%; Pred. No. 5.5e-189;  
Matches 809; Conservative 6; Mismatches 3; Indels 1; Gaps 1;  
QY 1 GAAAGAATGTTGGTGTCTCTTTTTCGTGACCTGCCATTCATGCTGAACTCTGTCAA 60  
Db 26 GAAAGAATGTTGGTGTCTCTTTTTCGTGACCTGCCATTCATGCTGAACTCTGTCAA 85  
QY 61 CAGGTGCAAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAA 120  
Db 86 CAGGTGCAAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAA 145  
QY 121 GCATATGCCCTGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 180  
Db 146 GCATATGCCCTGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 205  
QY 181 AGAAAGTTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACC 240  
Db 206 AGAAAGTTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTACTTTGCAATGTAACC 265  
QY 241 CAGAGGATCATCTCTGGTTTGGTTTACAGACCTTTCAAAAAATCACAACCCCTTCTGTCT 300  
Db 266 CAGAGGATCATCTCTGGTTTGGTTTACAGACCTTTCAAAAAATCACAACCCCTTCTGTCT 325  
QY 301 GTTGAGGTGCAATCAGCCATTAAGAATGAACAGAACCGGATCAACAATGCCCTTCTTTCTA 360  
Db 326 GTTGAGGTGCAATCAGCCATTAAGAATGAACAGAACCGGATCAACAATGCCCTTCTTTCTA 385  
QY 361 AATGACCAACTCTGGAATTTTAAATTCCTTCCACATCTTGCAACCCCATGGAACCA 420  
Db 386 AATGACCAACTCTGGAATTTTAAATTCCTTCCACATCTTGCAACCCCATGGAACCA 445  
QY 421 TCTGTGCCATCTGGATTTATTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 480  
Db 446 TCTGTGCCATCTGGATTTATTATTTGGTGTGATATTTTGCATCATCATAGTTGCAATT 505  
QY 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAAACCAAGAACCCATCTGAA 540  
Db 506 GCACTACTGATTTTATCAGGGATCTGGCAACGTADAARAAGAAACCAAGAACCCATCTGAA 565  
QY 541 GTGGATGACGCTGAAGATAGTGAACATGATCAACAATTTGAAATGGCATCCCTCT 600  
Db 566 GTGGATGACGCTGAARATAAATGTGAACATGATCAACAATTTGAAATGGCATCCCTCT 625  
QY 601 GATCCCTTGACATGAAGG-GGGCATATTAATGATGCCCTTCATGACAGAGATGAGAG 659  
Db 626 GATCCCTTGACATGAAGGAGGGGCATATTAATGATGCCCTTCATGACAGAGATGAGAG 685  
QY 660 CTCACCCCTCTGAAAGGGCTGTGTTCTGCTTCTCAAGAAATTAACAATTTGTTTCTG 719  
Db 686 CTCACCCCTCTGAAAGGGCTGTGTTCTGCTTCTCAARAATTAACAATTTGTTTCTG 745  
QY 720 TGTGACTGTGACATCCTGAAATACCAAGACAGATCATATATTTGTTTTCACCATCT 779  
Db 746 TGTGACTGTGACATCCTGAAATACCAAGACAGATCATATATTTGTTTTCACCATCT 805  
QY 780 TCTTTTGTATAAATTTTGAATGTGCTTGAAGTGA AAA 818  
Db 806 TCTTTTGTATAAATTTTGAATGTGCTTGA AAAAAAAAA 844

RESULT 6

US-09-513-999C-5  
; Sequence 5, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..697
; FEATURE:
; NAME/KEY: sig\_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: 540
; OTHER INFORMATION: d=a or g or t
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: 543
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: 581
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: 586
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: 725
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc\_feature
; LOCATION: 788
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 156
; OTHER INFORMATION: Xaa=Ile or Lys or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 170
; OTHER INFORMATION: Xaa=Asp or Asn
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 171
; OTHER INFORMATION: Xaa=Lys or Asn
; OTHER INFORMATION: Xaa=Lys or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 157
; OTHER INFORMATION: Xaa=Lys or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 156
; OTHER INFORMATION: Xaa=Ile or Lys or Arg
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 170
; OTHER INFORMATION: Xaa=Asp or Asn
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 171
; OTHER INFORMATION: Xaa=Lys or Asn
; OTHER INFORMATION: Xaa=Lys or Arg
; US-09-513-999C-5

Query Match 59.4%; Score 799.4; DB 4; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.5e-189;
Matches 809; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

Qy 1 GAAGAAGTGTGGCTCTTTTCTGTGACTGCGCTTCTGAGTGCATTCATGCTGAACTCTGTCAA 60
Db 26 GAAGAAGTGTGGCTCTTTTCTGTGACTGCGCTTCTGAGTGCATTCATGCTGAACTCTGTCAA 85
Qy 61 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 120
Db 86 CCAGGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAA 145
Qy 121 GCATATGCTGGGATACCAATGAAGAATACTCTTCAAAGCGATGGTAGCTTCTCCATG 180
Db 146 GCATATGCTGGGATACCAATGAAGAATACTCTTCAAAGCGATGGTAGCTTCTCCATG 205

Qy 181 AGAAAAGTTCACACAGAGAAGCAACAGAAATTTCCCATGTCCTTACTTTGCAATGTAAAC 240
Db 206 AGAAAAGTTCACACAGAGAAGCAACAGAAATTTCCCATGTCCTTACTTTGCAATGTAAAC 265
Qy 241 CAGAGGTATCATCTCTGTTTGTGTTACAGACCCCTTCAAAAATCAGCCCTTCCCTGCT 300
Db 266 CAGAGGTATCATCTCTGTTTGTGTTTACAGACCCCTTCAAAAAATCAGCCCTTCCCTGCT 325
Qy 301 GTTGAGGTGCAATCAGCCATAAAGAAATGAACAGAACCGGATCAACAATGCTTCTTCTA 360
Db 326 GTTGAGGTGCAATCAGCCATAAAGAAATGAACAGAACCGGATCAACAATGCTTCTTCTA 385
Qy 361 AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGCACCAATGAGGCCA 420
Db 386 AATGACCAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGCACCAATGAGGCCA 445
Qy 421 TCTGTGCCCATCTGGATTATATATTTGGTGTGATATTTTGCATCATATAGTTGCAATT 480
Db 446 TCTGTGCCCATCTGGATTATATATTTGGTGTGATATTTTGCATCATATAGTTGCAATT 505
Qy 481 GCCTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 540
Db 506 GCCTACTGATTTTATCAGGGATCTGGCAACGTAGAAGAAAGAACAAAGAACCATCTGAA 565
Qy 541 GTGGATGACGCTGAAGATAAGTGTGAAAAACATGATCAATTTGAAAAATGGCATCCCTCT 600
Db 566 GTGGATGACGCTGAARATAAATGTGAAAAACATGATCAATTTGAAAAATGGCATCCCTCT 625
Qy 601 GATCCCTGGACATGAAGGG- GGGCATATTAATGATGCTTTCATGACAGAGGATGAGAG 659
Db 626 GATCCCTGGACATGAAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 685
Qy 660 CTCACCCCTCTCTGAAGGGCTGTTTCTGCTTCTCAAGAAATTAACATTTCTGTTCTG 719
Db 686 CTCACCCCTCTCTGAAGGGCTGTTTCTGCTTCTCAAGAAATTAACATTTCTGTTCTG 745
Qy 720 TGTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATCT 779
Db 746 TGTGACTGCTGAGCATCTGAAATACCAAGAGCAGATCATATATTTTGTTCACCATCT 805
Qy 780 TCTTTTGTATAAATTTTGAATGTGCTTGAAGTGAATAA 818
Db 806 TCTTTTGTATAAATTTTGAATGTGCTTGAAGTGAATAA 844

RESULT 7
US-09-471-276-5
; Sequence 5, Application US/09471276
; Patent No. 6822072
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6822072
; FILE REFERENCE: GENSET.025CP1
; CURRENT APPLICATION NUMBER: US/09/471,276
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: 09/057,719
; EARLIER FILING DATE: 1998-04-09
; EARLIER APPLICATION NUMBER: 09/069,047
; EARLIER FILING DATE: 1998-04-28
; EARLIER APPLICATION NUMBER: PCT/IB99/00712
; EARLIER FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 1622
; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS

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; LOCATION: 32..697
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
; US-09-471-276-5

Query Match      59.4%; Score 799.4; DB 4; Length 848;
Best Local Similarity 98.8%; Pred. No. 5.5e-189;
Matches 809; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

QY 1 GAAAGAAATGTTGGTCTCTTTTCTGGTGACTGCCATTCATGCTGAACCTCTGTCAA 60
DB 26 GAAAGAAATGTTGGTCTCTTTTCTGGTGACTGCCATTCATGCTGAACCTCTGTCAA 85
QY 61 CCAAGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGACAGCTCTGGGAGATAAA 120
DB 86 CCAAGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGACAGCTCTGGGAGATAAA 145
QY 121 GCATATGCCCTGGGATACCAATGAAGAAATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 180
DB 146 GCATATGCCCTGGGATACCAATGAAGAAATACCTCTTCAAGCGATGGTAGCTTTCTCCATG 205
QY 181 AGAAAGTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGAAC 240
DB 206 AGAAAGTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGAAC 265
QY 241 CAGAGGGTATCATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 300
DB 266 CAGAGGGTATCATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 325
QY 301 GTTGAGTGCATCAGCCATGAAGTGAAGCAAGAACCGGATCAACATGCTCTTTCTTA 360
DB 326 GTTGAGTGCATCAGCCATGAAGTGAAGCAAGAACCGGATCAACATGCTCTTTCTTA 395
QY 361 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACACCCATGGACCCA 420
DB 386 AATGACCAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACACCCATGGACCCA 445
QY 421 TCTGTGCCATCTGGATATATATTTGGTGTGATATTTTGGCATCATCATAGTTGCAATT 480
DB 446 TCTGTGCCATCTGGATATATATTTGGTGTGATATTTTGGCATCATCATAGTTGCAATT 505
QY 481 GCACTACTGATTTTATCAGGGATCTGGCAACGTTAGAAAGAAAGAACCAACCATCTGAA 540
DB 506 GCACTACTGATTTTATCAGGGATCTGGCAACGTTAGAAAGAAAGAACCAACCATCTGAA 565
QY 541 GTGGATGACGCTGAAGATAAGTGTGAACACATGATCACAATGAAATGGCATCCCTCT 600
DB 566 GTGGATGACGCTGAARATAAKTGTGAACACATGATCACAAATGGCAATGGCATCCCTCT 625
QY 601 GATCCCTGGACATGAAGG- GGGCATATTAATGATGCCCTTCATGACAGGATGAGAG 659
DB 626 GATCCCTGGACATGAAGGAGGGCATATTAATGATGCCCTTCATGACAGGATGAGAG 685
QY 660 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCCTCAAGAAATTAACATTTGTTCTG 719
DB 686 CTCACCCCTCTCTGAAGGGCTGTTGTTCTGCTTCCCTCAARAAATTAACATTTGTTCTG 745
QY 720 TGTGACTGTGACATCCTGAAATACCAAGAGCAGATCATATATTTGTTTCCCAATCT 779
DB 746 TGTGACTGTGACATCCTGAAATACCAAGAGCAGATCATATATTTGTTTCCCAATCT 805
QY 780 TCTTTTGTAAATTTTGAATGCTTGAAGTGA 818
DB 806 TCTTTTGTAAATTTTGAATGCTTGAAGTGA 844
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## RESULT 8

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US-08-989-299-3
; Sequence 3, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.

; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MIA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2415 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-989-299-3

Query Match      9.3%; Score 125; DB 3; Length 2415;
Best Local Similarity 57.3%; Pred. No. 3.3e-21;
Matches 293; Conservative 0; Mismatches 200; Indels 18; Gaps 3;

QY 54 CTGTCAACCAAGTGCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
DB 1827 CTGGAGTCCATATGCAGACCAAGCATCAAAGTGAGGATAAGCCTAAAAATCAGCTCTGG 1886
QY 114 AGATAAGCATATGCTCTGGGATACCAATGAAGTACCTCTTCAAGCGATGCTAGCTTT 173
DB 1887 AGATAAGCATATGAATGAAGACGAATGAATGTACCTGTTCCGATCATCTCTTGCATA 1946
QY 174 CTCCATGAG--AAAAGTTCCTCCCAACAGAGAACAGAAATTTTCCC-----A 218
DB 1947 TCGTATGAGCGAGTACTTTTAAAGTAAATAATCAGATGATCTTTTGGGAGGAGGA 2006
QY 219 TGTCTTACTTTGCAATGTAAACCCAGAGGGTATCAITCTGGTTGTGTGGTTACAGACCTTC 278
DB 2007 TGTGCGAGTGGCTTAATTTGAAACCAAGAAATCTCTTAAATTTCTTTGTCACTCACCTAA 2066
QY 279 AAAAAA---TCACACCCCTTCTCTGCTTTCAGGTGCAATCAGCCATGAAGATGAACAGAA 335
DB 2067 AAATGTGTCTGATATCATTTCTTAGAACTGAAGTTGAAAGGCCATCAGGATGTCGGGAG 2126
QY 336 CCGGATCAACAATGCTCTCTTCTAAATGACCAAACTCTGGAATTTTAAAAATCCCTTC 395
DB 2127 CCGTATCAATGATGCTTTCCGCTGATGAACACAGCTTAGAGTTCTGGGATACAGCC 2186
QY 396 CACACTTGACCAACCCATGGAACCATCTGTGCCCATTCTGAGATTATTAATTTGGTGTGAT 455
DB 2187 AACACTTGGACCTCTCTAACAGAGCCCTCTTCCATATGGCTGATTTGTTTGGAGTTGT 2246
QY 456 ATTTTGCATCATATAGTTGCAATTCGACTACTGATTTTATCAGGATCTGGCAAGCTAG 515
DB 2247 GATGGGAGTGTAGTGGTTGGCAATTCATCTTGAATCTTCACTGGGATCAGATCGGAA 2306
QY 516 AAGAAAGAAACAAAGAACCATCTGAAGTGGAT 546
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Dn  
2307 GAAGAAAAATAACCAAGAAGTGGGAAAAT 2337

RESULT 9  
US-09-407-427-3  
; Sequence 3, Application US/09407427  
; Patent No. 6610497  
; GENERAL INFORMATION:  
; APPLICANT: Acton, Susan L.  
; INVENTOR: Robison, Keith E.  
; TITLE OF INVENTION: ANGIOGENESIS CONVERTING ENZYME HOMOLOGY AND THERAPEUTIC USES THEREOF  
; FILE REFERENCE: WNI-132CP2  
; CURRENT APPLICATION NUMBER: US/09/407,427  
; PRIORITY FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 09/163,648  
; PRIOR FILING DATE: 1998-09-30  
; PRIOR APPLICATION NUMBER: 08/989,299  
; PRIOR FILING DATE: 1997-12-11  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 2415  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-407-427-3

Query Match                  9.3%; Score 125; DB 4; Length 2415;  
Best Local Similarity      57.3%; Pred. No. 3.3e-21;  
Matches 293; Conservative 0; Mismatches 200; Indels 18; Gaps 3;

Qy    54 CTGTCAAACCAGGTGCAGAAATGCTTTTAAGTCAGACTTAGTATCAGAACAGCTCTGGG 113  
       ||| |  
Dn    1827 CTGGAGTCCATCATCGACACCACAACATCAAGTGAGGATAAGCCATAAATCAGCTCTGG 1886  
       ||| |

Qy    114 AGATAAGCATATGCCCTGGGNATCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTT 173  
  
Dn    1887 AGATAAGCATATGAATGGAAACGAATGAATTGACTGTTCGATCATCTGTTGCATA 1946  
       ||| |

Qy    174 CTCATCAG--AAAAGTTCCAACAGAGAGCACAGAAATTTCCC-----A 218  
       ||| |  
Dn    1947 TGCTATGAGGCAGTACTTTTTAAAGTAA AAAATCAGATGATCTTTTGGGGAGGAGGA 2006  
       ||| |

Qy    219 TGTCTACTTTTGCAATGTAA CCCCAGAGGGTATCAATCTCGTGTGTTTACAGACCCCTTC 278  
       ||| |

Dn    2007 TGTGCGAGTGGCTAATTTGAACCAAGAACTCCCTTAATTTCTTGTCACTGCACCTAA 2066  
       ||| |

Qy    279 AAAAA---TCACACCTTCTCTGTGTGGGTGCAATCAGCCNATAGAATGAACAAGAA 335  
       ||| |

Dn    2067 AAATGTGTCATATCATCTCTAGAACTGAAGTTGA AAAGGCCATCAGGATGTCCCGAG 2126  
       ||| |

Qy    336 CCAGATCAACATGCCCTTCTTTCAATGACCAACTCTGGAATTTTAAAAATCCCCCTC 395  
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Dn    2127 CCAGTATCAATGATGCTTTCCGCTGTAACGACCAAGCCCTAGAGTTCTGGGGATACAGCC 2186  
       ||| |

Qy    396 CACACTTGCACACCCATGAGACCCTCTGTGCCCATCTGGATATTATATTTGGTGTGAT 455  
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Dn    2187 AACACTTGGACCTCTCAACGCCCCCTGTTCATATGAGCTGATTTGTTGGAGTTGT 2246  
       ||| |

Qy    456 ATTTTGCATCATCATGTTGCAATGCACTACTGATTTTATCAGGGATCTGGCAACGTAG 515  
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Dn    2247 GATGGAGTGTAGTGTGGTTGSCATTTGTCATCTCTGATCTTCACTGGGATCAGATCGAA 2306  
       ||| |

Qy    516 AAGAAAGAACAAAGAACCATCTGAAGTGGAT 546  
       ||| |

Dn    2307 GAAGAAAAATAACCAAGAAGTGGGAAAAT 2337  
       ||| |

RESULT 10  
US-09-949-016-5413  
; Sequence 5413, Application US/09949016  
; Patent No. 6812339

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/989,299  
; FILING DATE: 11-DEC-1997  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold E., Beth  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: MIA-025.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3396 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 82..2496  
US-08-989-299-1

Query Match 9.3%; Score 125; DB 3; Length 3396;

Best Local Similarity 57.3%; Pred. No. 3.8e-21;  
Matches 293; Conservative 0; Mismatches 200; Indels 18; Gaps 3;

QY	54	CTGTCAACGAGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG	113
Db	1908	CTGGAGTCCATATGCGACGACAAAGCATCAAAGTGAGGATAAGCCTAAATCAGCTCTGG	1967
QY	114	AGATAAAGCATATGCGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGCTAGCTTT	173
Db	1968	AGATAAAGCATATGAATGGAACGACATGAATGTACCTGTTCCGATCATCTGTTGCATA	2027
QY	174	CTCCATGAG--AAAAGTTCCTCAACAGAGAACAGCAAGAAATTTCCC-----A	218
Db	2028	TGCTATGAGGCAGTACTTTTTTAAAGTAAATAATCAGATGATTTCTTTTGGGAGGAGGA	2087
QY	219	TGTCCTACTTTGCAATGTAAACCAGAGGGTATCATTTCTGTTTGTGGTTACAGACCTTC	278
Db	2088	TGTGCGAGTGGCTAAATTTGAACCAAGAAATCTCCTTTAAATTTCTTTGTCACTGCACCTAA	2147
QY	279	AAAAAA---TCACACCTCTCTGCTGTGTGAGGTGCAATCAGCCATAAGAAATGAACAAGAA	335
Db	2148	AAATGTGCTGATATCATTTCTTAGAAGTGAAGTGAAGGCCATCAGGATGTCCCGGAG	2207
QY	336	CCGGATCAACAATGCTCTTTCTAAATGACCAAACTCTGGAAATTTTTAAAAATCCCTTC	395
Db	2208	CCGTATCAATGATGCTTTCCGTCTGAATGACAAAGCCTAGAGTTTCTGGGGATACAGCC	2267
QY	396	CACACTTGACACCCCATGAGCCATCTGCGCCATCTGGATTATATATTTGGTGTGAT	455
Db	2268	AACACTTGGACCTCTTAACAGCCCTGTTTCCATATGCGCTGATTTTGGAGTTGT	2327
QY	456	ATTTTGCATCATATAGTTGCAATTCGACTACTGATTTTATCAGGGATCTGGCAAGCTAG	515
Db	2328	GATGGAGTGAATGTTGGCATTTGTCTGATCTTCACTGGGATCAGAGATCGGAA	2387
QY	516	AGAAAGAACAAAGAACCATCTGAAAGTGAAT	546
Db	2388	GAAGAAAAATAAGCAAGAGTGGAGAAAAAT	2418

## RESULT 13

US-09-407-427-1

; Sequence 1, Application US/09407427

; Patent No. 6610497

; GENERAL INFORMATION:

; APPLICANT: Acton, Susan L.

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC

; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR

; FILE REFERENCE: MNI-132CP2

## RESULT 12

US-10-158-847-141

; Sequence 141, Application US/10158847

; Patent No. 6592865

; GENERAL INFORMATION:

; APPLICANT: Tom Parry et al.

; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity

; FILE REFERENCE: PF557

; CURRENT APPLICATION NUMBER: US/10/158,847

; PRIOR FILING DATE: 2002-06-03

; PRIOR APPLICATION NUMBER: 60/295,004

; PRIOR FILING DATE: 2001-06-04

; NUMBER OF SEQ ID NOS: 158

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 141

; LENGTH: 3396

; TYPE: DNA

; ORGANISM: homo sapiens

US-10-158-847-141

Query Match 9.3%; Score 125; DB 4; Length 3396;

Best Local Similarity 57.3%; Pred. No. 3.8e-21;

Matches 293; Conservative 0; Mismatches 200; Indels 18; Gaps 3;

QY	54	CTGTCAACGAGTGCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG	113
Db	1908	CTGGAGTCCATATGCGACGACCAAGCATCAAAGTGAGGATAAGCCTAAATCAGCTCTGG	1967
QY	114	AGATAAAGCATATGCGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGCTAGCTTT	173
Db	1968	AGATAAAGCATATGAATGGAACGACATGAATGTACCTGTTCCGATCATCTGTTGCATA	2027
QY	174	CTCCATGAG--AAAAGTTCCTCAACAGAGAACAGCAAGAAATTTCCC-----A	218
Db	2028	TGCTATGAGGCAGTACTTTTTTAAAGTAAATAATCAGATGATTTCTTTTGGGAGGAGGA	2087
QY	219	TGTCCTACTTTGCAATGTAAACCAGAGGGTATCATTTCTGTTTGTGGTTACAGACCTTC	278
Db	2088	TGTGCGAGTGGCTAAATTTGAACCAAGAAATCTCCTTTAAATTTCTTTGTCACTGCACCTAA	2147
QY	279	AAAAAA---TCACACCTCTCTGCTGTGTGAGGTGCAATCAGCCATAAGAAATGAACAAGAA	335
Db	2148	AAATGTGCTGATATCATTTCTTAGAAGTGAAGTGAAGGCCATCAGGATGTCCCGGAG	2207
QY	336	CCGGATCAACAATGCTCTTTCTAAATGACCAAACTCTGGAAATTTTTAAAAATCCCTTC	395
Db	2208	CCGTATCAATGATGCTTTCCGTCTGAATGACAAAGCCTAGAGTTTCTGGGGATACAGCC	2267
QY	396	CACACTTGACACCCCATGAGCCATCTGCGCCATCTGGATTATATATTTGGTGTGAT	455
Db	2268	AACACTTGGACCTCTTAACAGCCCTGTTTCCATATGCGCTGATTTTGGAGTTGT	2327
QY	456	ATTTTGCATCATATAGTTGCAATTCGACTACTGATTTTATCAGGGATCTGGCAAGCTAG	515
Db	2328	GATGGAGTGAATGTTGGCATTTGTCTGATCTTCACTGGGATCAGAGATCGGAA	2387
QY	516	AGAAAGAACAAAGAACCATCTGAAAGTGAAT	546
Db	2388	GAAGAAAAATAAGCAAGAGTGGAGAAAAAT	2418

## RESULT 13

US-09-407-427-1

; Sequence 1, Application US/09407427

; Patent No. 6610497

; GENERAL INFORMATION:

; APPLICANT: Acton, Susan L.

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC

; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR

; FILE REFERENCE: MNI-132CP2

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; CURRENT APPLICATION NUMBER: US/09/407,427
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)..(2496)
US-09-407-427-1

Query Match      9.3%; Score 125; DB 4; Length 3396;
Best Local Similarity 57.3%; Pred. No. 3.8e-21;
Matches 293; Conservative 0; Mismatches 200; Indels 18; Gaps 3;

Qy 54 CTGTCAACACGAGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1908 CTGGAGTCCATATGCGACCAAGCATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1967
Qy 114 AGATAAAGCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGGATGGTAGCTTT 173
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1968 AGATAAAGCATATGAATGAAGCAAGCAATGAATGAATGAATGAATGAATGAATGAATGAAT 2027
Qy 174 CTCATGAG--AAAGTTCACACAGAGCAACAGAAATTTCCC-----A 218
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2028 TGCTATGAGGCGAGTACTTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2087
Qy 219 TGTCTACTTTGCAATGTAAACCCAGAGGGTATCATCTCTGTTTGTGGTTACAGACCCCTTC 278
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2088 TGTGGAGTGCTAATTGAAACCAAGAACTCTCTTAAATTTCTTGTCTACCTGCACTAA 2147
Qy 279 AAAAA--TCACACCTTCTCTGCTGTGTGAGTGCATACAGCAATGAAGTAAAGTAAAGTAA 335
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2148 AAATGTGTCTGATATCATCTCTAGAACTGAAAGTTGAAAGGCCATCAGGATGTCCTGGAG 2207
Qy 336 CCGGATCAACAACTGCTTCTTAAATGACCAACTCTGAAATTTTAAATTTTAAATTTTAAAT 395
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2208 CCGTATCAATGATGCTTTCGCTCTGAATGACCAAGCCCTAGAGTTCTCTGGGATACAGCC 2267
Qy 396 CACACTTGACCCACCCATGAGCCCATCTGTCCTCATCTGGATTTATTTATTTGTTGAT 455
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2268 AACACTTGGACCTCTTACAGCCCTCTGTTTCCATATGGCTGATTTGTTTGGAGTTGT 2327
Qy 456 ATTTTGCATCATATAGTTGCAATTGCACTACTGATTTTATCAGGATCTGGCAACGTAG 515
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2328 GATGGAGTGATAGTGGTTGGCAATTGTCATCTCTGATCTTCACTGGGATCAGAGATCGAA 2387
Qy 516 AAGAAAGCAACAAAGCAACCATCTGAAGTGGAT 546
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US-10-158-847-137
; Sequence 137, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
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; ORGANISM: homo sapiens
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; NAME/KEY: misc feature
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; OTHER INFORMATION: n equals any amino acid
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; OTHER INFORMATION: n equals any amino acid
; US-10-158-847-137

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Best Local Similarity 57.6%; Pred. No. 3.5e-19;
Matches 276; Conservative 0; Mismatches 185; Indels 18; Gaps 3;

Qy 54 CTGTCAACGAGTGCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGG 113
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1856 CTGGAGTCCATATGCGACCAAGCATCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1915
Qy 114 AGATAAAGCATATGCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTT 173
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1916 AGATAAAGCATATGAATGGNACGACATGAATGTACCTGTTCCGATCATCTGTTGCATA 1975
Qy 174 CTCATGAG--AAAAGTTCACACAGAGCAACAGAAATTTCCC-----A 218
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1976 TGCTATGAGGCGAGTACTTTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 2035
Qy 219 TGTCTACTTTGCAATGTAAACCCAGAGGGTATCATCTCTGTTTGTGGTTACAGACCCCTTC 278
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2036 TGTGGAGTGGCTAATTTGAAACCAAGAAATCTCCTTTAAATTTCTTGTCTACCTCACCTAA 2095
Qy 279 AAAAA--TCACACCTTCTCTGCTGTGAGTGCATCAGCCATCAGCAATGAAGTAAAGTAAAG 335
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2156 CCGTATCAATGATGCTTTCGCTCTGAATGACGACAGCTAGAGTCTTCTGGGATACAGCC 2215
Qy 396 CACACTTGACCAACCCATGAGCCCATCTGTGCCATCTGGATTTATTTATTTTGTGTGAT 455
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
2216 AACACTTGGACCTCTTAACCAAGCCCTCTGTTCCATATGCGCTGATTTGTTTGGAGTTGT 2275
Qy 456 ATTTTGCATCATATAGTTGCAATTCACCTACTGATTTTATCAGGATCTGGCAACGTA 514
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RESULT 15
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; Sequence 17155, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17155
; LENGTH: 43986
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17155

Query Match          5.8%; Score 77.4; DB 4; Length 43986;
Best Local Similarity 61.8%; Pred. No. 6.5e-09;
Matches 123; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

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Qy 376 GAATTTTAAATCCCTTCCACATTCGACCCCATGCCCATCTGTGCCCATCTGG 435
Db 38855 GAGTTTCTGGGGATACAGCCACACATTTGGACCTCTTAACCCAGCCCTGTTCATATGG 38914

Qy 436 ATTATTATATTGGTGTGATATTTGCATCATCATAGTTGCAATTCACCTACTGATTTTA 495
Db 38915 CTGATTGTTTTTGGAGTTGTGATGGGAGTGATAGTGTGGCAATGTGTCCTGATCTTC 38974

Qy 496 TCAGGGATCTGGCAACGTA 514
Db 38975 ACTGGGATCAGAGATCGA 38993
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Job time : 329 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 4, 2005, 05:14:03 ; Search time 884 Seconds  
(without alignments)  
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Perfect score: 1346  
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Gapop 10.0 , Gapext 1.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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521	1346	100.0	1346	22 US-10-950-374-386
522	1325.4	98.5	1432	14 US-10-097-065-17
523	1325.4	98.5	1432	17 US-10-372-876-17
524	1324.6	98.4	1447	10 US-09-892-877-22
525	1324.6	98.4	1447	10 US-09-948-783-22
Sequence 122, App				
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Sequence 205, App				
Sequence 27, Appl				
Sequence 27, Appl				
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Sequence 27, Appl				
Sequence 1744, Ap				
Sequence 570, App				
Sequence 1636, Ap				
Sequence 23160, A				
Sequence 6445, Ap				
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Sequence 842, App				
Sequence 2371, Ap				
Sequence 2496, Ap				
Sequence 71, Appl				
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Sequence 2, Appl				
Sequence 137, App				
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Sequence 1637, Ap				
Sequence 5, Appl				
Sequence 8, Appl				
Sequence 1556, Ap				
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Sequence 17676, A				
Sequence 1517, App				
Sequence 231, App				
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Sequence 5831, Ap				
Sequence 12112, A				
Sequence 1703, Ap				
Sequence 213, App				

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c1047	54.2	4.0	9180	15	US-10-311-455-1937	Sequence 1937, App	c1120	49.4	3.7	18997	19	US-10-311-507-31	Sequence 31, Appl
c1048	54	4.0	6106	15	US-10-311-455-1937	Sequence 1446, App	c1121	49.4	3.7	18997	20	US-10-480-846-17	Sequence 17, Appl
c1049	54	4.0	6106	17	US-10-311-455-1937	Sequence 114, App	c1122	49.2	3.7	476	10	US-09-814-353-4700	Sequence 4700, Ap
c1050	54	4.0	6106	18	US-10-257-166-114	Sequence 152, App	c1123	49.2	3.7	476	10	US-09-814-353-10999	Sequence 10999, A
c1051	54	4.0	11288	9	US-09-947-925A-4	Sequence 4, Appli	c1124	49.2	3.7	6106	15	US-10-311-455-1445	Sequence 1445, Ap
c1052	54	4.0	11288	9	US-09-822-634-1	Sequence 1, Appli	c1125	49.2	3.7	6106	17	US-10-257-166-113	Sequence 113, App
c1053	54	4.0	15056	9	US-09-392-822-4	Sequence 4, Appli	c1126	49.2	3.7	6106	18	US-10-221-714A-151	Sequence 151, App
c1054	54	4.0	15056	10	US-09-814-357-14	Sequence 14, Appl	c1127	49.2	3.7	6863	18	US-10-221-714A-339	Sequence 339, App
c1055	54	4.0	15056	14	US-09-814-351-14	Sequence 14, Appl	c1128	49.2	3.7	15548	15	US-10-311-455-2128	Sequence 2128, Ap
c1056	54	4.0	15056	14	US-10-045-116-25	Sequence 25, Appl	c1129	49.2	3.7	17183	15	US-10-311-455-459	Sequence 459, App
c1057	54	4.0	15056	14	US-10-226-820-10	Sequence 10, Appl	c1130	49.2	3.7	50000	21	US-10-706-635-23	Sequence 23, Appl
c1058	54	4.0	15056	22	US-10-691-045-14	Sequence 14, Appl	c1131	49.2	3.7	198522	13	US-10-087-192-244	Sequence 244, App
c1059	54	4.0	15056	22	US-10-938-227-3	Sequence 3, Appli	c1132	49	3.6	7351	15	US-10-311-455-2	Sequence 2, Appli
c1060	53.4	4.0	6641	15	US-10-311-455-288	Sequence 288, App	c1133	49	3.6	198522	13	US-10-087-192-244	Sequence 244, App
c1061	53.4	4.0	6641	16	US-10-240-452-36	Sequence 36, Appl	c1134	48.8	3.6	3197	22	US-10-499-554-3	Sequence 3, Appli
c1062	53.4	4.0	9642	15	US-10-311-455-329	Sequence 329, App	c1135	48.8	3.6	5398	15	US-10-311-455-115	Sequence 115, App
c1063	53.4	4.0	163382	19	US-10-367-094-179	Sequence 179, App	c1136	48.8	3.6	5611	19	US-10-433-793-100	Sequence 100, App
c1064	53	3.9	530	10	US-09-814-353-5294	Sequence 5294, Ap	c1137	48.8	3.6	6222	15	US-10-311-455-666	Sequence 666, App
c1065	53	3.9	530	10	US-09-814-353-11581	Sequence 11581, A	c1138	48.8	3.6	7851	15	US-10-311-455-1734	Sequence 1734, Ap
c1066	53	3.9	18817	15	US-10-240-488-48	Sequence 48, Appl	c1139	48.8	3.6	8222	21	US-10-486-319A-65	Sequence 65, Appl
c1067	52.8	3.9	26000	20	US-10-476-022-10	Sequence 10, Appl	c1140	48.8	3.6	8222	21	US-10-486-319A-65	Sequence 65, Appl
c1068	52.8	3.9	49979	19	US-10-741-601-5746	Sequence 5746, Ap	c1141	48.8	3.6	8305	15	US-10-311-455-1542	Sequence 1542, Ap
c1069	52.8	3.9	49979	21	US-10-741-601-17905	Sequence 17905, A	c1142	48.8	3.6	10279	18	US-10-311-455-1564	Sequence 1564, Ap
c1070	52.6	3.9	113515	15	US-10-311-455-2147	Sequence 2147, Ap	c1143	48.8	3.6	10279	18	US-10-240-589C-86	Sequence 86, Appl
c1071	52.4	3.9	11836	14	US-10-239-678-102	Sequence 102, App	c1144	48.8	3.6	11534	15	US-10-311-455-315	Sequence 315, App
c1072	52.4	3.9	11836	15	US-10-240-453-114	Sequence 114, App	c1145	48.8	3.6	15373	15	US-10-311-455-440	Sequence 440, App
c1073	52.2	3.9	15872	18	US-10-221-714A-242	Sequence 242, App	c1146	48.8	3.6	17280	18	US-10-221-714A-497	Sequence 497, App
c1074	52	3.9	6134	15	US-10-311-455-1138	Sequence 1138, Ap	c1147	48.8	3.6	3673778	16	US-10-312-841-1	Sequence 1, Appli
c1075	52	3.9	7597	15	US-10-311-455-986	Sequence 986, App	c1148	48.6	3.6	5033	20	US-10-473-126-139	Sequence 139, App
c1076	52	3.9	176096	22	US-10-981-277-34	Sequence 34, Appl	c1149	48.6	3.6	7001	15	US-10-172-086-60	Sequence 60, Appl
c1077	51.8	3.8	6175	15	US-10-311-455-1280	Sequence 1280, Ap	c1150	48.6	3.6	7001	19	US-10-311-507-2	Sequence 2, Appli
c1078	51.8	3.8	8056	20	US-10-473-128-240	Sequence 240, App	c1151	48.6	3.6	7001	20	US-10-480-846-60	Sequence 60, Appl
c1079	51.6	3.8	5143	15	US-10-311-455-321	Sequence 321, App	c1152	48.6	3.6	8033	17	US-10-221-613-73	Sequence 73, Appl
c1080	51.6	3.8	5143	15	US-10-240-485-17	Sequence 17, Appl	c1153	48.6	3.6	8033	18	US-10-221-714A-29	Sequence 29, Appl
c1081	51.6	3.8	11976	15	US-10-311-455-567	Sequence 567, App	c1154	48.6	3.6	14798	15	US-10-311-455-1005	Sequence 1005, Ap
c1082	51.6	3.8	16173	15	US-10-240-485-22	Sequence 22, Appl	c1155	48.6	3.6	19380	17	US-10-221-613-389	Sequence 389, App
c1083	51.6	3.8	168575	16	US-10-178-194-1	Sequence 1, Appli	c1156	48.6	3.6	50000	21	US-10-706-635-24	Sequence 24, Appl
c1084	51.4	3.8	1033	19	US-10-437-963-47635	Sequence 47635, A	c1157	48.4	3.6	6123	15	US-10-311-455-1009	Sequence 1009, Ap
c1085	51.4	3.8	6494	15	US-10-311-455-1366	Sequence 1366, Ap	c1158	48.4	3.6	7498	15	US-10-311-455-230	Sequence 230, App
c1086	51.4	3.8	8305	15	US-10-311-455-1541	Sequence 1541, Ap	c1159	48.4	3.6	49379	19	US-10-741-601-5746	Sequence 5746, Ap
c1087	51.4	3.8	11422	15	US-10-311-455-192	Sequence 192, App	c1160	48.4	3.6	49379	21	US-10-741-600-17905	Sequence 17905, A
c1088	51.4	3.8	11422	17	US-10-257-166-18	Sequence 18, Appl	c1161	48.2	3.6	4240	10	US-09-814-353-22023	Sequence 22023, A
c1089	51.4	3.8	13123	16	US-10-240-453-64	Sequence 64, Appl	c1162	48.2	3.6	6030	14	US-10-239-676-164	Sequence 164, App
c1090	51.4	3.8	15743	15	US-10-240-453-269	Sequence 269, App	c1163	48.2	3.6	6030	15	US-10-240-453-186	Sequence 186, App
c1091	51.2	3.8	13131	18	US-10-240-589C-58	Sequence 58, Appl	c1164	48.2	3.6	6030	17	US-10-221-613-310	Sequence 310, App
c1092	51	3.8	6239	15	US-10-311-455-1749	Sequence 1749, Ap	c1165	48.2	3.6	6314	16	US-10-240-452-14	Sequence 14, Appl
c1093	51	3.8	6239	18	US-10-240-453-171	Sequence 171, App	c1166	48.2	3.6	6731	17	US-10-257-166-44	Sequence 44, Appl
c1094	51	3.8	10595	15	US-10-221-714A-263	Sequence 263, App	c1167	48.2	3.6	11691	15	US-10-311-455-2213	Sequence 2213, Ap
c1095	51	3.8	15399	15	US-10-311-455-1487	Sequence 1487, Ap	c1168	48.2	3.6	17869	15	US-10-311-455-77	Sequence 77, Appl
c1096	51	3.8	18585	15	US-10-240-485-162	Sequence 162, App	c1169	48.2	3.6	17869	17	US-10-257-166-1	Sequence 1, Appli
c1097	50.8	3.8	6109	17	US-10-311-455-299	Sequence 299, App	c1170	48.2	3.6	40178	17	US-10-282-174-467	Sequence 467, App
c1098	50.8	3.8	6109	17	US-10-221-613-33	Sequence 33, Appl	c1171	48.2	3.6	40178	17	US-10-282-174-468	Sequence 468, App
c1099	50.8	3.8	6631	15	US-10-240-453-214	Sequence 214, App	c1172	48.2	3.6	40178	21	US-10-600-009-467	Sequence 467, App
c1100	50.8	3.8	7143	15	US-10-311-455-956	Sequence 956, App	c1173	48.2	3.6	40178	21	US-10-600-009-468	Sequence 468, App
c1101	50.6	3.8	176096	22	US-10-981-277-34	Sequence 34, Appl	c1174	48.2	3.6	40862	15	US-10-311-455-2046	Sequence 2046, Ap
c1102	50.4	3.7	6286	18	US-10-221-714A-313	Sequence 313, App	c1175	48.2	3.6	141158	20	US-10-719-993-6837	Sequence 6837, Ap
c1103	50.4	3.7	337344	19	US-10-388-838-58	Sequence 58, Appl	c1176	48.2	3.6	3673778	16	US-10-312-841-2	Sequence 2, Appli
c1104	50.2	3.7	1501	20	US-10-473-126-328	Sequence 328, App	c1177	48	3.6	65	10	US-09-908-975-25999	Sequence 25999, A
c1105	50.2	3.7	50000	21	US-10-706-635-25	Sequence 25, Appl	c1178	48	3.6	834	20	US-10-726-699-20	Sequence 20, Appl
c1106	50	3.7	391	20	US-10-357-930-8140	Sequence 8140, Ap	c1179	48	3.6	3076	9	US-09-745-763-71	Sequence 71, Appl
c1107	50	3.7	560	19	US-10-021-323-2253	Sequence 2253, Ap	c1180	48	3.6	7167	15	US-10-311-455-373	Sequence 373, App
c1108	49.8	3.7	5999	15	US-10-311-455-826	Sequence 826, App	c1181	48	3.6	14023	15	US-10-311-455-2078	Sequence 2078, Ap
c1109	49.8	3.7	5999	15	US-10-240-453-66	Sequence 66, Appl	c1182	48	3.6	19576	17	US-10-221-613-220	Sequence 220, App
c1110	49.8	3.7	6767	18	US-10-221-714A-330	Sequence 330, App	c1183	48	3.6	37515	19	US-10-433-793-28	Sequence 28, Appl
c1111	49.6	3.7	419	9	US-09-960-352-11234	Sequence 11234, A	c1184	48	3.6	83391	19	US-10-433-793-124	Sequence 124, App
c1112	49.6	3.7	994	14	US-10-198-846-6968	Sequence 6968, Ap	c1185	48	3.6	91697	20	US-10-417-375-36	Sequence 36, Appl
c1113	49.6	3.7	5388	15	US-10-311-455-218	Sequence 218, App	c1186	48	3.6	115218	21	US-10-278-698-255	Sequence 255, App
c1114	49.6	3.7	6591	18	US-10-221-714A-5	Sequence 5, Appli	c1187	48	3.6	115218	21	US-10-278-698-769	Sequence 769, App
c1115	49.4	3.7	7167	15	US-10-311-455-373	Sequence 373, App	c1188	47.8	3.6	614	19	US-10-437-963-57702	Sequence 57702, A
c1116	49.4	3.7	11805	15	US-10-311-455-1721	Sequence 1721, Ap	c1189	47.8	3.6	3586	18	US-10-240-454-61	Sequence 61, Appl
c1117	49.4	3.7	15387	15	US-10-311-455-158	Sequence 158, App	c1190	47.8	3.6	7131	17	US-10-221-613-324	Sequence 324, App
c1118	49.4	3.7	18997	15	US-10-172-086-17	Sequence 17, Appl	c1191	47.8	3.6	8238	15	US-10-311-455-1962	Sequence 1962, Ap

c1192	47.8	3.6	8238	18	US-10-240-454-44	Sequence 44, Appl	c1265	46.2	3.4	5689	15	US-10-240-453-100	Sequence 100, App
c1193	47.8	3.6	10020	15	US-10-311-455-2266	Sequence 2266, App	c1266	46.2	3.4	5689	18	US-10-221-714A-148	Sequence 148, App
c1194	47.8	3.6	40324	19	US-10-433-793-179	Sequence 179, App	c1267	46.2	3.4	5706	17	US-10-221-613-280	Sequence 280, App
c1195	47.8	3.6	109730	21	US-10-741-600-17809	Sequence 17809, A	c1268	46.2	3.4	6223	17	US-10-221-613-135	Sequence 135, App
c1196	47.6	3.5	1830	21	US-10-706-635-67	Sequence 67, Appl	c1269	46.2	3.4	13511	15	US-10-311-455-254	Sequence 254, App
c1197	47.6	3.5	4152	21	US-10-706-635-9	Sequence 9, Appli	c1270	46.2	3.4	13627	19	US-10-433-793-5	Sequence 5, Appli
c1198	47.6	3.5	6106	16	US-10-311-455-1445	Sequence 1445, App	c1271	46.2	3.4	105550	21	US-10-741-600-5630	Sequence 5630, App
c1199	47.6	3.5	6106	17	US-10-257-166-113	Sequence 113, App	c1272	46.2	3.4	105550	21	US-10-741-600-17620	Sequence 17620, A
c1200	47.6	3.5	6106	18	US-10-221-714A-151	Sequence 151, App	c1273	46	3.4	2298	9	US-09-960-352-1004	Sequence 1004, App
c1201	47.6	3.5	12237	15	US-10-311-455-2331	Sequence 2331, App	c1274	46	3.4	1461	19	US-10-767-701-13778	Sequence 13778, A
c1202	47.6	3.5	13712	15	US-10-311-455-1504	Sequence 1504, App	c1275	46	3.4	5807	15	US-10-311-455-1128	Sequence 1128, App
c1203	47.6	3.5	15567	13	US-10-047-676A-3	Sequence 3, Appli	c1276	46	3.4	6191	15	US-10-311-455-1189	Sequence 1189, App
c1204	47.6	3.5	15567	20	US-10-790-914-3	Sequence 3, Appli	c1277	46	3.4	6881	15	US-10-311-455-1353	Sequence 1353, App
c1205	47.6	3.5	21537	15	US-10-311-455-1972	Sequence 1972, App	c1278	46	3.4	6881	15	US-10-240-453-123	Sequence 123, App
c1206	47.6	3.5	32392	21	US-10-706-635-27	Sequence 27, Appl	c1279	46	3.4	7814	18	US-10-221-714A-252	Sequence 252, App
c1207	47.6	3.5	335913	10	US-09-754-853A-3	Sequence 3, Appli	c1280	46	3.4	8170	15	US-10-240-453-131	Sequence 131, App
c1208	47.6	3.5	335913	10	US-09-754-853A-3	Sequence 3, Appli	c1281	46	3.4	19087	15	US-10-311-455-766	Sequence 766, App
c1209	47.4	3.5	954	20	US-10-425-115-16752	Sequence 16752, A	c1282	46	3.4	42027	20	US-10-417-375-58	Sequence 58, Appl
c1210	47.4	3.5	5768	17	US-10-421-613-62	Sequence 62, Appl	c1283	46	3.4	43527	22	US-10-756-143-2369	Sequence 2369, App
c1211	47.4	3.5	7657	14	US-10-239-676-185	Sequence 185, App	c1284	46	3.4	71553	21	US-10-719-993-7039	Sequence 7039, App
c1212	47.4	3.5	7657	15	US-10-311-455-1995	Sequence 1995, App	c1285	46	3.4	71553	21	US-10-741-600-17960	Sequence 17960, A
c1213	47.4	3.5	15161	17	US-10-221-613-386	Sequence 386, App	c1286	46	3.4	1980090	20	US-10-719-993-6815	Sequence 6815, App
c1214	47.4	3.5	15373	15	US-10-311-455-440	Sequence 440, App	c1287	46	3.4	1980090	21	US-10-741-600-17676	Sequence 17676, A
c1215	47.4	3.5	337244	19	US-10-388-838-58	Sequence 58, Appl	c1288	45.8	3.4	457	9	US-09-770-444-508	Sequence 508, App
c1216	47.2	3.5	6123	15	US-10-311-455-794	Sequence 794, App	c1289	45.8	3.4	531	10	US-09-814-353-18996	Sequence 18996, A
c1217	47.2	3.5	6641	16	US-10-311-455-288	Sequence 288, App	c1290	45.8	3.4	921	20	US-10-425-113-38710	Sequence 38710, A
c1218	47.2	3.5	6641	16	US-10-240-452-36	Sequence 36, Appl	c1291	45.8	3.4	1559	18	US-10-351-334-42	Sequence 42, Appl
c1219	47.2	3.5	7445	15	US-10-311-455-824	Sequence 824, App	c1292	45.8	3.4	2056	15	US-10-106-698-2027	Sequence 2027, App
c1220	47.2	3.5	7445	17	US-10-257-166-92	Sequence 92, Appl	c1293	45.8	3.4	5795	15	US-10-311-455-1741	Sequence 1741, App
c1221	47.2	3.5	11049	15	US-10-311-455-642	Sequence 642, App	c1294	45.8	3.4	6419	15	US-10-311-455-240	Sequence 240, App
c1222	47.2	3.5	11049	18	US-10-240-5890C-28	Sequence 28, Appl	c1295	45.8	3.4	9155	15	US-10-311-455-436	Sequence 436, App
c1223	47.2	3.5	16217	15	US-10-311-455-597	Sequence 597, App	c1296	45.8	3.4	9707	15	US-10-311-455-1394	Sequence 1394, App
c1224	47.2	3.5	18434	15	US-10-311-455-1979	Sequence 1979, App	c1297	45.8	3.4	11178	17	US-10-221-613-16	Sequence 16, Appl
c1225	47	3.5	594	20	US-10-425-115-4325	Sequence 4325, App	c1298	45.8	3.4	15592	15	US-10-311-455-1299	Sequence 1299, App
c1226	47	3.5	5273	15	US-10-311-455-848	Sequence 848, App	c1299	45.8	3.4	15592	18	US-10-221-714A-175	Sequence 175, App
c1227	47	3.5	11787	18	US-10-240-5890C-52	Sequence 52, Appl	c1300	45.6	3.4	507	19	US-10-437-963-73825	Sequence 73825, A
c1228	47	3.5	13427	15	US-10-311-455-1900	Sequence 1900, App	c1301	45.6	3.4	599	20	US-10-425-113-163442	Sequence 163442, A
c1229	47	3.5	98716	21	US-10-741-600-17754	Sequence 17754, A	c1302	45.6	3.4	930	17	US-10-198-846-6625	Sequence 6625, App
c1230	46.8	3.5	472	28	US-10-424-599-116828	Sequence 116828, A	c1303	45.6	3.4	1730	14	US-10-369-493-29357	Sequence 29357, A
c1231	46.8	3.5	577	19	US-10-437-963-34329	Sequence 34329, A	c1304	45.6	3.4	3089	22	US-10-954-778-160	Sequence 160, App
c1232	46.8	3.5	858	14	US-10-198-846-7035	Sequence 7035, App	c1305	45.6	3.4	4654	15	US-10-311-455-2196	Sequence 2196, App
c1233	46.8	3.5	2911	17	US-10-264-049-283	Sequence 283, App	c1306	45.6	3.4	4654	18	US-10-221-714A-508	Sequence 508, App
c1234	46.8	3.5	6127	15	US-10-311-455-1587	Sequence 1587, App	c1307	45.6	3.4	4985	14	US-10-094-240-10	Sequence 10, Appl
c1235	46.8	3.5	6609	15	US-10-311-455-1276	Sequence 1276, App	c1308	45.6	3.4	4985	16	US-10-056-405-10	Sequence 10, Appl
c1236	46.8	3.5	8310	21	US-10-861-875-9	Sequence 9, Appli	c1309	45.6	3.4	5388	17	US-10-221-613-199	Sequence 199, App
c1237	46.8	3.5	9810	15	US-10-311-455-399	Sequence 399, App	c1310	45.6	3.4	5427	15	US-10-311-455-685	Sequence 685, App
c1238	46.8	3.5	15479	17	US-10-257-166-45	Sequence 45, Appl	c1311	45.6	3.4	6015	15	US-10-311-455-649	Sequence 649, App
c1239	46.8	3.5	17721	15	US-10-311-455-1701	Sequence 1701, App	c1312	45.6	3.4	7040	15	US-10-172-086-13	Sequence 13, Appl
c1240	46.6	3.5	474	20	US-10-425-115-64122	Sequence 64122, A	c1313	45.6	3.4	7040	18	US-10-221-714A-161	Sequence 161, App
c1241	46.6	3.5	960	14	US-10-198-846-6381	Sequence 6381, App	c1314	45.6	3.4	7040	19	US-10-311-507-47	Sequence 47, Appl
c1242	46.6	3.5	13148	18	US-10-424-599-30088	Sequence 30088, A	c1315	45.6	3.4	7040	20	US-10-480-846-13	Sequence 13, Appl
c1243	46.6	3.5	11787	18	US-10-240-5890C-52	Sequence 52, Appl	c1316	45.6	3.4	7040	20	US-10-473-126-173	Sequence 173, App
c1244	46.6	3.5	12507	15	US-10-311-455-271	Sequence 271, App	c1317	45.6	3.4	7040	20	US-10-473-126-319	Sequence 319, App
c1245	46.6	3.5	14307	15	US-10-311-455-702	Sequence 702, App	c1318	45.6	3.4	7990	15	US-10-311-455-131	Sequence 131, App
c1246	46.6	3.5	18060	16	US-10-240-5890C-21	Sequence 21, Appl	c1319	45.6	3.4	7990	16	US-10-240-452-7	Sequence 7, Appli
c1247	46.4	3.4	504	19	US-10-437-963-90499	Sequence 90499, A	c1320	45.6	3.4	8305	15	US-10-311-455-1541	Sequence 1541, App
c1248	46.4	3.4	794	20	US-10-739-930-3501	Sequence 3501, App	c1321	45.6	3.4	11260	14	US-10-239-676-19	Sequence 19, Appl
c1249	46.4	3.4	5518	15	US-10-240-453-180	Sequence 180, App	c1322	45.6	3.4	11260	14	US-10-240-453-27	Sequence 27, Appl
c1250	46.4	3.4	5551	17	US-10-421-613-55	Sequence 55, Appl	c1323	45.6	3.4	12393	15	US-10-311-455-1235	Sequence 1235, App
c1251	46.4	3.4	5647	14	US-10-311-455-1540	Sequence 1540, App	c1324	45.6	3.4	14032	15	US-10-311-455-1426	Sequence 1426, App
c1252	46.4	3.4	5647	17	US-10-221-613-282	Sequence 282, App	c1325	45.6	3.4	14919	18	US-10-221-714A-228	Sequence 228, App
c1253	46.4	3.4	5696	15	US-10-311-455-1079	Sequence 1079, App	c1326	45.6	3.4	17421	14	US-10-239-676-53	Sequence 53, Appl
c1254	46.4	3.4	5917	14	US-10-087-464-9	Sequence 9, Appli	c1327	45.6	3.4	17421	14	US-10-240-453-55	Sequence 55, Appl
c1255	46.4	3.4	6283	15	US-10-311-455-61	Sequence 61, Appl	c1328	45.6	3.4	567564	19	US-10-699-156-3	Sequence 3, Appli
c1256	46.4	3.4	7503	15	US-10-311-455-1522	Sequence 1522, App	c1329	45.4	3.4	294	10	US-09-814-353-5106	Sequence 5106, App
c1257	46.4	3.4	7503	19	US-10-433-793-40	Sequence 40, Appl	c1330	45.4	3.4	294	10	US-09-814-353-11398	Sequence 11398, A
c1258	46.4	3.4	11745	15	US-10-240-453-206	Sequence 206, App	c1331	45.4	3.4	445	20	US-10-357-930-5422	Sequence 5422, App
c1259	46.4	3.4	11996	15	US-10-240-485-46	Sequence 46, Appl	c1332	45.4	3.4	614	10	US-09-814-353-5117	Sequence 5117, App
c1260	46.4	3.4	32392	21	US-10-706-635-27	Sequence 27, Appl	c1333	45.4	3.4	614	10	US-09-814-353-11409	Sequence 11409, A
c1261	46.4	3.4	46951	16	US-10-091-281-2	Sequence 2, Appli	c1334	45.4	3.4	622	10	US-09-764-891-1673	Sequence 1673, App
c1262	46.4	3.4	50000	21	US-10-706-635-23	Sequence 23, Appl	c1335	45.4	3.4	622	15	US-10-205-428-148	Sequence 148, App
c1263	46.2	3.4	469	10	US-09-814-353-17965	Sequence 17965, A	c1336	45.4	3.4	1014	15	US-10-195-730-34	Sequence 34, Appl
c1264	46.2	3.4	5689	14	US-10-239-676-90	Sequence 90, Appl	c1337	45.4	3.4	1014	19	US-10-799-747-34	Sequence 34, Appl

1338	45.4	3.4	1014	21	US-10-979-183-34	Sequence 34, Appl	1411	44.8	3.3	755	17	US-10-027-632-128109	Sequence 128109,
c1339	45.4	3.4	3059	22	US-10-954-778-160	Sequence 160, App	1412	44.8	3.3	3095	20	US-10-602-494-313	Sequence 313, App
1340	45.4	3.4	3744	8	US-08-961-527-263	Sequence 263, App	c1413	44.8	3.3	5020	20	US-10-473-126-99	Sequence 99, Appl
1341	45.4	3.4	3744	17	US-10-158-844-263	Sequence 263, App	c1414	44.8	3.3	5020	20	US-10-473-126-245	Sequence 245, App
c1342	45.4	3.4	4985	14	US-10-094-240-10	Sequence 10, Appl	1415	44.8	3.3	5875	15	US-10-311-455-261	Sequence 261, App
c1343	45.4	3.4	4985	16	US-10-056-405-10	Sequence 10, Appl	1416	44.8	3.3	5917	14	US-10-087-464-9	Sequence 9, Appl1
c1344	45.4	3.4	5033	20	US-10-473-126-285	Sequence 285, App	1417	44.8	3.3	6222	15	US-10-311-455-211	Sequence 211, App
c1345	45.4	3.4	5231	15	US-10-311-455-1239	Sequence 1239, Ap	1418	44.8	3.3	6228	17	US-10-221-613-393	Sequence 393, App
c1346	45.4	3.4	5376	15	US-10-311-455-1239	Sequence 1239, Ap	c1419	44.8	3.3	6397	15	US-10-311-455-792	Sequence 792, App
c1347	45.4	3.4	5427	15	US-10-311-455-686	Sequence 686, App	1420	44.8	3.3	6627	15	US-10-311-455-1547	Sequence 1547, App
c1348	45.4	3.4	5675	15	US-10-311-455-1249	Sequence 1249, Ap	c1421	44.8	3.3	6662	15	US-10-311-455-371	Sequence 371, App
c1349	45.4	3.4	5909	15	US-10-311-455-1132	Sequence 1132, Ap	1422	44.8	3.3	6676	19	US-10-433-793-44	Sequence 44, Appl
c1350	45.4	3.4	6621	15	US-10-311-455-886	Sequence 886, App	c1423	44.8	3.3	6904	15	US-10-311-455-185	Sequence 185, App
c1351	45.4	3.4	7906	14	US-10-239-676-98	Sequence 98, Appl	c1424	44.8	3.3	7201	15	US-10-311-455-309	Sequence 309, App
c1352	45.4	3.4	7906	15	US-10-240-453-110	Sequence 110, App	c1425	44.8	3.3	7319	15	US-10-311-455-2018	Sequence 2018, App
c1353	45.4	3.4	8227	19	US-10-433-793-155	Sequence 155, App	c1426	44.8	3.3	7823	14	US-10-239-676-198	Sequence 198, App
c1354	45.4	3.4	8524	14	US-10-311-455-1814	Sequence 1814, Ap	c1427	44.8	3.3	7823	15	US-10-311-455-2034	Sequence 2034, App
c1355	45.4	3.4	8524	18	US-10-221-714A-310	Sequence 310, App	c1428	44.8	3.3	7823	15	US-10-240-453-292	Sequence 292, App
c1356	45.4	3.4	13574	15	US-10-311-455-1290	Sequence 1290, Ap	c1429	44.8	3.3	8952	18	US-10-221-714A-167	Sequence 167, App
1357	45.4	3.4	15853	17	US-10-221-613-422	Sequence 422, App	c1430	44.8	3.3	8962	15	US-10-311-455-660	Sequence 660, App
c1358	45.4	3.4	18218	15	US-10-311-455-1922	Sequence 1922, App	c1431	44.8	3.3	11092	15	US-10-311-455-1486	Sequence 1486, App
c1359	45.4	3.4	18855	15	US-10-311-455-583	Sequence 583, App	c1432	44.8	3.3	128034	17	US-10-282-174-187	Sequence 186, App
c1360	45.4	3.4	105550	19	US-10-741-601-5630	Sequence 5630, App	c1433	44.8	3.3	128034	17	US-10-282-174-187	Sequence 187, App
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1363	45.4	3.4	462586	22	US-10-476-264-420	Sequence 420, App	1436	44.8	3.3	202100	17	US-10-282-174-484	Sequence 484, App
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c1366	45.2	3.4	421	10	US-09-814-353-5169	Sequence 5169, App	c1439	44.6	3.3	363	10	US-09-814-353-10888	Sequence 10888, A
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c1368	45.2	3.4	505	14	US-10-060-036-2607	Sequence 2607, Ap	c1441	44.6	3.3	408	21	US-10-275-323A-13	Sequence 13, Appl
c1369	45.2	3.4	5001	15	US-10-172-086-69	Sequence 69, Appl	1442	44.6	3.3	440	20	US-10-425-115-173202	Sequence 173202, A
c1370	45.2	3.4	5001	16	US-10-240-452-73	Sequence 73, Appl	c1443	44.6	3.3	465	10	US-08-844-353-17748	Sequence 17748, A
c1371	45.2	3.4	5001	19	US-10-311-507-33	Sequence 33, Appl	c1444	44.6	3.3	648	13	US-10-027-632-132827	Sequence 132827, A
c1372	45.2	3.4	5001	20	US-10-480-846-69	Sequence 69, Appl	c1445	44.6	3.3	648	17	US-10-027-632-132827	Sequence 132827, A
c1373	45.2	3.4	5328	17	US-10-311-455-533	Sequence 533, App	1446	44.6	3.3	2802	20	US-10-425-115-35732	Sequence 35732, A
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c1375	45.2	3.4	5930	15	US-10-311-455-490	Sequence 490, App	c1448	44.6	3.3	6853	15	US-10-311-455-283	Sequence 283, App
1376	45.2	3.4	6171	15	US-10-311-455-761	Sequence 761, App	c1449	44.6	3.3	6853	16	US-10-240-452-31	Sequence 31, Appl
c1377	45.2	3.4	6200	15	US-10-311-455-2188	Sequence 2188, Ap	c1450	44.6	3.3	7351	15	US-10-311-455-1	Sequence 1, Appl1
c1378	45.2	3.4	7346	15	US-10-311-455-318	Sequence 318, App	c1451	44.6	3.3	8056	20	US-10-473-126-385	Sequence 385, App
c1379	45.2	3.4	7892	17	US-10-257-166-138	Sequence 138, App	c1452	44.6	3.3	8607	18	US-10-240-589C-111	Sequence 111, App
1380	45.2	3.4	9265	15	US-10-311-455-2125	Sequence 2125, Ap	c1453	44.6	3.3	11964	19	US-10-433-793-56	Sequence 56, Appl
c1381	45.2	3.4	9265	18	US-10-240-454-49	Sequence 49, Appl	c1454	44.6	3.3	11964	15	US-10-311-455-604	Sequence 604, App
c1382	45.2	3.4	12592	17	US-10-221-613-58	Sequence 58, Appl	c1455	44.6	3.3	15732	14	US-10-239-676-95	Sequence 95, Appl
c1383	45.2	3.4	19380	17	US-10-221-613-390	Sequence 390, App	c1456	44.6	3.3	15732	15	US-10-240-453-107	Sequence 107, App
c1384	45.2	3.4	40324	19	US-10-433-793-180	Sequence 180, App	c1457	44.6	3.3	15951	15	US-10-311-455-1654	Sequence 1654, App
c1385	45.2	3.4	163382	20	US-10-367-094-179	Sequence 179, App	c1458	44.6	3.3	17959	15	US-10-240-485-134	Sequence 134, App
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c1387	45	3.3	411	14	US-10-198-846-4590	Sequence 4590, Ap	c1460	44.6	3.3	17959	16	US-10-240-452-42	Sequence 42, Appl
c1388	45	3.3	485	20	US-10-425-115-170017	Sequence 170017, A	c1461	44.6	3.3	19082	15	US-10-311-455-599	Sequence 599, App
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1393	45	3.3	1501	20	US-10-473-126-328	Sequence 328, App	c1466	44.4	3.3	397	9	US-09-960-352-13784	Sequence 13784, A
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c1401	45	3.3	18154	15	US-10-311-455-227	Sequence 227, App	1474	44.4	3.3	2217	17	US-10-191-803-555	Sequence 555, App
1402	45	3.3	115218	21	US-10-278-698-255	Sequence 255, App	c1475	44.4	3.3	2217	18	US-10-152-319A-2185	Sequence 2185, App
1403	45	3.3	115218	21	US-10-278-698-769	Sequence 769, App	1476	44.4	3.3	5487	15	US-10-311-455-1571	Sequence 1571, App
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c1405	45	3.3	164910	22	US-10-981-277-53	Sequence 53, Appl	c1478	44.4	3.3	6132	15	US-10-311-455-835	Sequence 835, App
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1409	44.8	3.3	551	21	US-10-863-332-60	Sequence 60, Appl	c1482	44.4	3.3	6465	15	US-10-311-455-958	Sequence 958, App
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(without alignments)  
3382.452 Million cell updates/sec

Title: US-09-989-724-387

Perfect score: 1102

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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6	1089	98.8	666	6	AX083382	Sequence
7	1089	98.8	1345	9	AF229179	Homo sapi
8	1089	98.8	1347	6	AX083392	Sequence
9	1089	98.8	1377	9	BC050606	Homo sapi
10	1089	98.8	1440	9	BC015099	Homo sapi
11	1089	98.8	1605	9	BC014317	Homo sapi
12	1086	98.5	1401	6	BD083420	Secreted
13	1082	98.2	1447	6	BD205644	97 human
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23	1064	96.6	848	6	AX968599	Sequence
24	1064	96.6	848	6	AX969202	Sequence
25	1064	96.6	848	6	BD023757	Sequence
26	1064	96.6	848	6	BD073618	5' EST of
27	1064	96.6	848	6	BD075896	5' EST of
28	1064	96.6	848	6	BD076074	5' EST of
29	1064	96.6	848	6	BD076775	5' EST of
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33	1064	96.6	848	6	BD107926	EST and e
34	1064	96.6	848	6	BD131408	CDNA enco
35	1062	96.4	1356	6	BD135300	110 human
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37	936	84.9	545	6	CQ714932	Sequence
38	931	84.5	1222	10	BC049912	Mus muscu
39	931	84.5	1262	10	AF178085	Mus muscu
40	924	83.8	1181	10	AF178086	Rattus no
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49	376	34.1	2415	6	BD274685	Angiotens
50	376	34.1	2415	6	E43987	ACE-analog
51	376	34.1	2415	6	AR382342	Sequence
52	376	34.1	2415	6	AX418984	Sequence
53	376	34.1	2418	6	E39033	MPROT15 pol
54	376	34.1	2418	9	AY623811	Homo sapi
55	376	34.1	2599	6	E43988	ACE-analog
56	376	34.1	3325	9	AF291820	Homo sapi
57	376	34.1	3334	6	AX047758	Sequence
58	376	34.1	3339	9	BC048094	Homo sapi
59	376	34.1	3341	9	HSB000880	Homo sapi
60	376	34.1	3348	9	BC039902	Homo sapi
61	376	34.1	3375	9	BC059378	Homo sapi
62	376	34.1	3396	6	AR135177	Sequence
63	376	34.1	3396	6	BD274684	Angiotens
64	376	34.1	3396	6	AR353104	Sequence
65	376	34.1	3396	6	AR382341	Sequence
66	376	34.1	3396	6	AX418982	Sequence
67	376	34.1	3396	6	AX431513	Sequence
68	376	34.1	3405	6	CQ754222	Sequence
69	376	34.1	3405	9	AF241254	Homo sapi
70	373	33.8	2599	9	AB046569	Homo sapi
71	369	33.5	3732	6	AR528488	Sequence
72	369	33.5	3732	6	AX463938	Sequence
73	369	33.5	3732	6	AY358714	Homo sapi
74	361	32.8	2638	6	AX047762	Sequence
75	361	32.8	2638	6	AX047765	Sequence
76	361	32.8	2739	6	CQ754224	Sequence
77	361	32.8	2739	10	BC026801	Mus muscu

78	359	32.6	2920	6	AR353103 Sequence	151	92	8.3	189994	2	AC109209	AC109209 Mus muscu
79	358	32.5	1993	10	AB053182 Mus muscu	152	91.5	8.3	3564	6	AX379445	AX379445 Sequence
80	357	32.4	2760	10	AB053181 Mus muscu	153	91.5	8.3	4163	10	AX124460	AX124460 Mus muscu
c 81	340	30.9	159446	9	AC003669 Homo sapi	154	91.5	8.3	4858	6	AX379444	AX379444 Sequence
82	340	30.9	165730	2	AC061988 Homo sapi	155	91.5	8.3	4930	10	BC058716	BC058716 Mus muscu
c 83	335	30.4	213	6	CQ111904 Sequence	156	91	8.3	5149	6	CQ579236	CQ579236 Sequence
c 84	335	30.4	213	6	CQ150704 Sequence	c 157	91	8.3	6271	2	AC013078	AC013078 Drosophil
c 85	335	30.4	213	6	CQ184910 Sequence	c 158	91	8.3	9783	1	U39699	U39699 Mycoplasma
c 86	335	30.4	213	6	CQ234037 Sequence	c 159	91	8.3	110000	6	AR003426_1	Continuation (2 of
c 87	335	30.4	213	6	CQ271795 Sequence	c 160	91	8.3	9783	6	AR300198_2	Continuation (3 of
c 88	335	30.4	213	6	CQ309364 Sequence	c 161	91	8.3	179069	2	AC104144	AC104144 Drosophill
c 89	335	30.4	213	6	CQ346012 Sequence	c 162	91	8.3	182387	3	AC116543	AC116543 Drosophill
c 90	324	29.4	464	6	CQ098839 Sequence	c 163	91	8.3	262050	1	AP000985	AP000985 Sulfolobu
c 91	324	29.4	464	6	CQ137751 Sequence	c 164	90.5	8.2	163642	9	AC022748	AC022748 Homo sapi
c 92	324	29.4	464	6	CQ175049 Sequence	c 165	90	8.2	2812	10	NM02748	X95600 M.musculus
c 93	324	29.4	464	6	CQ221115 Sequence	c 166	90	8.2	3126	10	AB010436	AB010436 Rattus ra
c 94	324	29.4	464	6	CQ259275 Sequence	c 167	90	8.2	3136	6	I34425	I34425 Sequence 41
c 95	324	29.4	464	6	CQ296932 Sequence	c 168	90	8.2	3136	6	I55092	I55092 Sequence 41
c 96	324	29.4	464	6	CQ333335 Sequence	c 169	90	8.2	3352	10	BC057581	BC057581 Mus muscu
c 97	315	28.6	2134	6	CQ714933 Sequence	c 170	90	8.2	135940	2	AC119406	AC119406 Trypanoso
c 98	302	27.4	225558	2	AC103066 Rattus no	c 171	90	8.2	219517	2	AC098152	AC098152 Rattus no
c 99	302	27.4	226820	2	AC118872 Rattus no	c 172	90	8.2	234549	2	AC105497	AC105497 Rattus no
100	289	26.2	1119	5	EX935959 Gallus ga	c 173	89.5	8.1	483	10	AF148797	AF148797 Rattus no
101	289	26.2	112893	10	AL7322294 Mouse DNA	c 174	89.5	8.1	2545	9	HUMCABA	CQ824165 Sequence
102	289	26.2	234105	10	AC091606 Mus Muscu	c 175	89.5	8.1	2545	9	HUMCABA	I34060 Homo sapien
103	281	25.5	862	6	BD270445 Genes ass	c 176	89.5	8.1	2550	6	I34431	I34431 Sequence 53
104	278	25.2	2415	6	AX047760 Sequence	c 177	89.5	8.1	2550	6	I46829	I46829 Sequence 47
105	262	23.8	2282	6	E39034 MPROT15 pol	c 178	89.5	8.1	2550	6	I55098	I55098 Sequence 53
106	259	23.5	2415	6	AX047764 Sequence	c 179	89.5	8.1	3146	6	AR338786	AR338786 Sequence
107	238	21.6	3474	6	AX576256 Sequence	c 180	89.5	8.1	3150	6	AX332281	AX332281 Sequence
c 108	233.5	21.2	2350	6	AR263862 Sequence	c 181	89.5	8.1	3150	6	AX333742	AX333742 Sequence
c 109	232	21.1	1013	9	AK026461 Homo sapi	c 182	89.5	8.1	3150	6	AX3337415	AX3337415 Sequence
c 110	207.5	18.8	41572	9	AV217547 Homo sapi	c 183	89.5	8.1	3150	9	HUMINTEG8A	L36531 Homo sapien
c 111	207.5	18.8	194492	9	AC097625 Homo sapi	c 184	89.5	8.1	3668	6	AX377990	AX377990 Sequence
112	187	17.0	192676	10	AL671706 Mouse DNA	c 185	89.5	8.1	6868	3	AF056940	AF056940 Drosophill
113	179	16.2	1659	3	AK113405 Ciona int	c 186	89.5	8.1	136119	9	HS1028D15	AL121886 Human DNA
114	164	14.9	1155	5	EX934887 Gallus ga	c 187	89.5	8.1	198070	2	BX649326	BX649326 Danio rer
115	125.5	11.4	758	5	EX931879 Gallus ga	c 188	89.5	8.1	207701	2	BX545856	BX545856 Danio rer
116	118.5	10.8	109975	9	AC112497 Homo sapi	c 189	89	8.1	2317	6	CQ719194	CQ719194 Sequence
c 117	111	10.1	144046	2	AC068334 Homo sapi	c 190	89	8.1	2742	9	AB035305	AB035305 Homo sapi
c 118	111	10.1	166016	9	AX591378 Human DNA	c 191	89	8.1	2829	6	AB033856	AB033856 Sequence
c 119	106.5	9.7	3666	6	AX664156 Sequence	c 192	89	8.1	3502	9	AK124734	AK124734 Homo sapi
120	105	9.5	253354	2	AC096809 Rattus no	c 193	89	8.1	4558	3	AF177914	AF177914 Strongylo
121	104	9.4	164038	2	AC150011 Callithiri	c 194	89	8.1	110000	1	BX908798_21	Continuation (22 o
c 122	103	9.3	39233	6	AC005626 Homo sapi	c 195	89	8.1	154244	9	AL360231	AL360231 Human DNA
123	102	9.3	60	6	CQ539130 Sequence	c 196	89	8.1	171967	2	AC102710	AC102710 Mus muscu
124	100	9.1	110000	2	PFMAL8P1_09	c 197	89	8.1	212008	2	AC093271	AC093271 Homo sapi
c 125	100	9.1	146175	8	AC123527 Oryza sat	c 198	88.5	8.0	2897	14	AB026929	AB026929 TIV-like
c 126	99	9.0	82453	9	AC004558 Homo sapi	c 199	88.5	8.0	36056	3	DMC163A10	AL035436 Drosophill
c 127	99	9.0	110000	2	Continuation (5 of	c 200	88.5	8.0	158294	2	AC116789	AC116789 Mus muscu
c 128	99	9.0	266403	2	AC114693 Rattus no	c 201	88.5	8.0	169781	10	AF336378	AF336378 Mus muscu
129	98	8.9	531	6	CQ411925 Sequence	c 202	88.5	8.0	188287	9	HS32B1	AL023693 Human DNA
130	98	8.9	144239	9	AC004015 Homo sapi	c 203	88.5	8.0	204437	10	AC117678	AC117678 Mus muscu
131	97.5	8.8	3546	3	X97283 G.cydoriun	c 204	88.5	8.0	273740	2	AC132066	AC132066 Rattus no
132	96.5	8.8	3039	10	AF0411409 Mus muscu	c 205	88	8.0	1177	10	MUSCDA44A	M27129 Mouse CD44
133	95.5	8.7	5515	5	GGA238216 Gallus ga	c 206	88	8.0	1183	10	MUSCDA44B	M27130 Mouse CD44
134	94	8.5	34337	6	AX398707 Sequence	c 207	88	8.0	1208	10	MUSPGP1A	J05163 Mouse phosp
c 135	94	8.5	75425	2	AC135034 Homo sapi	c 208	88	8.0	1337	10	MUSPGP1	J05165 Mouse phago
c 136	94	8.5	166256	9	AC018922 Homo sapi	c 209	88	8.0	1418	10	NMPPGPI1M1M	X66081 M.musculus
137	94	8.5	167071	9	AC128649 Homo sapi	c 210	88	8.0	1520	10	NMPPGPI1M2M	X66082 M.musculus
138	94	8.5	184193	2	AC109720 Rattus no	c 211	88	8.0	1766	10	NMPPGPI1M3M	X66083 M.musculus
c 139	94	8.5	22083	2	AC118432 Rattus no	c 212	88	8.0	1997	10	NMPPGPI1M4M	X66084 M.musculus
c 140	94	8.5	230449	2	AC105504 Rattus no	c 213	88	8.0	2613	10	NM0251594	AX751594 Mus muscu
c 141	94	8.5	252988	2	AC105511 Rattus no	c 214	88	8.0	2799	10	BC005676	BC005676 Mus muscu
142	93.5	8.5	2790	6	CQ611604 Sequence	c 215	88	8.0	3518	10	BC051388	BC051388 Mus muscu
143	93	8.4	221179	2	AC099392 Rattus no	c 216	88	8.0	110000	3	AC116984_1	Continuation (2 of
144	93	8.4	274148	2	AC132554 Rattus no	c 217	88	8.0	195863	2	CR847978	CR847978 Danio rer
145	92.5	8.4	5070	3	AF012531 Lymnaea s	c 218	88	8.0	200340	9	AC009997	AC009997 Homo sapi
146	92.5	8.4	229752	2	AC127045 Rattus no	c 219	87.5	7.9	2908	6	CQ579237	CQ579237 Sequence
c 147	92	8.3	93010	10	AL627386 Mouse DNA	c 220	87.5	7.9	117409	2	AC138141	AC138141 Homo sapi
c 148	92	8.3	137271	2	AC102823 Mus muscu	c 221	87.5	7.9	128891	9	AF130866	AF130866 Homo sapi
149	92	8.3	159056	10	AL845368 Mouse DNA	c 222	87.5	7.9	147788	2	AC015840	AC015840 Homo sapi
c 150	92	8.3	188989	10	AC074224 Mus muscu	c 223	87.5	7.9	152309	9	AC138185	AC138185 Homo sapi

224	87.5	7.9	160612	9	AP005856	AP005856 Homo sapi	c 297	85.5	7.8	110980	8	ATF9K21	AL138657 Arabidops
225	87.5	7.9	161238	9	AP003127	AP003127 Homo sapi	c 298	85.5	7.8	113951	9	AC007552	AC007552 Homo sapi
226	87.5	7.9	168594	9	AP003970	AP003970 Homo sapi	c 299	85.5	7.8	191378	2	AC129960	AC129960 Bos tauri
c 227	87.5	7.9	178929	9	AL359252	Human DNA	c 300	85.5	7.8	239945	2	AC094050	AC094050 Rattus no
228	87.5	7.9	181827	2	AC022942	Homo sapi	c 301	85.5	7.8	248254	2	AC133448	AC133448 Rattus no
229	87.5	7.9	186812	2	AC023089	Homo sapi	c 302	85	7.7	4756	6	AR380916	AR380916 Sequence
c 230	87.5	7.9	192657	1	AP005377	Thermosyn	c 303	85	7.7	4756	6	AR380916	AR380916 Sequence
231	87.5	7.9	215789	2	AC103449	Rattus no	c 304	85	7.7	4756	6	AR380916	AR380916 Sequence
c 232	87	7.9	847	11	BV048781	S212P6020	c 305	85	7.7	24174	3	CBRG35124	D37781 Human mRNA
233	87	7.9	1089	10	CRUCD44	M33827 Hamster hya	c 306	85	7.7	58498	9	HS410B11	286063 Human DNA s
234	87	7.9	4129	1	AB098080	Paenibaci	c 307	85	7.7	110000	8	CR380951_5	Continuation (6 of
235	87	7.9	4631	6	BD261713	12 human	c 308	85	7.7	114738	8	AC002130	AC002130 Genomic s
236	87	7.9	184457	1	AF079317	Spingomo	c 309	85	7.7	152802	9	AC018923	AC018923 Homo sapi
237	87	7.9	196408	10	AC142114	Mus muscu	c 310	85	7.7	152895	2	AC139973	AC139973 Rattus no
c 238	87	7.9	200370	9	AC104035	Homo sapi	c 311	85	7.7	164846	2	AC107727	AC107727 Mus muscu
c 239	87	7.9	202000	1	AP000058	Aeropyrum	c 312	85	7.7	183051	2	AC120130	AC120130 Mus muscu
c 240	87	7.9	250519	2	AC094894	Rattus no	c 313	85	7.7	190371	2	AC116830	AC116830 Mus muscu
241	87	7.9	257860	2	AC127719	Rattus no	c 314	85	7.7	192141	2	AC019004	AC019004 Homo sapi
c 242	86.5	7.8	2147	10	BC010299	Mus muscu	c 315	85	7.7	213676	9	AC103975	AC103975 Homo sapi
243	86.5	7.8	3295	3	AF196553	Drosophil	c 316	85	7.7	255661	2	AC106084	AC106084 Rattus no
244	86.5	7.8	3521	3	DME289882	Chlorobiu	c 317	85	7.7	273225	2	AC129440	AC129440 Rattus no
c 245	86.5	7.8	11067	1	AB012888	Measles v	c 318	84.5	7.7	2097	9	IR0322987	AL359064 Homo sapi
246	86.5	7.8	15894	14	AB012948	Measles v	c 319	84.5	7.7	2907	1	BACFLG	M54965 Bacillus su
247	86.5	7.8	15894	14	AB012948	Measles v	c 320	84.5	7.7	3057	9	AF111799	AF111799 Homo sapi
c 248	86.5	7.8	110000	2	AC151852_1	Continuation (2 of	c 321	84.5	7.7	3564	6	AX379427	AX379427 Sequence
c 249	86.5	7.8	110000	8	CR382139_16	Continuation (17 o	c 322	84.5	7.7	3601	5	XL092006	U92006 Xenopus lae
c 250	86.5	7.8	114576	9	AC074397	Homo sapi	c 323	84.5	7.7	3983	6	CQ721401	CQ721401 Sequence
c 251	86.5	7.8	154324	2	AC122552	Mus muscu	c 324	84.5	7.7	3983	9	AF137378	AF137378 Homo sapi
c 252	86.5	7.8	157904	2	AC025150	Homo sapi	c 325	84.5	7.7	5042	6	AX379426	AX379426 Sequence
253	86.5	7.8	166197	10	AC132343	Mus muscu	c 326	84.5	7.7	38306	6	CQ812178	CQ812178 Sequence
254	86.5	7.8	167691	2	AC103349	Mus muscu	c 327	84.5	7.7	38306	6	CQ818355	CQ818355 Sequence
255	86.5	7.8	183188	2	AC147927	Ovis arie	c 328	84.5	7.7	80142	9	AL645465	AL645465 Human DNA
c 256	86.5	7.8	191635	10	BX119996	Mouse DNA	c 329	84.5	7.7	107947	8	NCB7N14	AL669986 Neurospor
257	86.5	7.8	218800	2	AC094410	Rattus no	c 330	84.5	7.7	110000	2	AC117024_3	Continuation (4 of
c 258	86.5	7.8	230116	10	AL732620	Mouse DNA	c 331	84.5	7.7	157138	2	AC144366	AC144366 Papio anu
c 259	86.5	7.8	244637	2	AC110473	Rattus no	c 332	84.5	7.7	165784	2	AC022527	AC022527 Homo sapi
260	86.5	7.8	274710	2	AC131884	Rattus no	c 333	84.5	7.7	175191	9	AC010251	AC010251 Homo sapi
c 261	86.5	7.8	303249	1	AP001515	Bacillus	c 334	84.5	7.7	198097	10	AC146602	AC146602 Mus muscu
262	86	7.8	1383	10	RNU52179	Rattus norv	c 335	84.5	7.7	199096	10	AC098718	AC098718 Mus muscu
263	86	7.8	1384	10	RNU46957	Rattus norv	c 336	84.5	7.7	204263	1	BSUB0009	299112 Bacillus su
264	86	7.8	1384	10	AF065147	Rattus norv	c 337	84.5	7.7	204350	10	AC125056	AC125056 Mus muscu
265	86	7.8	1690	1	AF061802	Pseudomon	c 338	84.5	7.7	207922	10	AL450399	AL450399 Mouse DNA
266	86	7.8	1932	10	MAU10881	Mesocricetu	c 339	84.5	7.7	211772	2	AC112148	AC112148 Mus muscu
267	86	7.8	1932	10	BC061531	Rattus no	c 340	84.5	7.7	212564	10	AC148983	AC148983 Mus muscu
268	86	7.8	2747	6	AX401912	Sequence	c 341	84.5	7.7	216325	10	AC112260	AC112260 Mus muscu
269	86	7.8	2747	10	RATCD44A	Rattus norv	c 342	84.5	7.7	248297	2	AC094564	AC094564 Rattus no
270	86	7.8	2962	10	MAU10880	Mesocricetu	c 343	84.5	7.7	255790	2	AC117112	AC117112 Rattus no
271	86	7.8	3164	10	RATMETAA	Rattus norv	c 344	84.5	7.7	257934	2	AC113300	AC113300 Rattus no
272	86	7.8	3207	6	I19505	Sequence 1	c 345	84.5	7.7	258486	2	AC113677	AC113677 Rattus no
273	86	7.8	3580	10	AF135439	Mus muscu	c 346	84.5	7.7	290573	2	AC110362	AC110362 Rattus no
274	86	7.8	4038	10	RNU96138	Rattus norv	c 347	84.5	7.7	311321	1	NMA322491	AL162754 Neisseria
c 275	86	7.8	134201	2	AC114976	Homo sapi	c 348	84.5	7.7	345730	1	BX957219	BX957219 Methanoco
276	86	7.8	141048	2	AC141679	Apis mell	c 349	84	7.6	2446	3	AB189721	AB189721 Plasmodi
c 277	86	7.8	150902	2	AC018391	Homo sapi	c 350	84	7.6	11445	1	AE010606	AE010606 Fusobacte
278	86	7.8	186535	9	AC022272	Homo sapi	c 351	84	7.6	60016	2	AC126381	AC126381 Homo sapi
c 279	86	7.8	210545	5	BX004772	Zebrafish	c 352	84	7.6	104939	9	AL590413	AL590413 Human DNA
280	86	7.8	253599	2	AC117827	Mus muscu	c 353	84	7.6	110000	2	AC151843_2	Continuation (3 of
281	86	7.8	259957	2	AC141698	Apis mell	c 354	84	7.6	110000	2	AL732358	AL732358 Homo sapi
c 282	86	7.8	266544	3	AC116956	Dictyoste	c 355	84	7.6	113880	3	PFMAL394_0	AL008970 Plasmodi
283	85.5	7.8	3212	9	BC038232	Homo sapi	c 356	84	7.6	161797	9	AP005209	AP005209 Homo sapi
284	85.5	7.8	3447	6	AX366689	Sequence	c 357	84	7.6	171158	2	AC023201	AC023201 Homo sapi
285	85.5	7.8	3557	6	BD160631	Primer fo	c 358	84	7.6	173657	2	AP001014	AP001014 Homo sapi
286	85.5	7.8	3557	6	CQ834028	Sequence	c 359	84	7.6	174409	2	AC107088	AC107088 Homo sapi
287	85.5	7.8	3557	6	AX302537	Sequence	c 360	84	7.6	177223	9	AC009890	AC009890 Genomic S
288	85.5	7.8	3557	6	AX366690	Sequence	c 361	84	7.6	179786	2	AP001015	AP001015 Homo sapi
289	85.5	7.8	3557	6	AX366696	Sequence	c 362	84	7.6	188615	9	AL590410	AL590410 Human DNA
290	85.5	7.8	3557	6	AX883959	Sequence	c 363	84	7.6	191206	10	AC124573	AC124573 Mus muscu
291	85.5	7.8	3557	6	AK024365	Homo sapi	c 364	84	7.6	217342	2	AC119700	AC119700 Rattus no
292	85.5	7.8	6395	9	AB046769	Homo sapi	c 365	84	7.6	237317	2	AC097420	AC097420 Rattus no
c 293	85.5	7.8	8186	6	AX344683	Sequence	c 366	84	7.6	271454	2	AC112098	AC112098 Rattus no
294	85.5	7.8	15894	14	AB016162	Measles v	c 367	84	7.6	300150	1	AP004598	AP004598 Oceanobac
295	85.5	7.8	15894	14	AB032167	Measles v	c 368	84	7.6	302836	1	AB017253	AB017253 Treponema
c 296	85.5	7.8	91274	8	ATF18N11	Arabidops	c 369	84	7.6	314415	2	AC106697	AC106697 Rattus no

370	84	7.6	340750	1	BX2941135	443	82.5	7.5	516	8	AY052191	Arabidops
371	83.5	7.6	720	8	CNS01ALC	444	82.5	7.5	1308	3	AF318611	Caenorhab
372	83.5	7.6	1335	8	BT015858	445	82.5	7.5	1345	5	BC067690	Danio rer
373	83.5	7.6	1630	8	BT015052	446	82.5	7.5	1538	5	AY598943	Retrodon
374	83.5	7.6	3529	5	GGINTA8	447	82.5	7.5	1590	6	AR396528	Sequence
375	83.5	7.6	4284	10	AB0622913	448	82.5	7.5	4373	1	SGU61158	Staphylococ
376	83.5	7.6	5117	6	AR109903	449	82.5	7.5	13884	6	BD193747	Enterococ
377	83.5	7.6	5117	6	AR308068	450	82.5	7.5	15045	8	SPAC959	S.pombe c
378	83.5	7.6	5117	6	AX817984	451	82.5	7.5	25321	3	CEF18E2	Caenorhabdi
379	83.5	7.6	5117	6	HSU10886	452	82.5	7.5	80598	9	AL158191	Human DNA
380	83.5	7.6	34551	6	AX647685	453	82.5	7.5	100170	9	AL161743	Human DNA
381	83.5	7.6	43622	9	AC105414	454	82.5	7.5	101295	3	CEY48B6A	Caenorhab
382	83.5	7.6	94074	9	HSBC17A96	455	82.5	7.5	129663	2	AC027081	Homo sapi
383	83.5	7.6	96967	9	AC127894	456	82.5	7.5	132155	9	AC026703	Homo sapi
384	83.5	7.6	114240	9	AC124890	457	82.5	7.5	145590	8	AC109601	Homo sapi
385	83.5	7.6	122159	5	EX470175	458	82.5	7.5	153539	2	AL591168	Oryza sat
386	83.5	7.6	123454	9	HSBC17A99	459	82.5	7.5	163566	4	AC139340	Atelerix
387	83.5	7.6	142882	9	AP003029	460	82.5	7.5	166859	2	AC116521	Mus muscu
388	83.5	7.6	145101	2	AC021775	461	82.5	7.5	171419	9	AC006961	Homo sapi
389	83.5	7.6	157043	2	AC013692	462	82.5	7.5	172951	2	AC026751	Homo sapi
390	83.5	7.6	170397	2	CR352232	463	82.5	7.5	173301	8	AP003539	Oryza sat
391	83.5	7.6	178035	2	AC068680	464	82.5	7.5	176778	10	AL845336	Mouse DNA
392	83.5	7.6	182205	2	BX901930	465	82.5	7.5	180480	9	AC027588	Homo sapi
393	83.5	7.6	182375	10	AL627089	466	82.5	7.5	181750	2	AC025506	Homo sapi
394	83.5	7.6	183088	9	AC007600	467	82.5	7.5	182267	2	AC021128	Homo sapi
395	83.5	7.6	191906	10	AC132304	468	82.5	7.5	191643	2	AC144874	Pongo pyg
396	83.5	7.6	194018	2	AC118477	469	82.5	7.5	192821	2	AC102684	Mus muscu
397	83.5	7.6	194198	2	AC013298	470	82.5	7.5	193276	2	BX088575	Mus muscu
398	83.5	7.6	194632	9	AC096996	471	82.5	7.5	202937	10	AL669961	Mouse DNA
399	83.5	7.6	200697	2	AC119512	472	82.5	7.5	203124	2	AC101849	Mus muscu
400	83.5	7.6	202343	2	AC123884	473	82.5	7.5	209071	2	AC134109	Rattus no
401	83.5	7.6	203605	2	AC119514	474	82.5	7.5	213604	2	AC100345	Mus muscu
402	83.5	7.6	203998	2	AC102681	475	82.5	7.5	214695	2	AC128559	Rattus no
403	83.5	7.6	215566	10	AC119805	476	82.5	7.5	224612	5	BX085195	Zebraphis
404	83.5	7.6	221958	2	AC021705	477	82.5	7.5	227111	5	BX085195	Zebraphis
405	83.5	7.6	235422	2	AC095877	478	82.5	7.5	228353	2	AL445283	Homo sapi
406	83.5	7.6	241170	2	AC111268	479	82.5	7.5	245046	2	CR846103	Danio rer
407	83.5	7.6	300900	1	AP005939	480	82.5	7.5	300225	1	AE016949	Enterococ
408	83.5	7.6	301629	2	AC103342	481	82.5	7.5	301068	1	AE017231	Mycobacte
409	83	7.5	1581	4	AF055347	482	82	7.4	1554	10	AY115572	Rattus norv
410	83	7.5	2789	9	AX125149	483	82	7.4	1748	6	AR508364	Sequence
411	83	7.5	5588	6	AX401889	484	82	7.4	2339	6	CQ583029	Sequence
412	83	7.5	5588	10	RNSCAL	485	82	7.4	3034	3	AF239722	Drosophi
413	83	7.5	10981	1	U32841	486	82	7.4	3105	3	BT003216	Drosophi
414	83	7.5	12857	1	U32841	487	82	7.4	3207	6	A30543	R.norvegicu
415	83	7.5	44530	8	AP004475	488	82	7.4	4986	9	AF109681	Homo sapi
416	83	7.5	87900	8	AP004475	489	82	7.4	4995	6	BD261705	Homo sapi
417	83	7.5	98070	9	AC025463	490	82	7.4	5820	6	CQ583028	12 human
418	83	7.5	110000	2	AC101676	491	82	7.4	6314	6	AX817991	Sequence
419	83	7.5	110000	2	AC101676	492	82	7.4	6314	10	RNU40790	Sequence
420	83	7.5	110000	6	BD426631_17	493	82	7.4	25297	3	AC024778	Rattus norv
421	83	7.5	110000	6	AR274513_17	494	82	7.4	42799	2	BX649329	Caenorhab
422	83	7.5	110000	6	AR541453_17	495	82	7.4	62178	8	NCG1501	Homo sapi
423	83	7.5	115173	2	AC012612	496	82	7.4	62178	8	AC087172	Homo sapi
424	83	7.5	133028	2	AC146840	497	82	7.4	78745	9	AL603882	Human DNA
425	83	7.5	146500	2	AC119500	498	82	7.4	101324	9	AC010386	Homo sapi
426	83	7.5	146798	2	AC116022	499	82	7.4	103814	2	AC009210	Drosophi
427	83	7.5	151040	10	AC126040	500	82	7.4	110000	2	PFMAL3_02	Continuation (3 of
428	83	7.5	157061	9	AC010250	501	82	7.4	110000	8	CR380947_0	Candida g
429	83	7.5	159922	9	AC008447	502	82	7.4	123153	2	AC069155	Homo sapi
430	83	7.5	162029	2	AC145046	503	82	7.4	152158	2	BX649301	Danio rer
431	83	7.5	171096	14	AY037858	504	82	7.4	152740	9	AF490843	Homo sapi
432	83	7.5	185908	9	AC136297	505	82	7.4	159145	2	AC027172	Homo sapi
433	83	7.5	190080	9	AC022463	506	82	7.4	164935	9	AC012513	Homo sapi
434	83	7.5	202328	10	AC102590	507	82	7.4	166178	3	AC011072	Drosophi
435	83	7.5	203971	10	AC132460	508	82	7.4	166954	5	BX470178	Zebraphis
436	83	7.5	223435	2	AC098360	509	82	7.4	168153	2	CRG28407	Danio rer
437	83	7.5	253305	3	PFMAL397	510	82	7.4	176068	10	AC099593	Mus muscu
438	83	7.5	269050	1	AP000987	511	82	7.4	179676	2	AC129889	Papio anu
439	83	7.5	272221	10	AC099597	512	82	7.4	183483	9	AL161628	Human DNA
440	83	7.5	307380	1	AE016939	513	82	7.4	192645	9	AC006763	Caenorhab
441	83	7.5	324165	2	AC010277	514	82	7.4	195273	10	AC113548	Mus muscu
442	82.5	7.5	386	6	AX333122	515	82	7.4	198073	2	AC109146	Mus muscu

c 516	82	7.4	19957	10	AL589735	AL589735 Mouse DNA	589	81	7.4	110000	8	CR380959_12	Continuation (13 o
c 517	82	7.4	214281	2	AC140050	AC140050 Mus muscu	c 590	81	7.4	118331	9	AL391336	ACU931336 Human DNA
518	82	7.4	258174	2	AC079429	AC079429 Mus muscu	591	81	7.4	121702	9	AC096723	AC096723 Homo sapi
519	82	7.4	303450	1	AP005085	AP005085 Vibrio pa	c 592	81	7.4	126150	9	AC005152	AC005152 Homo sapi
c 520	82	7.4	316961	3	AP003799	AP003799 Drosophil	c 593	81	7.4	140797	2	AC118723	AC118723 Mus muscu
521	82	7.4	343558	2	AC117032	AC117032 Rattus no	c 594	81	7.4	146545	2	AC115221	AC115221 Homo sapi
c 522	81.5	7.4	816	3	CH1HB85	M17695 C.thummi th	c 595	81	7.4	148471	2	AC099332	AC099332 Homo sapi
523	81.5	7.4	910	6	C0847339	C0847339 Sequence	c 596	81	7.4	149844	2	AC144682	AC144682 Rattus no
524	81.5	7.4	910	6	AX440868	AX440868 Sequence	c 597	81	7.4	153926	2	AC107866	AC107866 Mus muscu
525	81.5	7.4	1191	1	AF346727	AF346727 Staphyloc	598	81	7.4	158648	2	AC021853	AC021853 Homo sapi
c 526	81.5	7.4	1386	10	BC028255	BC028255 Mus muscu	599	81	7.4	170201	2	AC055885	AC055885 Homo sapi
527	81.5	7.4	1955	10	AB024427	AB024427 Mus muscu	600	81	7.4	170213	5	BX005062	BX005062 Zebrafish
528	81.5	7.4	2461	8	MSY428052	AY428052 Malassezi	601	81	7.4	170376	9	AC104430	AC104430 Homo sapi
529	81.5	7.4	2604	3	AF413623	AF413623 Drosophil	602	81	7.4	170435	9	AC100767	AC100767 Homo sapi
530	81.5	7.4	3040	3	AF413622	AF413622 Drosophil	c 603	81	7.4	171451	2	AC064838	AC064838 Homo sapi
531	81.5	7.4	3147	6	AX481398	AX481398 Sequence	604	81	7.4	176054	2	AC022377	AC022377 Homo sapi
532	81.5	7.4	3234	9	BC064366	BC064366 Homo sapi	c 605	81	7.4	177738	2	AC055886	AC055886 Homo sapi
533	81.5	7.4	3269	6	AX337787	AX337787 Sequence	606	81	7.4	178121	9	AL603840	AL603840 Human DNA
534	81.5	7.4	3269	9	HUMORPT	D26067 Homo sapien	c 607	81	7.4	179350	9	AC026351	AC026351 Homo sapi
535	81.5	7.4	3495	5	CHKVITAA	M60517 Chicken vit	608	81	7.4	180957	9	AF267168	AF267168 Homo sapi
536	81.5	7.4	4334	10	BC060200	BC060200 Mus muscu	c 609	81	7.4	183867	10	AC122237	AC122237 Mus muscu
537	81.5	7.4	5716	6	CQ713063	CQ713063 Sequence	c 610	81	7.4	187677	2	AC147321	AC147321 Pan trogl
538	81.5	7.4	5717	6	AR380788	AR380788 Sequence	611	81	7.4	187979	10	AC123854	AC123854 Mus muscu
539	81.5	7.4	5717	6	AX658103	AX658103 Sequence	612	81	7.4	188110	2	AC104152	AC104152 Rattus no
540	81.5	7.4	5717	9	HUMVTNR	M14648 Human cell	613	81	7.4	190644	10	AC122872	AC122872 Mus muscu
541	81.5	7.4	6952	6	CO493953	CO493953 Sequence	614	81	7.4	191379	10	AL845534	AL845534 Mouse DNA
542	81.5	7.4	6954	6	CO412497	CO412497 Sequence	615	81	7.4	194837	10	AL607066	AL607066 Mouse DNA
543	81.5	7.4	8302	1	BSFLAAO	X56049 B. subtilis	c 616	81	7.4	196044	9	AC018505	AC018505 Homo sapi
c 544	81.5	7.4	17528	2	AC020192	AC020192 Drosophil	617	81	7.4	198759	2	AC020772	AC020772 Homo sapi
545	81.5	7.4	21520	6	AX770894	AX770894 Sequence	618	81	7.4	202366	2	AL805939	AL805939 Mus muscu
546	81.5	7.4	68850	10	AL929258	AL929258 Mouse DNA	619	81	7.4	209876	9	AC011599	AC011599 Homo sapi
547	81.5	7.4	76410	2	AC016093	AC016093 Homo sapi	c 620	81	7.4	210979	10	AC132863	AC132863 Mus muscu
548	81.5	7.4	81677	3	AC004377	AC004377 Drosophil	c 621	81	7.4	237286	2	AC113645	AC113645 Rattus no
549	81.5	7.4	89836	8	AC007188	AC007188 Arabidops	c 622	81	7.4	240483	2	AC095955	AC095955 Rattus no
550	81.5	7.4	96642	8	AC002291	AC002291 Arabidops	c 623	81	7.4	250119	2	AC111874	AC111874 Rattus no
551	81.5	7.4	136124	9	HS394P21	AL021528 Human DNA	c 624	81	7.4	257991	2	AC114028	AC114028 Rattus no
552	81.5	7.4	138217	10	AL669905	AL669905 Mouse DNA	c 625	81	7.4	267546	2	AC125740	AC125740 Rattus no
c 553	81.5	7.4	139994	9	AC006462	AC006462 Homo sapi	626	81	7.4	268050	1	AL627266	AL627266 Salmonell
c 554	81.5	7.4	140327	2	AP003938	AP003938 Oryza sat	c 627	81	7.4	275460	2	AC114120	AC114120 Rattus no
555	81.5	7.4	147569	2	BX248417	BX248417 Homo sapi	c 628	81	7.4	288479	2	AC146814	AC146814 Zea mays
c 556	81.5	7.4	155112	2	AL357521	AL357521 Homo sapi	c 629	81	7.4	300029	1	AE016842	AE016842 Salmonell
c 557	81.5	7.4	182927	2	AL513545	AL513545 Homo sapi	c 630	80.5	7.3	568	6	CQ719682	CQ719682 Sequence
558	81.5	7.4	167442	2	AC112954	AC112954 Mus muscu	c 631	80.5	7.3	597	8	AX557646	AX557646 Saccharom
559	81.5	7.4	171015	5	BX005395	BX005395 Zebrafish	c 632	80.5	7.3	1636	6	AX366700	AX366700 Sequence
c 560	81.5	7.4	173373	3	AC008349	AC008349 Drosophil	633	80.5	7.3	2166	10	BC005441	BC005441 Mus muscu
c 561	81.5	7.4	174811	2	AC013259	AC013259 Homo sapi	634	80.5	7.3	2242	5	DRU41419	DRU41419 Danio rerio
c 562	81.5	7.4	175118	2	AC145247	AC145247 Didelphis	635	80.5	7.3	2280	5	AB056090	AB056090 Polyandro
563	81.5	7.4	177384	2	AC091786	AC091786 Mus muscu	636	80.5	7.3	2359	3	AB056090	AB056090 Polyandro
c 564	81.5	7.4	177747	10	AC122051	AC122051 Mus muscu	637	80.5	7.3	3141	5	DRE311886	DRE311886 Danio rer
565	81.5	7.4	187277	2	BX901971	BX901971 Danio rer	638	80.5	7.3	3613	6	CQ851438	CQ851438 Sequence
c 566	81.5	7.4	188802	2	AC113864	AC113864 Rattus no	639	80.5	7.3	3613	6	AK128681	AK128681 Homo sapi
567	81.5	7.4	192208	2	AC084792	AC084792 Homo sapi	640	80.5	7.3	4184	6	CQ851271	CQ851271 Sequence
568	81.5	7.4	208609	9	HS389A20	Z33242 Human DNA e	641	80.5	7.3	4184	9	AK128856	AK128856 Homo sapi
c 569	81.5	7.4	213541	9	HUAC004381	AC004381 Homo sapi	642	80.5	7.3	4294	8	SCYDR032C	SCYDR032C Homo sapi
c 570	81.5	7.4	216726	2	AC097270	AC097270 Pan trogl	643	80.5	7.3	5138	5	AF090432	AF090432 Danio rer
571	81.5	7.4	238643	2	AC133255	AC133255 Rattus no	644	80.5	7.3	5355	5	AF229450	AF229450 Danio rer
c 572	81.5	7.4	247730	2	AC112120	AC112120 Rattus no	645	80.5	7.3	5469	5	AF229449	AF229449 Danio rer
573	81.5	7.4	253522	2	AC130734	AC130734 Rattus no	646	80.5	7.3	10085	8	AB015471	AB015471 Arabidops
c 574	81.5	7.4	275209	2	AC097164	AC097164 Rattus no	c 647	80.5	7.3	13761	1	AB013212	AB013212 Thermoana
c 575	81.5	7.4	281904	2	AC132547	AC132547 Rattus no	c 648	80.5	7.3	15446	1	AE000710	AE000710 Aquifex a
c 576	81.5	7.4	301146	1	AE017311	AE017311 Desulfovi	649	80.5	7.3	15894	6	BD137592	BD137592 Mutation
c 577	81.5	7.4	307323	3	AC003457	AC003457 Arabidops	650	80.5	7.3	15894	6	BD137593	BD137593 Mutation
578	81.5	7.4	349944	1	BX571871	BX571871 Photorhab	651	80.5	7.3	21112	9	AF361486	AF361486 Homo sapi
579	81	7.4	1539	6	AR544985	AR544985 Sequence	652	80.5	7.3	24628	8	SC9673	SC9673 S. cerevisia
c 580	81	7.4	3241	3	AF005059	AF005059 Toxoplas	c 653	80.5	7.3	29548	3	AF022970	AF022970 Caenorhab
581	81	7.4	4010	10	MUSINTA7SU	L23423 Mouse (BALB	654	80.5	7.3	41523	2	AC101065	AC101065 Mus muscu
582	81	7.4	4262	3	AF067658	AF067658 Lytechinu	c 655	80.5	7.3	60000	9	AP003679	AP003679 Homo sapi
583	81	7.4	4262	3	LVU22152	U22152 Lytechinu	656	80.5	7.3	66765	6	CQ874958	CQ874958 Sequence
584	81	7.4	26880	10	AF067129	AF067129 Mus muscu	657	80.5	7.3	66765	9	AF414442	AF414442 Homo sapi
585	81	7.4	29047	3	CET05A10	Z68108 Caenorhabdi	658	80.5	7.3	110000	1	CR543861_24	Continuation (25 o
c 586	81	7.4	38784	2	AC014012	AC014012 Drosophil	c 659	80.5	7.3	110000	2	AC095920_03	Continuation (4 of
587	81	7.4	94728	2	OSIG00030	AL732334 Oryza sat	660	80.5	7.3	110000	2	AC134360_2	Continuation (3 of
588	81	7.4	99596	9	AC106873	AC106873 Homo sapi	661	80.5	7.3	110000	8	CR380951_1	Continuation (2 of

662	80.5	7.3	135980	8	AC126224	AC126224 Oryza sat
663	80.5	7.3	137617	9	AC092107	Homo sapi
664	80.5	7.3	152612	2	AC053515	Homo sapi
665	80.5	7.3	163310	2	AC016147	Homo sapi
666	80.5	7.3	168706	2	AC016151	Homo sapi
667	80.5	7.3	168794	2	AC026252	Homo sapi
668	80.5	7.3	171058	9	AC073068	Homo sapi
669	80.5	7.3	172949	10	AC122231	Mus muscu
670	80.5	7.3	174113	2	AC112810	Rattus no
671	80.5	7.3	177048	2	AC128925	Rattus no
672	80.5	7.3	179246	9	AC114877	Homo sapi
673	80.5	7.3	205985	2	AC148494	Ocolemur
674	80.5	7.3	207531	2	AC133061	Rattus no
675	80.5	7.3	228752	2	AC094632	Rattus no
676	80.5	7.3	248917	2	AC096017	Rattus no
677	80.5	7.3	252394	3	AE014833	Plasmodiu
678	80.5	7.3	254278	2	AC095693	Rattus no
679	80.5	7.3	286162	2	AC117293	Rattus no
680	80.5	7.3	340900	1	SMES91791	AL591791 Sino
681	80	7.3	669	3	GCSHOX	W79054 G.cyd
682	80	7.3	1327	3	AF076220	Drosophil
683	80	7.3	1349	6	Q575619	Q575619 Sequence
684	80	7.3	1427	3	AY058251	Drosophil
685	80	7.3	1599	3	AK116812	Clona int
686	80	7.3	3711	6	Q872812	Sequence
687	80	7.3	4775	5	XELNWTAS	L43057 Xenopus lae
688	80	7.3	10029	1	AE005313	Escherich
689	80	7.3	11578	1	AE008345	Agrobacte
690	80	7.3	11583	1	AE005277	Escherich
691	80	7.3	12013	1	AE009266	Agrobacte
692	80	7.3	47493	2	AC141834	Apis mell
693	80	7.3	76410	2	AC016093	Homo sapi
694	80	7.3	81149	2	AC023338	Homo sapi
695	80	7.3	81419	5	BX571840	Zebrafish
696	80	7.3	86248	6	BD184766	Nucleic a
697	80	7.3	87563	6	AR204161	Sequence
698	80	7.3	89479	8	AC006932	Genomic s
699	80	7.3	100795	5	BX323600	Zebrafish
700	80	7.3	108716	9	HS101A4	293341 Human DNA s
701	80	7.3	110000	8	CR380948_1	Continuation (2 of
702	80	7.3	135686	9	HS473J6	283827 Human DNA s
703	80	7.3	148090	10	AC100737	Mus muscu
704	80	7.3	158475	9	AC097463	Homo sapi
705	80	7.3	165791	10	AC129198	Homo sapi
706	80	7.3	169414	9	AC068707	Homo sapi
707	80	7.3	170535	9	CNS05TBO	AL163932 Human chr
708	80	7.3	170559	2	AC026989	Homo sapi
709	80	7.3	170924	2	AC148627	Callithri
710	80	7.3	171823	14	HHV507799	AJ507799 Human her
711	80	7.3	172281	14	EBV	V01555 Epstein-Bar
712	80	7.3	173775	2	AC079933	Trypanoso
713	80	7.3	174965	9	AC036222	Homo sapi
714	80	7.3	177248	5	AL929093	Zebrafish
715	80	7.3	182997	9	AL355332	Human DNA
716	80	7.3	184113	14	HS48958RAJ	M80517 Epstein-Bar
717	80	7.3	191729	2	AL590872	Homo sapi
718	80	7.3	198703	10	AC129570	Trypanoso
719	80	7.3	200340	9	AC100797	Homo sapi
720	80	7.3	201470	2	AC105683	Rattus no
721	80	7.3	204401	2	AC105524	Rattus no
722	80	7.3	206264	2	CR847572	Danio rer
723	80	7.3	207411	10	AC114916	Mus muscu
724	80	7.3	208458	10	AC118009	Mus muscu
725	80	7.3	212664	2	AC123005	Rattus no
726	80	7.3	212705	10	AC113600	Mus muscu
727	80	7.3	212879	2	AC148552	Callithri
728	80	7.3	229905	2	AC135819	Rattus no
729	80	7.3	232120	2	AC132712	Rattus no
730	80	7.3	237952	2	AL591116	Homo sapi
731	80	7.3	247728	2	AC134204	Rattus no
732	80	7.3	250541	2	AC114390	Rattus no
733	80	7.3	276326	8	AV574035	Zea mays
734	80	7.3	279331	2	AC097172	Rattus no
CR847807	Danio rer					
AE017323	Listeria					
AC113653	Rattus no					
Q873161	Sequence					
AP002554	Escherich					
Q847194	Sequence					
AX440723	Caenorhab					
AF440518	Caenorhab					
U64092	Cercopithe					
AY513386	Centrucho					
AF142497	Trypanoso					
U14135	Mus muscu					
BC048857	Mus muscu					
Z50755	Caenorhabdi					
U40797	Caenorhabdi					
AY714857	Unculture					
AC107923	Homo sapi					
BX294028	Neurospor					
AL096763	Human DNA					
Continuation (32 o						
AC087807	Felis cat					
AC139626	Takifugu					
AP001017	Homo sapi					
AC109289	Mus muscu					
AL451070	Human DNA					
AC147925	Oryza sat					
AL161422	Human DNA					
AC119214	Mus muscu					
AC018520	Homo sapi					
AC097347	Homo sapi					
AC109289	Mus muscu					
AC037484	Homo sapi					
AC103922	Homo sapi					
AL954157	Oryza sat					
AC138070	Homo sapi					
AC148444	Rhinoloph					
AC027634	Homo sapi					
AC022030	Homo sapi					
AF220294	Mus muscu					
BX001060	Oryza sat					
AC136432	Homo sapi					
AC121725	Rattus no					
AC114907	Mus muscu					
AL845483	Mouse DNA					
AC023150	Homo sapi					
AC121564	Mus muscu					
AC022274	Homo sapi					
BX510909	Danio rer					
AP002896	Homo sapi					
AC117033	Rattus no					
AC141966	Rattus no					
AC124556	Mus muscu					
AC091103	Homo sapi					
AC027438	Homo sapi					
BX571675	Zebrafish					
BX005008	Zebrafish					
AC072048	Mus muscu					
AY223810	Rhodococc					
BX842696	Zebrafish					
AC129635	Rattus no					
AC127197	Rattus no					
AC130711	Mus muscu					
AC094273	Rattus no					
AC094389	Rattus no					
AC027438	Homo sapi					
CR392035	Danio rer					
AC097396	Rattus no					
AC096239	Rattus no					
AC093479	Mus muscu					
AC137598	Oryza sat					
AC137598	Oryza sat					
BX005328	Zebrafish					
AC11812	Rattus no					
AC137193	Rattus no					



808	79.5	7.2	295050	1	AL591982	AL591982 Listeria	c 881	79	7.2	186751	9	AC023344	AC023344 Homo sapi
c 809	79.5	7.2	300425	1	AF005038	Streptomy	c 882	79	7.2	187314	2	AC036590	AC036590 Homo sapi
810	79.5	7.2	320205	1	AC106178	Rattus no	c 883	79	7.2	187936	2	AC080003	AC080003 Homo sapi
811	79.5	7.2	348632	2	AC096299	Rattus no	c 884	79	7.2	191028	8	PPU38804	PPU38804 Porphyra pu
812	79.5	7.2	349980	6	AX641671	Sequence	c 885	79	7.2	199897	2	AC118296	AC118296 Rattus no
813	79	7.2	65	6	CQ556364	Sequence	c 886	79	7.2	203183	3	AC005721	AC005721 Drosophil
c 814	79	7.2	543	3	AF301159	AF301159 Eriochoir	c 887	79	7.2	203374	2	AC102546	AC102546 Mus muscu
c 815	79	7.2	1032	5	AY059001	AY059001 Walterinn	c 888	79	7.2	206733	2	AC110553	AC110553 Mus muscu
816	79	7.2	1155	10	AF537215	Mus muscu	c 889	79	7.2	206945	2	AC146022	AC146022 Pan trogl
817	79	7.2	1301	10	AF234830	Mus muscu	c 890	79	7.2	215447	10	AC125541	AC125541 Mus muscu
818	79	7.2	1512	6	AX433776	Sequence	c 891	79	7.2	219664	2	AC146911	AC146911 Mus muscu
c 819	79	7.2	1695	6	CQ573504	Sequence	c 892	79	7.2	222195	2	AC112890	AC112890 Rattus no
c 820	79	7.2	1749	3	AF242735	Drosophil	c 893	79	7.2	224650	1	AL596164	AL596164 Listeria
c 821	79	7.2	2108	10	BC031488	BC031488 Mus muscu	c 894	79	7.2	245453	2	AC131004	AC131004 Rattus no
822	79	7.2	2198	3	AF275814	Drosophil	c 895	79	7.2	246585	2	AC108954	AC108954 Rattus no
823	79	7.2	2296	9	AK074419	Homo sapi	c 896	79	7.2	253278	2	AC097310	AC097310 Rattus no
824	79	7.2	2546	9	AK074243	Homo sapi	c 897	79	7.2	254961	3	AE003706	AE003706 Drosophil
825	79	7.2	2664	6	AX285092	Sequence	c 898	79	7.2	290667	3	AE003663	AE003663 Drosophil
826	79	7.2	2932	6	BD159735	Primer fo	c 899	79	7.2	291073	1	AE017323	AE017323 Listeria
827	79	7.2	2932	6	AX882457	Sequence	c 900	79	7.2	304758	3	AE003784	AE003784 Drosophil
828	79	7.2	2932	9	AK027587	Homo sapi	c 901	79	7.2	349527	1	CR378678	CR378678 Photobact
829	79	7.2	3298	10	AF170316	Mus muscu	c 902	79	7.2	349980	6	CQ655073	CQ655073 Sequence
c 830	79	7.2	3750	6	CQ573503	Sequence	c 903	79	7.2	349980	6	AX417041	AX417041 Sequence
831	79	7.2	4952	10	BC050836	Mus muscu	c 904	79	7.2	349980	6	AX453571	AX453571 Sequence
832	79	7.2	5018	10	BC050836	Mus muscu	c 905	79	7.2	349980	6	AX954533	AX954533 Sequence
833	79	7.2	5205	6	AX451422	Sequence	c 906	78.5	7.1	1060	6	AX366801	AX366801 Sequence
834	79	7.2	6228	3	AY051985	Drosophil	c 907	78.5	7.1	1173	6	CQ805812	CQ805812 Sequence
835	79	7.2	6490	3	DMDLAR9	U36857 Drosophila	c 908	78.5	7.1	1204	8	AY117314	AY117314 Arabidops
c 836	79	7.2	7265	6	AX602153	Sequence	c 909	78.5	7.1	1257	8	AB118147	AB118147 Saurea
837	79	7.2	7606	3	DNOLARM	M27700 D.melanogas	c 910	78.5	7.1	1320	8	AB118141	AB118141 Saurea
838	79	7.2	7630	6	CQ614817	Sequence	c 911	78.5	7.1	1365	8	AY064047	AY064047 Arabidops
839	79	7.2	7934	9	AY327116	Homo sapi	c 912	78.5	7.1	1419	8	AF419594	AF419594 Arabidops
840	79	7.2	10002	9	AB107369	Homo sapi	c 913	78.5	7.1	1761	6	BD265001	BD265001 Compositi
841	79	7.2	10002	9	AY327115	Homo sapi	c 914	78.5	7.1	1761	6	AR238404	AR238404 Sequence
c 842	79	7.2	12978	2	AC014229	AC014229 Drosophil	c 915	78.5	7.1	1761	6	AX478743	AX478743 Sequence
843	79	7.2	17284	9	HSRINGG	Y07829 Homo sapien	c 916	78.5	7.1	1761	6	AX366620	AX366620 Sequence
844	79	7.2	21495	1	AE014285	AE014285 Streptoco	c 917	78.5	7.1	2159	5	CR760664	CR760664 Xenopus t
845	79	7.2	24766	2	AC014976	AC014976 Drosophil	c 918	78.5	7.1	2608	6	BD265000	BD265000 Compositi
846	79	7.2	25119	2	AY714839	AY714839 Unculture	c 919	78.5	7.1	2608	6	AR238403	AR238403 Sequence
c 847	79	7.2	34284	8	SPAC3H5	Z99296 S.pombe chr	c 920	78.5	7.1	2608	6	AR478742	AR478742 Sequence
848	79	7.2	39434	2	AL162911	Human DNA	c 921	78.5	7.1	2608	6	AX366619	AX366619 Sequence
849	79	7.2	52712	2	AC149925	AC149925 Strongylo	c 922	78.5	7.1	2996	6	BD264926	BD264926 Compositi
850	79	7.2	73481	9	AC011891	AC011891 Homo sapi	c 923	78.5	7.1	2996	6	AR238329	AR238329 Sequence
851	79	7.2	80501	9	AC097314	AC097314 Homo sapi	c 924	78.5	7.1	2996	6	AR257870	AR257870 Sequence
852	79	7.2	87726	2	AC014337	AC014337 Drosophil	c 925	78.5	7.1	2996	6	AR478668	AR478668 Sequence
853	79	7.2	89050	1	SAG766855	AL766855 Streptoco	c 926	78.5	7.1	2996	6	AX156348	AX156348 Sequence
c 854	79	7.2	110000	1	AE01197_05	Continuation (6 of	c 927	78.5	7.1	2996	6	AX366544	AX366544 Sequence
c 855	79	7.2	110000	1	AE017333_39	Continuation (40 o	c 928	78.5	7.1	2996	6	AX366695	AX366695 Sequence
c 856	79	7.2	110000	1	CP000002_39	Continuation (40 o	c 929	78.5	7.1	3101	4	AF317199	AF317199 Bos tauru
c 857	79	7.2	125528	2	AC027389	AC027389 Homo sapi	c 930	78.5	7.1	3144	4	AF239958	AF239958 Bos tauru
c 858	79	7.2	129642	3	AGA438610	AJ438610 Anopheles	c 931	78.5	7.1	3489	10	MUSOSF4	D21253 Mus musculu
c 859	79	7.2	132354	2	AC017130	AC017130 Drosophil	c 932	78.5	7.1	3581	6	AR034821	AR034821 Sequence
c 860	79	7.2	138264	10	AC132579	AC132579 Mus muscu	c 933	78.5	7.1	3581	6	E07381	E07381 cDNA encodi
c 861	79	7.2	145327	9	AF004285	AF004285 Homo sapi	c 934	78.5	7.1	3646	10	BC046314	BC046314 Mus muscu
c 862	79	7.2	146572	10	AC118259	AC118259 Mus muscu	c 935	78.5	7.1	3755	6	CQ604115	CQ604115 Sequence
c 863	79	7.2	147322	2	AC137764	AC137764 Mus muscu	c 936	78.5	7.1	3862	6	CQ574215	CQ574215 Sequence
c 864	79	7.2	147530	9	AP008766	AP008766 Homo sapi	c 937	78.5	7.1	3863	3	AF184227	AF184227 Drosophil
c 865	79	7.2	152130	9	AP000856	AP000856 Homo sapi	c 938	78.5	7.1	4102	3	AY070899	AY070899 Drosophil
c 866	79	7.2	154890	3	AC008136	AC008136 Drosophil	c 939	78.5	7.1	4127	6	AX306074	AX306074 Sequence
c 867	79	7.2	155361	2	AC142174	AC142174 Rattus no	c 940	78.5	7.1	4127	10	MMCADL	W7557 M.musculus
c 868	79	7.2	163990	3	AC009255	AC009255 Drosophil	c 941	78.5	7.1	4129	9	BC047454	BC047454 Homo sapi
c 869	79	7.2	164936	2	AC141529	AC141529 Rattus no	c 942	78.5	7.1	4285	5	BC084201	BC084201 Xenopus l
c 870	79	7.2	170190	3	AC009911	AC009911 Drosophil	c 943	78.5	7.1	5513	9	AC098796	AC098796 Homo sapi
c 871	79	7.2	170803	9	H5T344J20	AL080285 Human DNA	c 944	78.5	7.1	5755	11	BV179236	BV179236 sgml0444
c 872	79	7.2	177487	2	AC117601	AC117601 Mus muscu	c 945	78.5	7.1	10622	6	AX366802	AX366802 Sequence
c 873	79	7.2	180699	3	AC008339	AC008339 Drosophil	c 946	78.5	7.1	11288	6	AR134885	AR134885 Sequence
c 874	79	7.2	181498	8	OSJN00162	AL662960 Oryza sat	c 947	78.5	7.1	11288	6	AR182304	AR182304 Sequence
c 875	79	7.2	182603	10	ACJ11893	AC141893 Mus muscu	c 948	78.5	7.1	11288	6	AR370519	AR370519 Sequence
c 876	79	7.2	183982	2	AC021884	AC021884 Homo sapi	c 949	78.5	7.1	11288	6	AX479027	AX479027 Sequence
c 877	79	7.2	184872	10	AL672243	AL672243 Mouse DNA	c 950	78.5	7.1	11288	6	AX269130	AX269130 Sequence
c 878	79	7.2	185769	10	AC129178	AC129178 Mus muscu	c 951	78.5	7.1	11288	9	HSCCAN7A	Z21818 H.sapiens C
c 879	79	7.2	186066	9	AC090579	AC090579 Homo sapi	c 952	78.5	7.1	11743	6	CQ592355	CQ592355 Sequence
c 880	79	7.2	186154	2	AC102651	AC102651 Mus muscu	c 953	78.5	7.1	12216	6	CQ594536	CQ594536 Sequence

C 954	78.5	7.1	15056	6	BD195539	Adenoviru	BD195539	c1027	78.5	7.1	222613	2	AC150742	Zea mays
C 955	78.5	7.1	15056	6	BD224258	Adenoviru	BD224258	c1028	78.5	7.1	223308	10	AC110920	Mus muscu
C 956	78.5	7.1	15056	6	AR266427	Sequence	AR266427	1029	78.5	7.1	225880	2	AC131693	Mus muscu
C 957	78.5	7.1	15056	6	AR474484	Sequence	AR474484	c1030	78.5	7.1	230232	2	AC104292	Rattus no
C 958	78.5	7.1	15056	6	AX259954	Sequence	AX259954	c1031	78.5	7.1	233589	10	AL683824	Mus muscu
C 959	78.5	7.1	15056	6	AX262359	Sequence	AX262359	1032	78.5	7.1	237899	10	AC102622	Mouse DNA
C 960	78.5	7.1	47687	2	AC013074	Drosophil	AC013074	1033	78.5	7.1	240256	2	AC123729	Mus muscu
C 961	78.5	7.1	55374	9	AL645474	Human DNA	AL645474	1034	78.5	7.1	259619	2	AC108308	Mus muscu
C 962	78.5	7.1	63940	2	AC017795	Drosophil	AC017795	c1035	78.5	7.1	282610	1	RPX001	Rickettsi
C 963	78.5	7.1	84961	2	AC014810	Drosophil	AC014810	c1036	78.5	7.1	284268	3	AE003565	Drosophil
C 964	78.5	7.1	98303	2	AP004642	Oryza sat	AP004642	1037	78.5	7.1	313050	1	EX321857	Nitrosomo
C 965	78.5	7.1	110000	8	CR382128_02	Continuation (3 of	CR382128_02	1038	78.5	7.1	344530	2	AC133390	Rattus no
C 966	78.5	7.1	110000	8	CR382135_06	Continuation (7 of	CR382135_06	c1039	78.5	7.1	348873	3	AE003790	Drosophil
C 967	78.5	7.1	117931	2	AC111066	Mus muscu	AC111066	1040	78	7.1	872	5	AE090396	Paralabid
C 968	78.5	7.1	128785	9	AC105328	Homo sapi	AC105328	1041	78	7.1	872	5	AE090397	Paralabid
C 969	78.5	7.1	132635	2	AC007577	Drosophil	AC007577	1042	78	7.1	872	5	AE090398	Paralabid
C 970	78.5	7.1	143798	9	AL157409	Human DNA	AL157409	1043	78	7.1	872	5	AE090425	Gaurochro
C 971	78.5	7.1	147002	10	AL928882	Mouse DNA	AL928882	1044	78	7.1	872	5	AE090427	Astatotil
C 972	78.5	7.1	148498	9	AP003473	Homo sapi	AP003473	1045	78	7.1	903	6	CO847198	Sequence
C 973	78.5	7.1	149284	5	BX323015	Zebrafish	BX323015	1046	78	7.1	903	6	AX440727	Sequence
C 974	78.5	7.1	149804	9	AC020984	Homo sapi	AC020984	1047	78	7.1	1138	5	AY207478	Euchilogl
C 975	78.5	7.1	150221	9	AC004593	Homo sapi	AC004593	1048	78	7.1	1138	5	AY207479	Euchilogl
C 976	78.5	7.1	150727	2	CR381531	Danio rer	CR381531	1049	78	7.1	1838	10	RATNTA	M35297 Rat poc. G
C 977	78.5	7.1	151512	2	AC142376	Rattus no	AC142376	1050	78	7.1	1989	9	BC001293	Homo sapi
C 978	78.5	7.1	152430	9	AC087432	Homo sapi	AC087432	1051	78	7.1	2436	5	GC0ADHB	Chickens mRN
C 979	78.5	7.1	154768	9	AC015476	Homo sapi	AC015476	1052	78	7.1	2615	5	AF001406	Carassius
C 980	78.5	7.1	157620	9	BS000109	Pan trogl	BS000109	1053	78	7.1	3126	3	AF515783	Aplysia c
C 981	78.5	7.1	159758	9	AP005356	Homo sapi	AP005356	1054	78	7.1	3307	5	NASPA	A. anguilla
C 982	78.5	7.1	160264	10	AC108412	Mus muscu	AC108412	1055	78	7.1	3900	1	AE633552	Spingomo
C 983	78.5	7.1	160410	2	AC020753	Homo sapi	AC020753	1056	78	7.1	3926	5	AB000470	Gallus ga
C 984	78.5	7.1	162223	8	AC108870	Oryza sat	AC108870	c1057	78	7.1	7173	1	STU94729	Salmonella
C 985	78.5	7.1	163438	2	AC147759	Macropus	AC147759	c1058	78	7.1	7437	14	RHDVCGS	Z29514 Rabbit hemo
C 986	78.5	7.1	163613	2	AC091702	Trypanoso	AC091702	1059	78	7.1	11876	9	AB110940	Homo sapi
C 987	78.5	7.1	163996	8	AP003333	Oryza sat	AP003333	1060	78	7.1	11877	9	AB110939	Homo sapi
C 988	78.5	7.1	165174	8	AP005730	Oryza sat	AP005730	c1061	78	7.1	20029	1	AE008755	Salmonell
C 989	78.5	7.1	165855	3	AC009342	Drosophil	AC009342	c1062	78	7.1	22700	3	CEF366G3	Z47069 Caenorhabdi
C 990	78.5	7.1	166162	9	AC018814	Homo sapi	AC018814	1063	78	7.1	36626	9	HS31BE23	AL132993 Homo sapi
C 991	78.5	7.1	168421	10	AC113328	Mus muscu	AC113328	c1064	78	7.1	42074	9	AC004202	Homo sapi
C 992	78.5	7.1	168618	8	AC116689	Mus muscu	AC116689	1065	78	7.1	52928	9	BX322644	Human DNA
C 993	78.5	7.1	169550	2	AP005617	Oryza sat	AP005617	1066	78	7.1	57264	9	EX005441	Human DNA
C 994	78.5	7.1	171072	9	CNS05ETE6	Rattus chr	AL358335	1067	78	7.1	69294	2	AC091032	Homo sapi
C 995	78.5	7.1	171810	2	AC128062	Rattus no	AL380622	1068	78	7.1	73009	9	EX927221	Human DNA
C 996	78.5	7.1	171973	2	AC013571	Homo sapi	AC013571	c1069	78	7.1	74841	10	AL806529	Mouse DNA
C 997	78.5	7.1	172127	2	AC013572	Homo sapi	AC013572	1070	78	7.1	78743	2	CR753815	Homo sapi
C 998	78.5	7.1	173910	2	AC115902	Mus muscu	AC115902	1071	78	7.1	78827	9	CR788282	Human DNA
C 999	78.5	7.1	174729	3	AC008203	Drosophil	AC008203	1072	78	7.1	82272	5	EX001004	Zebrafish
C 1000	78.5	7.1	174751	3	AC008288	Drosophil	AC008288	1073	78	7.1	83684	9	AC105290	Homo sapi
C 1001	78.5	7.1	176212	2	AC141778	Apis mell	AC141778	c1074	78	7.1	100000	9	AP000518	Homo sapi
C 1002	78.5	7.1	177380	6	AX706985	Sequence	AX706985	c1075	78	7.1	101333	8	AP004030	Oryza sat
C 1003	78.5	7.1	177380	6	AX707915	Sequence	AX707915	1076	78	7.1	104125	3	AC084468	Caenorhab
C 1004	78.5	7.1	177380	9	AC002457	Homo sapi	AC002457	1077	78	7.1	104924	9	CR759838	Human DNA
C 1005	78.5	7.1	180700	2	AC084136	Homo sapi	AC084136	1078	78	7.1	110000	2	AC087331_3	Continuation (4 of
C 1006	78.5	7.1	181535	9	AL592203	Human DNA	AL592203	1079	78	7.1	110000	2	AC097795_2	Continuation (3 of
C 1007	78.5	7.1	181833	2	AC141405	Homo sapi	AC141405	c1080	78	7.1	110000	2	AL672261_1	Continuation (2 of
C 1008	78.5	7.1	182223	3	AC023674	Drosophil	AC023674	1081	78	7.1	120206	9	HS439F8	Human DNA
C 1009	78.5	7.1	183763	9	AC104036	Homo sapi	AC104036	1082	78	7.1	121587	1	CR522871	Deulgota
C 1010	78.5	7.1	188432	2	AC018497	Homo sapi	AC018497	1083	78	7.1	123460	8	AB073166	Arabidops
C 1011	78.5	7.1	188555	10	AC122417	Mus muscu	AC122417	c1084	78	7.1	128032	9	AC091730	Homo sapi
C 1012	78.5	7.1	194034	9	AP005901	Homo sapi	AP005901	c1085	78	7.1	139033	2	AC150739	Zea mays
C 1013	78.5	7.1	196967	2	AC108589	Rattus no	AC108589	1086	78	7.1	144169	9	AL671859	Human DNA
C 1014	78.5	7.1	197173	2	AC131036	Mus muscu	AC131036	1087	78	7.1	149035	8	AC131343	Oryza sat
C 1015	78.5	7.1	200933	10	AL805910	Mouse DNA	AL805910	1088	78	7.1	151042	8	AC114011	Oryza sat
C 1016	78.5	7.1	201456	10	AC124669	Mus muscu	AC124669	1089	78	7.1	152487	9	AP000431	Homo sapi
C 1017	78.5	7.1	202645	2	AL513330	Homo sapi	AL513330	1090	78	7.1	153420	10	AL591426	Mouse DNA
C 1018	78.5	7.1	2032593	10	AL663053	Mouse DNA	AL663053	1091	78	7.1	159178	9	AL669914	Human DNA
C 1019	78.5	7.1	204278	10	AC124507	Mus muscu	AC124507	1092	78	7.1	159620	9	AL354835	Human DNA
C 1020	78.5	7.1	206749	2	AC102059	Mus muscu	AC102059	1093	78	7.1	161099	10	AC132624	Mus muscu
C 1021	78.5	7.1	208885	2	AC101703	Mus muscu	AC101703	c1094	78	7.1	162383	9	AB023054	Homo sapi
C 1022	78.5	7.1	211492	2	AC140877	Homo sapi	AC140877	c1095	78	7.1	162383	9	AB023055	Homo sapi
C 1023	78.5	7.1	216493	2	AC013550	Homo sapi	AC013550	c1096	78	7.1	162760	9	AC007969	Homo sapi
C 1024	78.5	7.1	216811	2	AC140808	Homo sapi	AC140808	1097	78	7.1	165241	10	AC117802	Mus muscu
C 1025	78.5	7.1	218498	3	AE003746	Drosophil	AE003746	c1098	78	7.1	165516	2	AC105938	Homo sapi
C 1026	78.5	7.1	220251	2	AC140363	Mus muscu	AC140363	c1099	78	7.1	167850	2	AC140114	Rattus no

c1100	78	7.1	170225	10	AC122512	1173	77.5	7.0	4613	5	CHKCRYP	L32780 Gallus gall
c1101	78	7.1	174539	2	AC113298	1174	77.5	7.0	6798	8	AY219227	AY219227 Leavenwor
c1102	78	7.1	176464	2	AC102297	1175	77.5	7.0	6957	7	BD183310	BD183310 Novel gen
c1103	78	7.1	176901	9	AC107623	c1176	77.5	7.0	7548	10	BC079889	BC079889 Mus muscu
c1104	78	7.1	177681	10	AC122810	c1177	77.5	7.0	7799	9	AF211174	AF211174 Homo sapi
c1105	78	7.1	178237	9	AF245226	c1178	77.5	7.0	8671	9	AB051462	AB051462 Homo sapi
c1106	78	7.1	183386	9	AC005229	c1179	77.5	7.0	10410	1	AE010782	AE010782 Mechanosa
c1107	78	7.1	183729	2	AC116352	c1180	77.5	7.0	13729	1	AE002415	AE002415 Neisseria
c1108	78	7.1	184346	10	AC122283	c1181	77.5	7.0	15894	6	AR049868	AR049868 Sequence
c1109	78	7.1	184672	2	AF002508	c1182	77.5	7.0	15894	6	BD137590	BD137590 Mutation
c1110	78	7.1	187831	2	AC149640	c1183	77.5	7.0	15894	6	BD137591	BD137591 Mutation
c1111	78	7.1	188782	10	AL713870	c1184	77.5	7.0	15894	6	BD137594	BD137594 Mutation
c1112	78	7.1	189768	2	CR753421	c1185	77.5	7.0	15894	6	BD137595	BD137595 Mutation
c1113	78	7.1	190130	10	AC122808	c1186	77.5	7.0	15894	6	BD137596	BD137596 Mutation
c1114	78	7.1	191901	9	BS000101	c1187	77.5	7.0	15894	6	BD137597	BD137597 Mutation
c1115	78	7.1	192106	9	AC090229	c1188	77.5	7.0	15894	6	E04903	E04903 DNA coding
c1116	78	7.1	196204	9	AC073957	c1189	77.5	7.0	15894	6	I59432	I59432 Sequence 1
c1117	78	7.1	196398	10	AL604027	c1190	77.5	7.0	15894	14	AB046218	AB046218 Measles v
c1118	78	7.1	197069	2	AC090370	c1191	77.5	7.0	15894	14	AF266286	AF266286 Measles v
c1119	78	7.1	200477	9	AC090079	c1192	77.5	7.0	15894	14	AF266287	AF266287 Measles v
c1120	78	7.1	204430	2	CR792453	c1193	77.5	7.0	15894	14	AF266288	AF266288 Measles v
c1121	78	7.1	204839	2	AC119260	c1194	77.5	7.0	15894	14	AF266289	AF266289 Measles v
c1122	78	7.1	206137	2	AC142455	c1195	77.5	7.0	15894	14	AF266290	AF266290 Measles v
c1123	78	7.1	207058	2	AF001394	c1196	77.5	7.0	15894	14	AF266291	AF266291 Measles v
c1124	78	7.1	214250	2	AC103314	c1197	77.5	7.0	15894	14	AY486083	AY486083 Measles v
c1125	78	7.1	214648	2	AC105570	c1198	77.5	7.0	15894	14	AY486084	AY486084 Measles v
c1126	78	7.1	217309	10	AL928632	c1199	77.5	7.0	15894	14	MV8DMBCDN	266517 Measles vir
c1127	78	7.1	218882	2	AC133692	c1200	77.5	7.0	15894	14	S58435	S58435 nucleocapsi
c1128	78	7.1	218974	2	AC133946	c1201	77.5	7.0	18967	6	CQ753911	CQ753911 Sequence
c1129	78	7.1	221586	2	EX957332	c1202	77.5	7.0	18967	6	CQ754454	CQ754454 Sequence
c1130	78	7.1	224292	2	AC026873	c1203	77.5	7.0	18967	6	CQ754932	CQ754932 Sequence
c1131	78	7.1	226611	10	AC122878	c1204	77.5	7.0	18967	6	CQ755017	CQ755017 Sequence
c1132	78	7.1	227495	2	AC148480	c1205	77.5	7.0	31731	3	U21318	U21318 Caenorhabdi
c1133	78	7.1	230258	2	AC110106	c1206	77.5	7.0	35040	1	BACVACA	L77246 Bacillus su
c1134	78	7.1	230682	2	EX510307	c1207	77.5	7.0	36462	14	AY530876	AY530876 Simian ad
c1135	78	7.1	230956	2	AC090614	c1208	77.5	7.0	37570	8	ATU53501	ATU53501 Aradidopsis
c1136	78	7.1	233050	1	AL627271	c1209	77.5	7.0	38775	3	U46671	U46671 Caenorhabdi
c1137	78	7.1	236428	10	AC147563	c1210	77.5	7.0	44645	8	AC108058	AC108058 Homo sapi
c1138	78	7.1	236844	2	AC098096	c1211	77.5	7.0	71347	2	AC025308	AC025308 Homo sapi
c1139	78	7.1	256581	2	CR394526	c1212	77.5	7.0	74645	2	AC009592	AC009592 Homo sapi
c1140	78	7.1	256303	2	AC114244	c1213	77.5	7.0	79976	9	EX537339	EX537339 Human DNA
c1141	78	7.1	286098	2	AC099280	c1214	77.5	7.0	79990	9	AC010457	AC010457 Homo sapi
c1142	78	7.1	286164	2	AC113507	c1215	77.5	7.0	82144	9	AC099660	AC099660 Homo sapi
c1143	78	7.1	274975	2	AC099279	c1216	77.5	7.0	94487	8	AC012394	AC012394 Aradidops
c1144	78	7.1	279560	2	AC113689	c1217	77.5	7.0	100806	8	AC015450	AC015450 Aradidops
c1145	78	7.1	280815	2	AC107562	c1218	77.5	7.0	104418	9	AC119740	AC119740 Homo sapi
c1146	78	7.1	300523	1	AE016838	c1219	77.5	7.0	109694	8	F23A5	AC011713 Aradidops
c1147	78	7.1	301877	2	AC096091	c1220	77.5	7.0	109694	8	F23A5	AC011713 Aradidops
c1148	78	7.1	313143	2	AC120453	c1221	77.5	7.0	110000	1	CR628337_13	Continuation (14 o
c1149	78	7.1	316869	2	AC124509	c1222	77.5	7.0	110000	2	LMFLCHR34_02	Continuation (3 of
c1150	78	7.1	324876	2	AC114164	c1223	77.5	7.0	110000	8	CR380955_04	Continuation (5 of
c1151	78	7.1	340000	9	AP001674	c1224	77.5	7.0	116459	8	AC093956	AC093956 Oryza sat
c1152	78	7.1	349877	2	AC115218	c1225	77.5	7.0	121257	2	AC146307	AC146307 Medicago
c1153	78	7.1	349980	6	AX344556	c1226	77.5	7.0	122269	9	HS653H13	AL031466 Human DNA
c1154	77.5	7.0	945	6	AX489386	c1227	77.5	7.0	131175	2	CNS08C7L	AL731736 Oryza sat
c1155	77.5	7.0	1020	1	AF426455	c1228	77.5	7.0	133786	9	AC091839	AC091839 Homo sapi
c1156	77.5	7.0	1055	4	CFCD44AG	c1229	77.5	7.0	137139	9	HSB455A7	AL121580 Human DNA
c1157	77.5	7.0	1089	5	AY062004	c1230	77.5	7.0	137908	10	AL607024	AL607024 Mouse DNA
c1158	77.5	7.0	1102	5	AF103007	c1231	77.5	7.0	139155	2	AC149815	AC149815 Zea mays
c1159	77.5	7.0	1850	9	BC018652	c1232	77.5	7.0	140572	9	AL354743	AL354743 Homo sapi
c1160	77.5	7.0	1925	10	BC024072	c1233	77.5	7.0	147350	2	AC069332	AC069332 Homo sapi
c1161	77.5	7.0	1941	10	BC031717	c1234	77.5	7.0	148000	9	AP003464	AP003464 Homo sapi
c1162	77.5	7.0	1957	10	BC024123	c1235	77.5	7.0	148057	5	BX649341	BX649341 Zebrafish
c1163	77.5	7.0	1977	10	AB055004	c1236	77.5	7.0	148376	2	AC138898	AC138898 Homo sapi
c1164	77.5	7.0	2025	10	AY027919	c1237	77.5	7.0	150528	2	AC149242	AC149242 Macaca mu
c1165	77.5	7.0	2313	6	AX046352	c1238	77.5	7.0	150789	2	AC006885	AC006885 Caenorhab
c1166	77.5	7.0	2651	9	BC050328	c1239	77.5	7.0	152276	10	AC131763	AC131763 Mus muscu
c1167	77.5	7.0	2677	5	BC084337	c1240	77.5	7.0	154112	9	AC074378	AC074378 Homo sapi
c1168	77.5	7.0	3395	9	HS4420243	c1241	77.5	7.0	154605	2	AC046161	AC046161 Homo sapi
c1169	77.5	7.0	3421	1	AF467290	c1242	77.5	7.0	156153	10	AC107715	AC107715 Mus muscu
c1170	77.5	7.0	3857	6	AX046398	c1243	77.5	7.0	156677	2	AC092550	AC092550 Homo sapi
c1171	77.5	7.0	4023	9	HUMHWC2B	c1244	77.5	7.0	159286	5	BX470149	BX470149 Zebrafish
c1172	77.5	7.0	4433	10	AK129390	c1245	77.5	7.0	160378	2	AC090076	AC090076 Homo sapi

c1246	77.5	7.0	160603	9	AC096630	AC096630 Pan trogl	c1319	77	7.0	5595	10	BC008538	BC008538 Mus muscu
c1247	77.5	7.0	165277	5	AL954184	AL954184 Zebrafish	1320	77	7.0	6030	6	CQ591240	CQ591240 Sequence
c1248	77.5	7.0	166371	2	BX936382	BX936382 Danio rer	1321	77	7.0	10029	1	AE0015875	AE0015875 Shewanell
1249	77.5	7.0	166637	9	AC008657	AC008657 Homo sapi	c1322	77	7.0	10840	1	AE000908	AE000908 Methanoba
c1250	77.5	7.0	167726	2	CR812892	CR812892 Danio rer	c1323	77	7.0	11684	1	AE006647	AE006647 Sulfolobu
c1251	77.5	7.0	167835	2	AC151085	AC151085 Bos tauru	c1324	77	7.0	11865	1	AE014797	AE014797 Bifidobac
1252	77.5	7.0	168797	2	AC104882	AC104882 Mus muscu	c1325	77	7.0	13867	1	AE014737	AE014737 Bifidobac
c1253	77.5	7.0	168889	10	AL7311779	AL7311779 Mouse DNA	1326	77	7.0	13987	1	AE014745	AE014745 Bifidobac
c1254	77.5	7.0	171550	9	AC079322	AC079322 Homo sapi	c1327	77	7.0	14023	1	AE007841	AE007841 Clostridi
c1255	77.5	7.0	172044	2	AC151530	AC151530 Mus muscu	1328	77	7.0	14835	1	AE010390	AE010390 Methanopy
1256	77.5	7.0	172667	2	CR361541	CR361541 Danio rer	c1329	77	7.0	15205	1	AE010390	AE010390 Methanocald
c1257	77.5	7.0	172732	10	AC113039	AC113039 Mus muscu	1330	77	7.0	33026	9	AF156673	AF156673 Homo sapi
1258	77.5	7.0	175426	2	AC113235	AC113235 Canis fam	c1331	77	7.0	56105	1	SS56KBER	SS56KBER Y08257 S.solfatari
c1259	77.5	7.0	176436	2	AC148535	AC148535 Macaca mu	c1332	77	7.0	62070	8	NC2E4	NC2E4 AL451022 Neurospor
1260	77.5	7.0	177171	2	AC1281176	AC1281176 Rattus no	c1333	77	7.0	65182	2	AC101488	AC101488 Mus muscu
c1261	77.5	7.0	178071	2	AC145536	AC145536 Lemur cat	1334	77	7.0	81209	10	AL805942	AL805942 Mouse DNA
1262	77.5	7.0	179271	2	AC136883	AC136883 Sus scrof	c1335	77	7.0	82944	9	AL354999	AL354999 Human DNA
c1263	77.5	7.0	179779	2	AC026012	AC026012 Homo sapi	1336	77	7.0	88546	9	AC008435	AC008435 Homo sapi
1264	77.5	7.0	180606	2	AC073406	AC073406 Homo sapi	c1337	77	7.0	110000	2	AC105546	AC105546 Continuation (2 of
c1265	77.5	7.0	181470	9	AC016659	AC016659 Homo sapi	1338	77	7.0	110000	2	AC105546	AC105546 Continuation (3 of
c1266	77.5	7.0	182559	9	AC096590	AC096590 Homo sapi	c1339	77	7.0	110000	2	AC114343	AC114343 Rattus no
1267	77.5	7.0	182871	3	AC117176	AC117176 Dictyoste	1340	77	7.0	110000	2	AC115635	AC115635 Rattus no
c1268	77.5	7.0	184361	2	AC012481	AC012481 Homo sapi	c1341	77	7.0	110000	2	AC115635	AC115635 Continuation (3 of
c1269	77.5	7.0	185020	5	BX649431	BX649431 Zebrafish	c1342	77	7.0	110000	6	AR271569	AR271569 Continuation (9 of
c1270	77.5	7.0	186720	2	AC122735	AC122735 Mus muscu	1343	77	7.0	115560	9	AC073905	AC073905 Homo sapi
1271	77.5	7.0	187938	2	AC117973	AC117973 Rattus no	1344	77	7.0	116951	9	AC114788	AC114788 Homo sapi
c1272	77.5	7.0	188532	2	AC145036	AC145036 Homo sapi	c1345	77	7.0	123077	8	OSJN00275	OSJN00275 Oryza sat
c1273	77.5	7.0	189710	10	AL805967	AL805967 Mouse DNA	1346	77	7.0	132097	9	AC005589	AC005589 Homo sapi
1274	77.5	7.0	190256	10	AC121302	AC121302 Mus muscu	c1347	77	7.0	132319	10	AL805904	AL805904 Mouse DNA
c1275	77.5	7.0	191704	2	AC053529	AC053529 Homo sapi	1348	77	7.0	135873	9	AC008915	AC008915 Homo sapi
1276	77.5	7.0	191710	10	AC122489	AC122489 Mus muscu	c1349	77	7.0	141810	2	CR847153	CR847153 Danio rer
c1277	77.5	7.0	193872	9	AC087369	AC087369 Homo sapi	c1350	77	7.0	142331	2	AF307157	AF307157 Homo sapi
1278	77.5	7.0	194727	2	AC148553	AC148553 Callithr	c1351	77	7.0	143549	2	AC118287	AC118287 Oryza sat
c1279	77.5	7.0	195642	2	AC125828	AC125828 Rattus no	c1352	77	7.0	147172	9	AC022234	AC022234 Homo sapi
c1280	77.5	7.0	201375	1	BSUB0012	Z99115 Bacillus su	c1353	77	7.0	148033	2	AC121513	AC121513 Mus muscu
c1281	77.5	7.0	201861	9	AC067796	AC067796 Homo sapi	c1354	77	7.0	149907	4	AC091436	AC091436 Felis cat
1282	77.5	7.0	202267	9	DJ293M10	AF111167 Homo sapi	c1355	77	7.0	150582	2	AC147805	AC147805 Mus muscu
c1283	77.5	7.0	203638	2	AC135953	AC135953 Macaca mu	c1356	77	7.0	160589	10	AL663066	AL663066 Mouse DNA
1284	77.5	7.0	204741	10	AC145569	AC145569 Mus muscu	1357	77	7.0	160881	10	AL844140	AL844140 Mouse DNA
c1285	77.5	7.0	205910	2	AC044847	AC044847 Mus muscu	1358	77	7.0	165051	9	AC026950	AC026950 Homo sapi
c1286	77.5	7.0	208369	1	AE017195	AE017195 Bacillus	1359	77	7.0	165723	2	AC150538	AC150538 Bos tauru
c1287	77.5	7.0	212637	2	CR749167	CR749167 Danio rer	c1360	77	7.0	168470	2	AC147309	AC147309 Pan trogl
1288	77.5	7.0	214406	2	AC140672	AC140672 Mus muscu	1361	77	7.0	172828	10	AC124187	AC124187 Mus muscu
c1289	77.5	7.0	216409	2	AC136132	AC136132 Rattus no	c1362	77	7.0	175026	2	AL512409	AL512409 Homo sapi
1290	77.5	7.0	220407	2	AC121626	AC121626 Rattus no	1363	77	7.0	177893	9	AC005089	AC005089 Homo sapi
c1291	77.5	7.0	220903	2	CR293532	CR293532 Danio rer	c1364	77	7.0	179919	2	AC114383	AC114383 Rattus no
c1292	77.5	7.0	227008	2	AP001771	AP001771 Homo sapi	1365	77	7.0	181279	2	CR382383	CR382383 Danio rer
c1293	77.5	7.0	227430	2	AC091590	AC091590 Homo sapi	c1366	77	7.0	182706	2	AC127983	AC127983 Rattus no
1294	77.5	7.0	229771	2	AC129242	AC129242 Rattus no	c1367	77	7.0	185928	2	AC127983	AC127983 Rattus no
c1295	77.5	7.0	230768	2	AC122571	AC122571 Rattus no	1368	77	7.0	187509	2	AC131327	AC131327 Mus muscu
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c1301	77.5	7.0	250029	3	AE014820	AE014820 Plasmodiu	1374	77	7.0	196263	2	AC131385	AC131385 Homo sapi
c1302	77.5	7.0	252410	2	AC095553	AC095553 Rattus no	1375	77	7.0	196413	2	AC139927	AC139927 Rattus no
1303	77.5	7.0	253924	3	AE014822	AE014822 Plasmodiu	c1376	77	7.0	197013	2	AC079552	AC079552 Mus muscu
1304	77.5	7.0	257028	2	AC129248	AC129248 Rattus no	1377	77	7.0	198264	9	AC018841	AC018841 Homo sapi
1305	77.5	7.0	263238	2	AC136483	AC136483 Rattus no	c1378	77	7.0	202548	10	AL672026	AL672026 Mouse DNA
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c1310	77.5	7.0	349980	6	AX044030	AX044030 Sequence	c1383	77	7.0	207161	2	AL20651	AL20651 Rattus no
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c1312	77	7.0	2337	3	AK114286	AK114286 Clona int	c1385	77	7.0	207909	10	AC122318	AC122318 Mus muscu
1313	77	7.0	2383	8	AK103518	AK103518 Oryza sat	c1386	77	7.0	208014	10	AL691519	AL691519 Mouse DNA
1314	77	7.0	2640	3	AY051488	AY051488 Drosophll	1387	77	7.0	211668	2	AC115146	AC115146 Rattus no
1315	77	7.0	2979	4	BD096360	BD096360 wri inter	1388	77	7.0	212930	2	AC123986	AC123986 Mus muscu
c1316	77	7.0	3189	14	PRR23078	AY232078 Porcine r	c1389	77	7.0	212343	2	AC130007	AC130007 Rattus no
1317	77	7.0	3320	5	AY057072	AY057072 Fundulus	1390	77	7.0	214118	9	BS000047	BS000047 Pan trogl
1318	77	7.0	4117	5	PWINTAV	X81108 P.waltl mRN	1391	77	7.0	214178	5	BX640577	BX640577 Zebrafish

c1392	77	7.0	217372	2	AC148224	Colobus g	1465	76.5	6.9	27518	9	HS1032FL13	AL031903 Human DNA	
c1393	77	7.0	218291	10	AC146610	Mus muscu	c1466	76.5	6.9	32501	9	HSAP2B	U09912 H.sapiens A	
c1394	77	7.0	218686	1	AC137954	Mus muscu	c1467	76.5	6.9	33087	3	U00055	U00055 Caenorhabdi	
c1395	77	7.0	218696	9	BS000031	Pan trogl	1468	76.5	6.9	36535	14	AY530878	AY530878 Simian ad	
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c1435	76.5	6.9	648	9	AY327582	Homo sapi	RESULT 1	AR252633	Sequence	386	from patent	US 6478825.	linear	PAT 20-DEC-2002
c1436	76.5	6.9	885	5	EX931788	Gallus ga	LOCUS	AR252633	Sequence	1346	bp	DNA		
c1437	76.5	6.9	912	6	C0847093	Sequence	DEFINITION	AR252633	Sequence	386	from patent	US 6478825.		
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c1442	76.5	6.9	1300	1	STU20795	Sequence	ORGANISM	Unclassified.						
c1443	76.5	6.9	1330	9	AK074197	Homo sapi	REFERENCE	1 (bases 1 to 1346)						
c1444	76.5	6.9	1344	5	XLU90895	Sequence	AUTHORS	Winterbottom, J.M., Shimp, L., Boyce, T.M. and Kaes, D.						
c1445	76.5	6.9	1399	8	AF151454	Xenopus lae	TITLE	Implant, method of making same and use of the implant for the						
c1446	76.5	6.9	1650	6	AX411427	Sequence		Implant, method of making same and use of the implant for the						
c1447	76.5	6.9	1650	6	AX411429	Sequence	JOURNAL	Patent: US 6478825-A 386 12-NOV-2002;						
c1448	76.5	6.9	1650	9	AF282874	Homo sapi	FEATURES	Location/Qualifiers						
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c1453	76.5	6.9	3032	6	CQ720852	Sequence	Pred. No.:	9.02e-114	Length:	1346				
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c1457	76.5	6.9	3552	3	DR010BTBN	L13305	Query Match:	100.00%	Indels:	0				
c1458	76.5	6.9	3742	4	CFU55028	Canis fami	DB:	6	Gaps:	0				
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c1463	76.5	6.9	15894	14	MEANPCG	Measles vir								
c1464	76.5	6.9	22348	1	AE008699	Salmonell								

Qy 1 MeLeuTripleLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20

Db	7	ATGTTGTGGCTGCTCTTTTCTGTGACTGCCATTATGCTGAACCTCTGTCAACCAAGGT	66
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Qy	41	AlaTrpAspThrAsnGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60
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Qy	101	ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp	120
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Qy	121	GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal	140
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Qy	161	LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp	180
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Qy	181	AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro	200
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RESULT 3			
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DEFINITION	Sequence 386 from Patent WO0073454.		
ACCESSION	AX403499		
VERSION	AX403499.1 GI:21436987		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
AUTHORS	1 Ashkenazi, A.J., Baker, K.P., Botstein, D., Desnovers, L., Eaton, D., Ferrara, N., Gerber, H., Gerritsen, M., Goddard, A., Godowski, P., Grimaldi, C.J., Gurney, A.L., Kljavin, I., Napier, M.A., Pan, J., Paoni, N.F., Roy, M., Stewart, T.A., Tumas, D., Watanabe, C.K., Williams, P., Wood, W.I. and Zhang, Z.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same		
JOURNAL	Patent: WO 0073454-A 386 07-DEC-2000; Genentech Inc. (US)		
FEATURES	Location/Qualifiers		
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ORIGIN			
Alignment Scores:			
Pred. No.:	9.02e-114	Length:	1346
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
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US-09-989-724-387 (1-212) x AR528692 (1-1346)			
Qy	1	MetLeuTrpLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly	20

Db	7																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
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Score: 1102.00 Mates: 212
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-989-724-387 (1-212) x AX403499 (1-1346)

Qy 1 MetLeuTrpLeuLeuPheLeuValThraAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGGTGGCTGCTCTTTTCTGGTGAATCATGCTGAACCTCTGTCACACAGGT 66
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThraAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGATACCATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGCTCTACTTGCATGTAAACCCAGAG 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATTTCTGGTTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCGCTGTG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCATCAGCCATAAGATGAACAGAACCGGATCAACATGCTTCTTCTAAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACCCATGAGCCATCTGTG 426
Qy 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTAATATTTGGTGTGATATTTGGCATCATATGCAATGGCACTA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAACCAACCATCTGAAGTGGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GAGCTGAAGATAAGTGTGAAAACATGATCACAATTTGAAATGGCATCCCTCTGATCCC 606
Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTAAATGATGCTTCA 642

RESULT 4
AX464348
LOCUS AX464348 1346 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 481 from Patent WO0140466.
ACCESSION AX464348
VERSION AX464348.1 GI:21899190
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Beresini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 481 07-JUN-2001;
Genentech Inc. (US)
FEATURES Location/Qualifiers

source 1. 1346
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 9,02e-114 Length: 1346
Score: 1102.00 Matches: 212
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-989-724-387 (1-212) x AX464348 (1-1346)

Qy 1 MetLeuTrpLeuLeuPheLeuValThraAlaIleHisAlaGluLeuCysGlnProGly 20
Db 7 ATGTTGGTGGCTGCTCTTTTCTGGTGAATCATGCTGAACCTCTGTCACACAGGT 66
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThraAlaLeuGlyAspLysAlaTyr 40
Db 67 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAAGCATAT 126
Qy 41 AlaTrpAspThrAsnGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 127 GCCTGGATACCATGAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAAA 186
Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 187 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGCTCTACTTGCATGTAAACCCAGAG 246
Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 247 GTATCATTTCTGGTTTGTGGTTACAGACCTTCAAAAAATCACACCTTCTCGCTGTG 306
Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 307 GTGCATCAGCCATAAGATGAACAGAACCGGATCAACATGCTTCTTCTAAATGAC 366
Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 367 CAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACCCATGAGCCATCTGTG 426
Qy 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu 160
Db 427 CCCATCTGGATTAATATTTGGTGTGATATTTGGCATCATATGCAATGGCACTA 486
Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180
Db 487 CTGATTTTATCAGGATCTGGCAACGTAGAAGAAAGAACCAACCATCTGAAGTGGAT 546
Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 547 GAGCTGAAGATAAGTGTGAAAACATGATCACAATTTGAAATGGCATCCCTCTGATCCC 606
Qy 201 LeuAspMetLysGlyGlyIleLeuMetMetProSer 212
Db 607 CTGGACATGAAGGGGGGCATATTAAATGATGCTTCA 642

RESULT 5
AX359060
LOCUS AX359060 1346 bp mRNA linear PRI 03-OCT-2003
DEFINITION Homo sapiens clone DNA61873 NX-17 (UNG678) mRNA, complete cds.
ACCESSION AY359060
VERSION AY359060.1 GI:37183237
KEYWORDS FLI CDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1346)
AUTHORS Clark, H.F., Gurney, A.L., Abaya, E., Baker, K., Baldwin, D., Brush, J.,

```

Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Hass, P. E., Heldens, S., Huang, A., Kim, H. S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seehagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wleand, D., Woods, K., Xie, M. H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W. I. and Godowaki, P.

The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment

Genome Res. 13 (10), 2265-2270 (2003)

12975309

2 (bases 1 to 1346)

Clark, H. F.

Direct Submission

Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

1..1346

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="DNA61873"

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7..645

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/notes="PRO1312"

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NEEYLFKAMVAFMRVPRREATEIISHLVCNVTQVRSFVFTDPSKNTLPVAVEVQ

SAIRMKNRINNAFFNDOTLEPLKIPSTLAPMDSPVPIIIFGVIFCIIVAI

LILSGIWQRRRNKEFSEVDDAEDKCNMTIENGIPSDPLDMKGGILMWS"

## ORIGIN

## Alignment Scores:

Pred. No.: 9.02e-114 Length: 1346

Score: 1102.00 Matches: 212

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x AV359060 (1-1346)

QY 1 MetLeuTriLeuLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20

DB 7 ATGTTGGCTGCTCTTTTCTGGTGACTGCCATTCATGCTGAACCTGTGTCACACAGGT 66

QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40

DB 67 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGAGTAAGCATAT 126

QY 41 AlaTriPheThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60

DB 127 GCCTGGGATACCAATGAAGAATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAA 186

QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80

DB 187 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAACCCAGAG 246

QY 81 ValSerPheTriPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100

DB 247 GTATCATCTGGTTTGGTTTACAGACCTTCAAAAATACACCCCTTCTCTGCTGTGAG 306

QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120

DB 307 GTGCAATCAGCCATAAGATGAACAGAACCGGATCAACAATGCCTTCTTCTTAATGAC 366

QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProMetAspProSerVal 140

DB 367 CAAACTCTGGAATTTTAAATCCCTTCCACACTTGACACCCATGCACCATCTGTG 426

QY 141 ProIleTriPheIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160

DB 427 CCATCTGGAATTTATATATTGCTGTGATATTTTGCATCATCATATGTCATATGCAC 486

QY 161 LeuIleLeuSerGlyIleTriPheGlnArgArgGlyAsnLysGluProSerGluValAsp 180

DB 487 CTGATTTTATCAGGGATCTGGCAACGTAGAGAAAGAACAAAGAACCATCTGAAGTGGAT 546

QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200

DB 547 GACGCTGAAGATAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCC 606

QY 201 LeuAspMetLysGlyIleLeuMetMetProSer 212

DB 607 CTGGACATGAAGGGGGCATATTAAATGATGCCTTCA 642

## RESULT 6

## AX083382

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## 1..666

## /organism="Homo sapiens"

## /mol\_type="unassigned DNA"

## /db\_xref="taxon:9606"

## ORIGIN

## Alignment Scores:

Pred. No.: 1.11e-112 Length: 666

Score: 1089.00 Matches: 212

Percent Similarity: 99.53% Conservative: 0

Best Local Similarity: 99.53% Mismatches: 0

Query Match: 98.82% Indels: 1

DB: 6 Gaps: 0

US-09-989-724-387 (1-212) x AX083382 (1-666)

QY 1 MetLeuTriLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20

DB 1 ATGTTGGCTGCTCTTTTCTGGTGACTGCCATTCATGCTGAACCTGTGTCACACAGGT 60

QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40

DB 61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 120

QY 41 AlaTriPheThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60

DB 121 GCCTGGGATACCAATGAAGAATACCTTTCAGAGCGATGGTAGCTTCTCCATGAGAAA 180

QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80

DB 181 GTTCCCAACAGAGAGCAACAGAAATTTCCCATGTCTCTACTTTGCAATGTAACCCAGAG 240

QY 81 ValSerPheTriPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100

DB 241 GTATCATCTGGTTTGGTTTACAGACCTTCAAAAAATCACACCTTCTCTGCTGTGAG 300



Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120  
 Db 301 GTGCAATCAGCATAAGAAATGAACAGAACCGGATCAACAAATGCTTCTTCTTAATGAC 360  
 Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140  
 Db 361 CAAACTCTGGAAATTTTAAATAATCCCTTCCACACTTGCACACCCATGGAGCCCATCTGTG 420  
 Qy 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160  
 Db 421 CCCATCTGGATTATATTTGGTGTGATATTTTGGATCATCATAGTTGCAATGGCACTA 480  
 Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180  
 Db 481 CTGATTTTATCAGGATCTGGCAACGTAGAAAGAAAGAACCAACCATCTGAAGTGGAT 540  
 Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200  
 Db 541 GACGCTGAAGATAAGTGTGAACATGATCAAAATGGAAATGGCATCCCTCTGTATCCC 600  
 Qy 201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212  
 Db 601 CTGGACATGAAGGAGGCATATTAATGATGCCTTCA 637

## RESULT 7

AF229179 1345 bp mRNA linear PRI 05-APR-2002  
 LOCUS AF229179 Homo sapiens collectrin mRNA, complete cds.

DEFINITION AF229179  
 ACCESSION AF229179.1 GI:9957753

VERSION AF229179.1  
 KEYWORDS

SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 (bases 1 to 1345)  
 Zhang, H., Wada, J., Hida, K., Tsuchiyama, Y., Hiragushi, K.,  
 Shikata, K., Wang, H., Lin, S., Kanwar, Y. S. and Makino, H.  
 Collectrin, a collecting duct-specific transmembrane glycoprotein,  
 is a novel homolog of ACE2 and is developmentally regulated in  
 embryonic kidneys

J. Biol. Chem. 276 (20), 17132-17139 (2001)  
 21264468

## JOURNAL

MEDLINE

PUBMED

11278314

2 (bases 1 to 1345)

Zhang, H., Wada, J. and Makino, H.

Human kidney specific membrane protein (NX-17)

Unpublished

3 (bases 1 to 1345)

Zhang, H., Wada, J. and Makino, H.

Direct Submission

Submitted (28-JAN-2000) Department of Medicine III, Okayama

University Medical School, 2-5-1 Shikata-cho, Okayama 700-8558,

Japan

## FEATURES

Location/Qualifiers

1..1345

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

24..692

/note="kidney-specific membrane protein NX-17; similar to  
 the Mus musculus and Rattus norvegicus products encoded by  
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 respectively"

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/protein\_id="AAG09466.1"

/db\_xref="GI:9957754"

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 LILSGIWQRKRKKEPSEVDADKCNMITIENGIPSDPLDMKGGHINDAFMTEDER

## CDS

## LTPL"

ORIGIN  
 Alignment Scores: 2 6e-112 Length: 1345  
 Pred. No.: 1089.00 Matches: 212  
 Score: 1089.00  
 Percent Similarity: 99.53% Conservative: 0  
 Best Local Similarity: 99.53% Mismatches: 0  
 Query Match: 98.82% Indels: 1  
 DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x AF229179 (1-1345)

Qy 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20  
 Db 24 ATGTTGTGGTCTCTCTTTTCTGTGACTGCCATTCTGCTGAACCTCTCTCAACAGGT 83  
 Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40  
 Db 84 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 143  
 Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60  
 Db 144 GCCTGGATACCAATGAGATATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAA 203  
 Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80  
 Db 204 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTCTTTCGAATGTAAACAGAGG 263  
 Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100  
 Db 264 GTATCATTTCTGGTTTGTGGTTACAGACCCCTTCAAAAATCACACCTTCTCTGTGTGAA 323  
 Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAlaPhePheLeuAsnAsp 120  
 Db 324 GTGCATCAGCCATAGATAGAACAGACCGGATCAACATGCTCTTCTTAAATGAC 383  
 Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140  
 Db 384 CAAACTCTGGAAATTTTAAATAATCCCTTCCACACTTGCACACCCATGGAGCCCATCTGTG 443  
 Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160  
 Db 444 CCATCTGGATTATATTTGTGTGATATTTTGCATCATCATAGTTGCAATGGCACTA 503  
 Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180  
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AX083392 Sequence 84 from Patent WO0112660.  
 AX083392  
 AX083392.1 GI:13185232

LOCUS AX083392 1347 bp DNA linear PAT 28-FEB-2001

DEFINITION

AX083392

ACCESSION

AX083392.1

VERSION

AX083392.1

KEYWORDS

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1

Kato, S. and Kimura, T.

Human proteins having hydrophobic domains and dnas encoding these

proteins

Patent: WO 0112660-A 84 22-FEB-2001;

JOURNAL



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ORIGIN
Alignment Scores:
Pred. No.: 2,68e-112 Length: 1377
Score: 1089.00 Matches: 212
Percent Similarity: 99.53% Conservative: 0
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Query Match: 98.82% Indels: 1
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x BC050606 (1-1377)

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Qy 21 AlaGluAenAlaPheLeuValArgLeuSerIleArgThrAlaLeuGluValAspLeuAlaTyr 40
Db 69 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 128

Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
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Db 189 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTCTTCAATGTGAACCCAGAGG 248

Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
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RESULT 10
BC015099 1440 bp mRNA linear PRI 29-JUN-2004
LOCUS BC015099
DEFINITION Homo sapiens transmembrane protein 27, mRNA (cDNA clone MGC:22827
IMAGE:3829035), complete cds.
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ACCESSION BC015099
VERSION BC015099.1 GI:15929328
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1440)
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Holtzman, R.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.B.,
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Worley, K.C., Hale, S., Garcia, A.M., Gunaratne, P.H., Richards, S.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1440)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAL Plate: 31 Row: d Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: GenomeScan gene
prediction, similarity but not identity to protein.
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ORIGIN

Alignment Scores:  
Pred. No.: 2,83e-112 Length: 1440  
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Percent Similarity: 99.53% Conservative: 0  
Best Local Similarity: 99.53% Mismatches: 1  
Query Match: 98.82% Indels: 1  
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x BC015099 (1-1440)

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Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40  
Db 149 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAGCATAT 208  
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RESULT 11  
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DEFINITION Homo sapiens transmembrane protein 27, mRNA (cdna clone MGC:22707  
IMAGE:4048217), complete cds.  
ACCESSION BC014317  
VERSION BC014317.1 GI:15680012  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1605)  
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,  
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.P., Bhat,N.K.,  
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,  
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,  
Stapleton,M., Soares,M.B., Bonaldo,M.P., Casavant,T.L.,  
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,  
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,  
Abramson,R.D., Mullaby,S.J., Bosak,S.A., McEwan,P.J.,  
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,  
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Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,  
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,  
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,  
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,  
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,  
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalish,D.E.,  
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1605)  
AUTHORS Strausberg,R.  
DIRECT SUBMISSION  
SUBMITTED (17-SEP-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgabbs@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Institute for Systems Biology  
http://www.systemsbio.org  
Contact: anadan@systemsbiology.org  
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha  
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov  
Series: IRAL Plate: 31 Row: n Column: 3  
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ORIGIN

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Best Local Similarity: 99.53% Mismatches: 0  
Query Match: 98.82% Indels: 1  
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x BC014317 (1-1605)

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BD083420  
LOCUS BD083420 1401 bp DNA linear PAT 27-AUG-2002  
DEFINITION Secreted proteins and polynucleotides encoding them.  
ACCESSION BD083420  
VERSION BD083420.1 GI:22629030  
KEYWORDS JP 2001523950-A/2.  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial  
1 (bases 1 to 1401)  
REFERENCE Jacoby,K., McCoy,J.M., Lavallie,E.R., Racie,L.A., Merberg,D.,  
Treacy,M., Spaulding,V. and Agostino,M.J.

TITLE  
JOURNAL

Secreted proteins and polynucleotides encoding them  
GENETICS INSTITUTE INC

COMMENT

PN JP 2001523950-A/2  
PD 27-NOV-2001  
PF 23-JAN-1998 JP 1998532177  
PR 24-JAN-1997 US 08/788789  
PI KENNETH JACOBS, JOHN M MCCOY, EDWARD R LAVALLIE, LISA A RACIE, PI  
DAVID MERBERG,  
PI MAURICE TREACY, VIKKI SPAULDING, MICHAEL J AGOSTINO PC  
C12N15/12, C12N5/10, C07K14/47, C12Q1/68, A61K38/17 CC Strandedness:  
Double;  
CC Topology: Linear;

FEATURES

Location/Qualifiers.

source

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Query Match: 98.55% Indels: 1  
DB: 6 Gaps: 0

US-09-989-724-387 (1-212) x BD083420 (1-1401)

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RESULT 13  
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LOCUS  
DEFINITION  
97 human secreted proteins.  
ACCESSION  
BD205644.1 GI:33015414  
VERSION  
JP 2002533058-A/21.  
KEYWORDS  
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SOURCE  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1447)  
Ruben,S.M., Florence,K., Ni,J., Rosen,C.A., Carter,K.C.,  
Moore,P.A., Olsen,H.S., Shi,Y., Young,P.E., Wei,F.F., Brewer,L.A.,  
Soppet,D.R., Lafleur,D.W., Endress,G.A. and Ebner,R.  
97 human secreted proteins  
Patent: JP 2002533058-A 21 08-OCT-2002;  
JOURNAL  
HUMAN GENOME SCIENCES INC  
COMMENT  
OS Homo sapiens (human)  
PN JP 2002533058-A/21  
PD 08-OCT-2002  
PR 06-MAY-1999 JP 2000548451 60/085093,12-MAY-1998 US 60/085094 PR  
PR 12-MAY-1998 US 60/085105,12-MAY-1998 US 60/085180 PR  
12-MAY-1998 US 60/085927,18-MAY-1998 US 60/085906 PR  
18-MAY-1998 US 60/085924,18-MAY-1998 US 60/085922 PR  
18-MAY-1998 US 60/085923,18-MAY-1998 US 60/085921 PR  
18-MAY-1998 US 60/085925,18-MAY-1998 US 60/085928 PR  
18-MAY-1998 US 60/085920  
PI STEVEN M RUBEN,KIMBERLY FLORENCE,JIAN NI,CRAIG A ROSEN,KENNETH  
PI C CARTER,  
PI PAUL A MOORE,HENRIK S OLSEN,YANGGU SHI,PAUL E YOUNG,FING FEI  
PI WEI,  
PI LAURIE A BREWER,DANIEL R SOPPET,DAVID W LAFLEUR,GREGORY A PI  
ENDRESS.  
PI REINHARD EBNER  
PC C12N1/21,  
PC C12N15/09,C07K14/00,C07K14/435,C07K16/18,C12N1/15,C12N1/19, PC  
C12N1/21,  
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FH Key Location/Qualifiers  
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Best Local Similarity: 99.06% Mismatches: 1  
Query Match: 98.19% Indels: 1  
DB: 6 Gaps: 0

US-09-989-724-387 (1-212) x BD205644 (1-1447)

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ACCESSION  
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VERSION  
ARI77334.1  
KEYWORDS  
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SOURCE  
Unknown.  
ORGANISM  
Unclassified.  
REFERENCE  
1 (bases 1 to 848)  
AUTHORS  
Edwards,J.-B.,Dumas,Milne., Duclert,A. and Bougueleret,L.  
TITLE  
Complementary DNAs  
JOURNAL  
Patent: US 6312922-A 27 06-NOV-2001;  
FEATURES  
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ORIGIN  
Alignment Scores:  
Pred. No.: 9-55e-110 Length: 848  
Score: 1064.00 Matches: 208  
Percent Similarity: 97.65% Conservative: 0  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
DB: 6 Gaps: 0

US-09-989-724-387 (1-212) x ARI77334 (1-848)

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Db 92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACACAGCTCTGGAGATAAGCATAT 151  
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60

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DEFINITION Extended cDNA of secretory protein.
ACCESSION BD139270
VERSION BD139270.1 GI:23234215
KEYWORDS JP 2002508182-A/22.
SOURCE Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 848)
Bougueleret, L., Duclert, A. and Edwards, J. B. D. M.
Extended cDNA of secretory protein
Patent: JP 2002508182-A 22 19-MAR-2002;
GENSET
OS Homo sapiens (human)
PN JP 2002508182-A/22
PD 19-MAR-2002
PF 17-DEC-1998 JP 2000539136
PR 17-DEC-1998 US 60/069957, 09-FEB-1998 US 60/074121 PR
13-APR-1998 US 60/081563, 10-AUG-1998 US 60/096116 PI LYDIE
BOUGUELERET, AYMERIC DUCLERT, JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, PC
C12N1/21,
PC C12N5/10, C12P21/02, C12Q1/68, C12N15/00, C12N5/00, C12N15/00 CC
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## FEATURES

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## ORIGIN

Alignment Scores:  
Pred. No.: 9.55e-110 Length: 848

Score: 1064.00 Matches: 208  
Percent Similarity: 97.65% Conservative: 0  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
DB: 6 Gaps: 0

US-09-989-724-387 (1-212) x BD139270 (1-848)

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Qy 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 32 ATGTTGTGGTGTCTCTTTTCTGTGGTACGCCATTATCATGCTGAACCTCTGTCACACAGGT 91
Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 92 GCAGAAAAATCTTTTAAAGTGAGACTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151
Qy 41 AlaTrpAspThrAsnGluTyrLeuPheLysAlaMetValAlaPheSerMetAtqLys 60
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Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
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2973.898 Million cell updates/sec

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Scoring table: BIOSUM62  
Searched: 4390206 seqs, 2959870667 residues  
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Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries  
1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1	ID	AAZ65097	standard; cDNA; 1346 BP.			
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PN	WO9963088-A2.					
PA	(GETH ) GENENTECH INC.					
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Query Match:	100.00%	Indels:	0			
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PN	WO200053758-A2.					
PD	14-SEP-2000.					
PA	(GETH ) GENENTECH INC.					
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Query Match:	100.00%	Indels:	0			
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PD	08-JUN-2000.					
PA	(GETH ) GENENTECH INC.					
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PD	07-JUN-2001.					
PA	(GETH ) GENENTECH INC.					
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PN	WO200073454-A1.					
PD	07-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Best Local Similarity:	100.00%	Mismatches:	0			
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PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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ID ACA03843 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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ID ABX89381 standard; cDNA; 1346 BP.  
DE DNA encoding novel secreted and transmembrane protein PRO1312.  
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PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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ID ABX80875 standard; cDNA; 1346 BP.  
DE Human secreted/transmembrane protein cDNA, #157.  
PN US2003027162-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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ID ACD44384 standard; cDNA; 1346 BP.  
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PN US2002127576-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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DE Human secreted/transmembrane protein (PRO) cDNA #241.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
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PA (GETH ) GENENTECH INC.  
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PD 30-JAN-2003.  
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PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
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PN US2003032155-A1.

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PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
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DE Novel human secreted and transmembrane protein PRO1312 cDNA.
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PA (GETH ) GENENTECH INC.
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Query Match: 100.00% Indels: 0
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ID ABX17158 standard; cDNA; 1346 BP.
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PN US2002123463-A1.
PD 05-SEP-2002.
PA (GETH ) GENENTECH INC.
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Query Match: 100.00% Indels: 0
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PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
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Query Match: 100.00% Indels: 0
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DE Human secreted and transmembrane polypeptide PRO1312 cDNA.
PN US2002197615-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
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Query Match: 100.00% Indels: 0
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PN US2003017981-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
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Query Match: 100.00% Indels: 0
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PD 30-JAN-2003.
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Query Match: 100.00% Indels: 0
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PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match: 100.00% Indels: 0
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DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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PA (GETH ) GENENTECH INC.
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PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
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PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
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Query Match: 100.00% Indels: 0
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PD 01-MAY-2003.
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Query Match: 100.00% Indels: 0
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PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 39
ID ADA87612 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 40
ID ADA16814 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 41
ID ADA28022 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003054359-A1.
PD 20-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 42
ID ADA91906 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 43
ID ADB14969 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 44
ID ADB18930 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 45
ID ADA94145 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 46
ID ADB20041 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 47
ID ADB13353 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 48
ID ACD98664 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 49
ID ADA94602 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003059832-A1.
PD 27-MAR-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 50
ID ADA74607 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 51
ID ADB24840 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 52
ID ADA82364 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Query Match: 100.00% Indels: 0  
RESULT 53  
ID ADA75327 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US200307721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 54  
ID ADA85405 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 55  
ID ADA84853 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 56  
ID ADB31019 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 57  
ID ADA80637 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 58  
ID ADA75879 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 59  
ID ADA38827 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003059780-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 60  
ID ADA47104 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 61  
ID ADB25400 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide SEQ ID NO 481.  
PN US2003077715-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 62

ID ADA93576 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US200307721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 63  
ID ADB26926 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 64  
ID ADB31213 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 65  
ID ADA92948 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003060407-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 66  
ID ADA61141 standard; cDNA; 1346 BP.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 67  
ID ADB24288 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide SEQ ID NO 481.  
PN US200307714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 68  
ID ADA96617 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 69  
ID ADA81189 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 70  
ID ADA96065 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 71  
ID ADB26374 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.

PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 72  
ID ADB21859 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 73  
ID ADA77638 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 74  
ID ADB18378 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 75  
ID ADA87061 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 76  
ID ADA88164 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 77  
ID ADA46552 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 78  
ID ADB28582 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 79  
ID ADB29134 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 80  
ID ACH65530 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003044806-A1.

PD 06-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 81  
ID ADA77086 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003059909-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 82  
ID ADA22509 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane polypeptide PRO1312.  
PN US2003040473-A1.  
PD 27-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 83  
ID ADA88716 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 84  
ID ADA97721 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 85  
ID ADB27478 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003022339-A1.  
PD 30-JAN-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 86  
ID ADB22411 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 87  
ID ACD39520 standard; cDNA; 1346 BP.  
DE Human cDNA encoding PRO1192.  
PN US2003017982-A1.  
PD 23-JAN-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 88  
ID ADA06675 standard; cDNA; 1346 BP.  
DE Human secreted/transmembrane PRO polypeptide cDNA #121.  
PN US2003049638-A1.  
PD 13-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 89  
ID ADA39368 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003059782-A1.  
PD 27-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 90  
ID ADA67102 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003068793-A1.

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PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 91
ID ADB22963 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 92
ID ADB23736 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 93
ID ADA92458 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 94
ID ADB15521 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 95
ID ADB38773 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 96
ID ADB96394 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003054403-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 97
ID ADB38221 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 98
ID ADB66693 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 99
ID ADB89773 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 100
ID ADB90505 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 101
ID ADB39606 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 102
ID ADB47229 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 103
ID ADB86836 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 104
ID ADB77441 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 105
ID ADB34598 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 106
ID ADB35702 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 107
ID ADB34046 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 108
ID ADB35150 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide SEQ ID NO 481.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Query Match: 100.00% Indels: 0  
RESULT 109  
ID ADB36254 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide SEQ ID NO 481.  
PN US200307720-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 110  
ID ADB46649 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003082692-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 111  
ID ADC57866 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #121.  
PN US2003027754-A1.  
PD 06-FEB-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 112  
ID ADC55230 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #121.  
PN US2003045463-A1.  
PD 06-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 113  
ID ADC12097 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003049681-A1.  
PD 13-MAR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 114  
ID ADC56519 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #121.  
PN US2003064375-A1.  
PD 03-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 115  
ID ADC07574 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003068647-A1.  
PD 10-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 116  
ID ADC11564 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003069403-A1.  
PD 10-APR-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 117  
ID ADC50522 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 118  
ID ADC72069 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 119  
ID ADC60048 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 120  
ID ADC53055 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 121  
ID ADC57409 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 122  
ID ADC60600 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 123  
ID ADC51075 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 124  
ID ADC65602 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 125  
ID ADC54700 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 126  
ID ADC53661 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 127  
ID ADC59184 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID481.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 100.00% Indels: 0
RESULT 128
ID ADC56062 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 129
ID ADC58632 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 130
ID ADC58632 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID481.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 131
ID ADC14686 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003082546-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 132
ID ADD08218 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003068623-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 133
ID ADD03306 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 134
ID ADC82043 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003083461-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 135
ID ADC69717 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 136
ID ADC48606 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 137
ID ADD10135 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 138
ID ADD07685 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002193299-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 139
ID ADD04710 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 140
ID ADC82576 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003059833-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 141
ID ADC80666 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 142
ID ADD11173 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 143
ID ADC48054 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 144
ID ADD08756 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003073090-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 145
ID ADC80114 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 146
ID ADD07005 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2002193300-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 147
ID ADD09583 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
PN US2003194775-A1. Indels: 0
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 148
ID ADC83252 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003059783-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 149
ID ADD41296 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 150
ID ADD52435 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 151
ID ADD53175 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 152
ID ADD53727 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 153
ID ADD53559 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003077593-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 154
ID ADD56317 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003077594-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 155
ID ADD51883 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 156
ID ADD02682 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199056-A1.
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DE Human PRO polynucleotide #241.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 157
ID ADD02116 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 158
ID ADD54298 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 159
ID ADD54755 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003203432-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 160
ID ADD92615 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 161
ID ADD91511 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 162
ID ADE04125 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 163
ID ADE26909 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087304-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 164
ID ADE32422 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 165
ID ADE22354 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199056-A1.
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PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 166
ID ADD79578 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 167
ID ADE42114 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 168
ID ADE17931 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 169
ID ADD92063 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 170
ID ADE33526 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 171
ID ADE34078 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 172
ID ADD80130 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 173
ID ADD93167 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 174
ID ADE19587 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 175
ID ADE19035 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 176
ID ADE43231 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 177
ID ADD96020 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 178
ID ADE22906 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 179
ID ADD79024 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 180
ID ADE26376 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087305-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 181
ID ADE32974 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 182
ID ADE42666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 183
ID ADD80682 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Query Match: 100.00% Indels: 0
RESULT 184
ID AD89710 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 185
ID ADE40994 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 186
ID ADE04793 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 187
ID ADE92922 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 188
ID ADE67313 standard; cDNA; 1346 BP.
DE Human PRO1312 nucleotide sequence SEQ ID NO:386.
PN US2002198148-A1.
PD 26-DEC-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 189
ID ADG21631 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 190
ID ADG23272 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 191
ID ADP97607 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 192
ID ADG06071 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 193
ID ADG80119 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 194
ID ADH55411 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 195
ID ADH55963 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 196
ID ADI35567 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003050457-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 197
ID ADI64182 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 198
ID ADI65131 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 199
ID ADI63630 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 200
ID ADH82044 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 201
ID ADI00060 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003049682-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 202
ID ADH81492 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
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PN US2003207377-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 203
ID ABX77959 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #121.
PN US2003027163-A1.
PD 06-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 204
ID ABX80371 standard; DNA; 1346 BP.
DE Novel human secreted or transmembrane protein PRO1192 DNA.
PN US2002132252-A1.
PD 19-SEP-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 205
ID ACA69277 standard; cDNA; 1346 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO1312.
PN US2003032023-A1.
PD 13-FEB-2003.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 206
ID ACD24093 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 207
ID ABX90348 standard; cDNA; 1346 BP.
DE Human secreted/transmembrane protein cDNA, #157.
PN US2002160384-A1.
PD 31-OCT-2002.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 208
ID ABX64194 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2002103125-A1.
PD 01-AUG-2002.
PA (GETH ) GENENTECH LTD.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 209
ID ACA67234 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 210
ID ADM82661 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 211
ID ADN16060 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 212
ID ADN16689 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 213
ID ADN15508 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 214
ID ADN14956 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 215
ID ADC81218 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 216
ID ADD76666 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 217
ID ADD88030 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 218
ID ADD86434 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 219
ID ADE75882 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 220
ID ADE23458 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Query Match: 100.00% Indels: 0
RESULT 221
ID ADE24010 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199052-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 222
ID ADE24653 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003092111-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 223
ID ADE93474 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199060-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 224
ID ADE87478 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003203439-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 225
ID ADE89344 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199062-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 226
ID ADE18483 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003194794-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 227
ID ADE88792 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199054-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 228
ID ADE94812 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199027-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 229
ID ADE91223 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199061-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 230
ID ADE91223 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003194760-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 231
ID ADE93474 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199060-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 232
ID ADE93474 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003199029-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 233
ID ADE92370 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003199051-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 234
ID ADE90671 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003199063-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 235
ID ADE91818 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003199058-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 236
ID ADG11762 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO1312 polypeptide.
PN US2003228655-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 237
ID ADG02397 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207352-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 238
ID ADG22183 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207360-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 239
ID ADG20253 standard; cDNA; 1346 BP.
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DE cDNA encoding human PRO polypeptide #241.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 240
ID ADF98159 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 241
ID ADG24376 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 242
ID ADF98730 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 243
ID ADG03561 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 244
ID ADF99282 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 245
ID ADG16867 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 246
ID ADG05326 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 247
ID ADG19593 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 248
ID ADG13430 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 249
ID ADG08487 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 250
ID ADG15657 standard; cDNA; 1346 BP.
DE cDNA encoding human PRO polypeptide #241.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 251
ID ADF97055 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 252
ID ADG06240 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 253
ID ADG23824 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 254
ID ADG04113 standard; cDNA; 1346 BP.
DE Human PRO polynucleotide #241.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 255
ID ADG25014 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 256
ID ADG07311 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 257
ID ADG07863 standard; cDNA; 1346 BP.
DE Novel human secreted and transmembrane protein PRO1312 cDNA.
PN US2003207356-A1.
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PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 258  
ID ADG55358 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 259  
ID ADG61022 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 260  
ID ADG62126 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 261  
ID ADG82327 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 262  
ID ADG57566 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 263  
ID ADG57014 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 264  
ID ADG55910 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 265  
ID ADG58670 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 266  
ID ADG71036 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207420-A1.  
PD 06-NOV-2003.

PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 267  
ID ADG58118 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 268  
ID ADG53702 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 269  
ID ADG71588 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 270  
ID ADG81775 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 271  
ID ADH19632 standard; cDNA; 1346 BP.  
DE Human cDNA encoding secreted/transmembrane protein PRO1312.  
PN US2003228656-A1.  
PD 11-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 272  
ID ADH30737 standard; cDNA; 1346 BP.  
DE Human PRO polynucleotide #241.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 273  
ID ADH12104 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 274  
ID ADG52526 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
RESULT 275  
ID ADG54254 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 100.00% Mismatches: 0

Query Match:	100.00%	Indels:	0
RESULT 276			
ID ADG81223 standard; cDNA; 1346 BP.			
DE Human PRO polynucleotide #241.			
PN US2003194793-A1.			
PD 16-OCT-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 277			
ID ADG56462 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2003207366-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 278			
ID ADH12728 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2003207378-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 279			
ID ADH21125 standard; cDNA; 1346 BP.			
DE Human cDNA encoding secreted/transmembrane protein PRO1312.			
PN US2003224358-A1.			
PD 04-DEC-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 280			
ID ADG61574 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2003207429-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 281			
ID ADH20165 standard; cDNA; 1346 BP.			
DE Human cDNA encoding secreted/transmembrane protein PRO1312.			
PN US2003219856-A1.			
PD 27-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 282			
ID ADH28661 standard; cDNA; 1346 BP.			
DE Human PRO polynucleotide #241.			
PN US2003022331-A1.			
PD 30-JAN-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 283			
ID ADG54806 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2003207367-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 284			
ID ADG59846 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2003207369-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 285			
ID ADM27845 standard; cDNA; 1346 BP.			

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ID ADI81270 standard; cDNA; 1346 BP.			
DE cDNA encoding human PRO polypeptide #241.			
PN US2003207361-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 286			
ID ADG10013 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2004009548-A1.			
PD 15-JAN-2004.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 287			
ID ADI15484 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2003207382-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 288			
ID ADG09361 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2004009547-A1.			
PD 15-JAN-2004.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 289			
ID ADI14816 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2003207383-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 290			
ID ADI18411 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2003207349-A1.			
PD 06-NOV-2003.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 291			
ID ADJ63692 standard; cDNA; 1346 BP.			
DE Novel human secreted and transmembrane protein PRO1312 cDNA.			
PN US2004039164-A1.			
PD 26-FEB-2004.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 292			
ID ADJ77587 standard; cDNA; 1346 BP.			
DE Human PRO polynucleotide #241.			
PN US2004038336-A1.			
PD 26-FEB-2004.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 293			
ID ADJ65709 standard; cDNA; 1346 BP.			
DE cDNA encoding human PRO polypeptide #241.			
PN US2004038335-A1.			
PD 26-FEB-2004.			
PA (GETH ) GENENTECH INC.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	100.00%	Indels:	0
RESULT 294			
ID ADM27845 standard; cDNA; 1346 BP.			



DE cDNA encoding human PRO polypeptide #241.  
PN US2004048333-A1.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00%  
RESULT 295  
ID ADM42569 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00%  
RESULT 296  
ID ADM28431 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00%  
RESULT 297  
ID ADI95913 standard; cDNA; 1346 BP.  
DE cDNA encoding human PRO polypeptide #241.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00%  
RESULT 298  
ID ADI96465 standard; cDNA; 1346 BP.  
DE Novel human secreted and transmembrane protein PRO1312 cDNA.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00%  
RESULT 299  
ID ADT94383 standard; cDNA; 1346 BP.  
DE Human PRO1312 cDNA sequence.  
PN AU2003259607-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00%  
RESULT 300  
ID AAF94460 standard; cDNA; 666 BP.  
DE Human hydrophobic domain containing protein clone HPI0720 cDNA #74.  
PN WO200112660-A2.  
PD 22-FEB-2001.  
PA (SAGA ) SAGAMI CHEM RES CENT. Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00%  
RESULT 301  
ID ADI02664 standard; cDNA; 1312 BP.  
DE Human cDNA differentially expressed in the vascular endothelium #205.  
PN US2003166903-A1.  
PD 04-SEP-2003.  
PA (ASTR/) ASTROMOFF A. Mismatches: 0  
PA (BAND/) BANDMAN O. Indels: 1  
PA (COCK/) COCKS B G. Mismatches: 0  
Best Local Similarity: 99.53% Indels: 1  
Query Match: 98.82%  
RESULT 302  
ID ABZ78127 standard; cDNA; 1345 BP.  
DE Human cancer-related coding sequence, 156PID4.  
PN WO200283921-A2.  
PD 24-OCT-2002.  
PA (AGEN-) AGENSYS INC. Mismatches: 0  
Best Local Similarity: 99.53% Indels: 1  
Query Match: 98.82%

RESULT 303  
ID AAF94470 standard; cDNA; 1347 BP.  
DE Human hydrophobic domain containing protein clone HPI0720 cDNA #84.  
PN WO200112660-A2.  
PD 22-FEB-2001.  
PA (SAGA ) SAGAMI CHEM RES CENT. Mismatches: 0  
Best Local Similarity: 99.53% Indels: 1  
Query Match: 98.82%  
RESULT 304  
ID ADA39900 standard; cDNA; 1432 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 0  
Best Local Similarity: 99.53% Indels: 1  
Query Match: 98.82%  
RESULT 305  
ID ADAL1489 standard; DNA; 1432 BP.  
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 17.  
PN US2003055236-A1.  
PD 20-MAR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 0  
Best Local Similarity: 99.53% Indels: 1  
Query Match: 98.82%  
RESULT 306  
ID ADD37613 standard; cDNA; 1432 BP.  
DE Human secreted protein encoding sequence #95.  
PN WO200290526-A2.  
PD 14-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 0  
Best Local Similarity: 99.53% Indels: 1  
Query Match: 98.82%  
RESULT 307  
ID ADA56090 standard; DNA; 1432 BP.  
DE Gene encoding human secreted protein #269.  
PN WO2002102994-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 0  
Best Local Similarity: 99.53% Indels: 1  
Query Match: 98.82%  
RESULT 308  
ID AAV40540 standard; cDNA; 1401 BP.  
DE Homo sapiens secreted protein clone AM42\_3.  
PN WO9832853-A2.  
PD 30-JUL-1998.  
PA (GEMY ) GENETICS INST INC. Mismatches: 0  
Best Local Similarity: 99.06% Indels: 1  
Query Match: 98.55%  
RESULT 309  
ID AAZ65261 standard; DNA; 1447 BP.  
DE Human secreted protein gene 12.  
PN WO9958660-A1.  
PD 18-NOV-1999.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 1  
Best Local Similarity: 99.06% Indels: 1  
Query Match: 98.19%  
RESULT 310  
ID ADE11650 standard; cDNA; 1447 BP.  
DE Human secreted polypeptide cDNA #12.  
PN US2003100051-A1.  
PD 29-MAY-2003.  
PA (RUBE/) RUBEN S M. Mismatches: 0  
PA (FLOR/) FLORENCE K A. Indels: 1  
PA (NIJU/) NI J. Mismatches: 0  
PA (ROSE/) ROSEN C A. Indels: 1  
PA (CART/) CARTER K C. Mismatches: 0  
PA (MOOR/) MOORE P A. Indels: 1  
PA (OLSE/) OLSEN H S. Mismatches: 0  
PA (SHIY/) SHI Y. Indels: 1  
PA (YOUN/) YOUNG P E. Mismatches: 0  
PA (WEIY/) WEI Y. Indels: 1  
PA (BREW/) BREWER L A. Mismatches: 0

PA (SOPP/) SOPPET D R.  
PA (LAFI/) LAFLEUR D W.  
PA (ENDR/) ENDRESS G A.  
PA (EBNE/) EBNER R.  
PA (BIRS/) BIRSE C E.  
Best Local Similarity: 99.06% Mismatches: 1  
Query Match: 98.19% Indels: 1  
RESULT 311  
ID AAX98224 standard; cDNA; 1365 BP.  
DE Human EST-derived coding sequence SEQ ID NO: 81.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 98.60% Mismatches: 0  
Query Match: 97.28% Indels: 2  
RESULT 312  
ID AAX19983 standard; cDNA; 848 BP.  
DE Human secreted protein 5' EST SEQ ID NO: 27.  
PN WO9906439-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 313  
ID AAX39430 standard; DNA; 848 BP.  
DE Human secreted protein 5' EST SEQ ID NO: 27.  
PN WO9906551-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 314  
ID AAX41369 standard; cDNA; 848 BP.  
DE Extended cDNA obtained from 5' EST, SEQ ID NO: 27 from WO 9906553.  
PN WO9906553-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 315  
ID AAX97564 standard; DNA; 848 BP.  
DE Extended human secreted protein coding sequence, SEQ ID NO: 27.  
PN WO9931236-A2.  
PD 24-JUN-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 316  
ID AAX40770 standard; DNA; 848 BP.  
DE Secreted protein extended EST coding sequence #6.  
PN WO9940189-A2.  
PD 12-AUG-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 317  
ID AAX26672 standard; RNA; 848 BP.  
DE Extended cDNA derived from a 5' EST encoding a secreted protien.  
PN WO9906554-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 318  
ID AAX51777 standard; cDNA; 848 BP.  
DE Human secreted protein 5' EST clone 58-35-2-F10-FL2.  
PN WO9906552-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 319  
ID AAX88191 standard; cDNA; 848 BP.

DE Human secreted protein 6 extended cDNA.  
PN WO9925825-A2.  
PD 27-MAY-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 320  
ID AAX51449 standard; DNA; 848 BP.  
DE Human secreted protein 5' EST SEQ ID NO: 27.  
PN WO9906549-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 321  
ID AAX40428 standard; cDNA; 848 BP.  
DE Extended cDNA derived from 5' EST.  
PN WO9906550-A2.  
PD 11-FEB-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 322  
ID AAX42251 standard; cDNA; 848 BP.  
DE Human full length cDNA 58-35-2-F10-FL2.  
PN WO9953051-A2.  
PD 21-OCT-1999.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 323  
ID AAC00012 standard; cDNA; 848 BP.  
DE Human secreted protein cDNA sequence #3.  
PN EF1033401-A2.  
PD 06-SEP-2000.  
PA (GEST) GENSET.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 324  
ID ADJ45874 standard; cDNA; 848 BP.  
DE Novel human secreted protein-related cDNA sequence SeqID27.  
PN US2003144490-A1.  
PD 31-JUL-2003.  
PA (EDNA/) EDWARDS J D M.  
PA (DUCL/) DUCLEF A.  
PA (BOUG/) BOUGUELERET L.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 325  
ID ADM7746 standard; cDNA; 848 BP.  
DE EST encoding signal sequence #6.  
PN US2003162176-A1.  
PD 28-AUG-2003.  
PA (EDNA/) EDWARDS J D M.  
PA (DUCL/) DUCLEF A.  
PA (BOUG/) BOUGUELERET L.  
Best Local Similarity: 97.65% Mismatches: 4  
Query Match: 96.55% Indels: 1  
RESULT 326  
ID AAX97957 standard; DNA; 1356 BP.  
DE Human secreted protein gene 42.  
PN WO9931117-A1.  
PD 24-JUN-1999.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 99.06% Mismatches: 1  
Query Match: 96.37% Indels: 2  
RESULT 327  
ID ADA40381 standard; cDNA; 1356 BP.  
DE Human secreted protein encoding cDNA.  
PN WO2002102993-A2.  
PD 27-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 99.06% Mismatches: 1

Query Match:	96.37%	Indels:	2
RESULT 328			
ID ADA11594 standard; DNA; 1356 BP.			
DE Human cDNA encoding a novel secreted protein, SEQ ID NO 122.			
PN US2003055236-A1.			
PD 20-MAR-2003.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity: 99.06%		Mismatches:	1
Query Match:	96.37%	Indels:	2
RESULT 329			
ID ADD37752 standard; cDNA; 1356 BP.			
DE Human secreted protein encoding sequence #234.			
PN WO200290526-A2.			
PD 14-NOV-2002.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity: 99.06%		Mismatches:	1
Query Match:	96.37%	Indels:	2
RESULT 330			
ID ADA56545 standard; DNA; 1356 BP.			
DE Gene encoding human secreted protein #269.			
PN WO2002102994-A2.			
PD 27-DEC-2002.			
PA (HUMA-) HUMAN GENOME SCI INC.			
Best Local Similarity: 99.06%		Mismatches:	1
Query Match:	96.37%	Indels:	2
RESULT 331			
ID AAX30083 standard; cDNA; 847 BP.			
DE Human secreted protein 5' EST SEQ ID NO:27.			
PN WO9906548-A2.			
PD 11-FEB-1999.			
PA (GEST ) GENSET.			
Best Local Similarity: 97.18%		Mismatches:	5
Query Match:	95.83%	Indels:	1
RESULT 332			
ID ADO07092 standard; cDNA; 774 BP.			
DE Human protein modification and maintenance molecule 26 (PMOM-26) cDNA.			
PN WO2004033636-A2.			
PD 22-APR-2004.			
PA (INCY-) INCYTE CORP.			
Best Local Similarity: 87.19%		Mismatches:	1
Query Match:	94.46%	Indels:	31
RESULT 333			
ID ABT42042 standard; DNA; 1181 BP.			
DE Toxicity modelling related rat gene SEQ ID NO 1744.			
PN WO200295000-A2.			
PD 28-NOV-2002.			
PA (GENE-) GENE LOGIC INC.			
Best Local Similarity: 83.57%		Mismatches:	21
Query Match:	83.85%	Indels:	1
RESULT 334			
ID AAX40832 standard; cDNA; 439 BP.			
DE Human secreted protein 5' EST SEQ ID NO: 44.			
PN WO9906554-A2.			
PD 11-FEB-1999.			
PA (GEST ) GENSET.			
Best Local Similarity: 100.00%		Mismatches:	0
Query Match:	62.98%	Indels:	0
RESULT 335			
ID AAV86301 standard; cDNA; 462 BP.			
DE EST clone AM42.			
PN WO9845435-A2.			
PD 15-OCT-1998.			
PA (GEMY ) GENETICS INST INC.			
Best Local Similarity: 94.89%		Mismatches:	4
Query Match:	61.16%	Indels:	0
RESULT 336			
ID ABS69507 standard; DNA; 532 BP.			
DE Novel murine polynucleotide isolated using gene trap technology #570.			
PN US2002102543-A1.			
PD 01-AUG-2002.			
PA (FRIE/) FRIEDRICH G.			
PA (ZAMB/) ZAMBROWICZ B.			
PA (SAND/) SANDS A T.			

  

Best Local Similarity: 83.70%	Mismatches:	16	
Query Match:	Indels:	0	
RESULT 337			
ID ADN43035 standard; cDNA; 379 BP.			
DE Human secreted protein SECP-21 cDNA.			
PN WO2004037987-A2.			
PD 08-MAY-2004.			
PA (INCY-) INCYTE CORP.			
Best Local Similarity: 51.17%	Mismatches:	0	
Query Match:	Indels:	104	
RESULT 338			
ID ABL78658 standard; cDNA; 355 BP.			
DE Human ovarian cancer related cDNA clone SEQ ID NO:1636.			
PN WO200192581-A2.			
PD 06-DEC-2001.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 81.51%	Mismatches:	10	
Query Match:	Indels:	4	
RESULT 339			
ID ADL95396 standard; cDNA; 2415 BP.			
DE Angiotensin converting enzyme-2 (ACE-2) coding sequence.			
PN US6610497-B1.			
PD 26-AUG-2003.			
PA (MILL-) MILLENNIUM PHARM INC.			
Best Local Similarity: 47.88%	Mismatches:	48	
Query Match:	Indels:	6	
RESULT 340			
ID AAZ59465 standard; DNA; 2418 BP.			
DE Human MPROT15 coding sequence #1.			
PN JPI1318472-A.			
PD 24-NOV-1999.			
PA (SMIK ) SMITHKLINE BEECHAM PLC.			
Best Local Similarity: 47.88%	Mismatches:	48	
Query Match:	Indels:	6	
RESULT 341			
ID ACN43792 standard; cDNA; 3064 BP.			
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2667.			
PN WO2004023973-A2.			
PD 25-MAR-2004.			
PA (INCY-) INCYTE CORP.			
Best Local Similarity: 47.88%	Mismatches:	48	
Query Match:	Indels:	6	
RESULT 342			
ID ACH03967 standard; cDNA; 3324 BP.			
DE Human cDNA differentially expressed in lung cancer #172.			
PN US2003065157-A1.			
PD 03-APR-2003.			
PA (LASE/) LASEK A W.			
Best Local Similarity: 47.88%	Mismatches:	48	
Query Match:	Indels:	6	
RESULT 343			
ID ADC38727 standard; cDNA; 3325 BP.			
DE Human cDNA encoding a secreted protein #41.			
PN US2002193567-A1.			
PD 19-DEC-2002.			
PA (GEMY ) GENETICS INST INC.			
Best Local Similarity: 47.88%	Mismatches:	48	
Query Match:	Indels:	6	
RESULT 344			
ID AAC84366 standard; cDNA; 3334 BP.			
DE Human Zace2 protein encoding cDNA.			
PN WO200070032-A1.			
PD 23-NOV-2000.			
PA (ZYMO ) ZYMOGENETICS INC.			
Best Local Similarity: 47.88%	Mismatches:	48	
Query Match:	Indels:	6	
RESULT 345			
ID ASX93333 standard; cDNA; 3334 BP.			
DE cDNA encoding human zinc metalloproteinase Zace2.			
PN US2002177211-A1.			
PD 28-NOV-2002.			
PA (ZYMO ) ZYMOGENETICS INC.			
Best Local Similarity: 47.88%	Mismatches:	48	

Query Match: 34.12% Indels: 6  
RESULT 346  
ID AAA12764 standard; cDNA; 3396 BP.  
DE cDNA encoding a human angiotensin converting enzyme-2 (ACE-2).  
PN WO200018899-A2.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 47.88% Mismatches: 48  
Query Match: 34.12% Indels: 6  
RESULT 347  
ID AAD02758 standard; cDNA; 3396 BP.  
DE Human angiotensin converting enzyme-2 (ACE-2) cDNA.  
PN US6194556-B1.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 47.88% Mismatches: 48  
Query Match: 34.12% Indels: 6  
RESULT 348  
ID AAD32586 standard; cDNA; 3396 BP.  
DE Human ACE-2 full-length cDNA.  
PN WO200212471-A2.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 47.88% Mismatches: 48  
Query Match: 34.12% Indels: 6  
RESULT 349  
ID ABK87623 standard; cDNA; 3396 BP.  
DE cDNA encoding human angiotensin converting enzyme-2 (ACE-2) protein.  
PN WO200239997-A2.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 47.88% Mismatches: 48  
Query Match: 34.12% Indels: 6  
RESULT 350  
ID ADA03343 standard; DNA; 3396 BP.  
DE Human angiotensin converting enzyme 2-like protein gene.  
PN WO200298448-A1.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 47.88% Mismatches: 48  
Query Match: 34.12% Indels: 6  
RESULT 351  
ID ACC79022 standard; cDNA; 3396 BP.  
DE Human ACE-2 protein encoding cDNA SEQ ID NO:141.  
PN WO200298906-A1.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 47.88% Mismatches: 48  
Query Match: 34.12% Indels: 6  
RESULT 352  
ID ADL95394 standard; cDNA; 3396 BP.  
DE Human angiotensin converting enzyme-2 (ACE-2) cDNA.  
PN US6610497-B1.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 47.88% Mismatches: 48  
Query Match: 34.12% Indels: 6  
RESULT 353  
ID ADH51356 standard; DNA; 3404 BP.  
DE Human angiotensin-converting enzyme homologue ACE2 DNA.  
PN WO2004000367-A1.  
PA (UYHE-) UNIV HEALTH NETWORK.  
Best Local Similarity: 47.88% Mismatches: 48  
Query Match: 34.12% Indels: 6  
RESULT 354  
ID ABS60632 standard; cDNA; 3405 BP.  
DE Human cDNA encoding angiotensin converting enzyme 2 variant #1.  
PN WO200261131-A2.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.

Best Local Similarity: 47.88% Mismatches: 48  
Query Match: 34.12% Indels: 6  
RESULT 355  
ID ABS60371 standard; cDNA; 3405 BP.  
DE Human cDNA encoding angiotensin converting enzyme 2.  
PN WO200261131-A2.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO.  
PA (TSUC/) TSUCHIHASHI Z.  
PA (HUIL/) HUI L.  
Best Local Similarity: 47.88% Mismatches: 48  
Query Match: 34.12% Indels: 6  
RESULT 356  
ID AAS21279 standard; cDNA; 3732 BP.  
DE Human cDNA sequence encoding for PRO1885 polypeptide.  
PN WO200140466-A2.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 357  
ID ACA03638 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003036180-A1.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 358  
ID ABX89176 standard; cDNA; 3732 BP.  
DE DNA encoding novel secreted and transmembrane protein PRO1885.  
PN US2003017563-A1.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 359  
ID ACD41830 standard; cDNA; 3732 BP.  
DE Human secreted/transmembrane protein (PRO) cDNA #36.  
PN US2003036179-A1.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 360  
ID ACA04059 standard; cDNA; 3732 BP.  
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 71.  
PN US2003032155-A1.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 361  
ID ADA45590 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003022328-A1.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 362  
ID ADA76021 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003073212-A1.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 363  
ID ADA18671 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003054517-A1.  
PA (HUIL/) HUI L.

PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 364					
ID ADA61294 standard; cDNA; 3732 BP.					
DE Homo sapiens.					
PN US2003049816-A1.					
PD 13-MAR-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 365					
ID ADB19079 standard; cDNA; 3732 BP.					
DE Novel human secreted and transmembrane protein PRO1885 cDNA.					
PN US2003068796-A1.					
PD 10-APR-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 366					
ID ADB27620 standard; cDNA; 3732 BP.					
DE cDNA encoding human PRO polypeptide #36.					
PN US2003082704-A1.					
PD 01-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 367					
ID ADA86099 standard; cDNA; 3732 BP.					
DE Novel human secreted and transmembrane protein PRO1885 cDNA.					
PN US2003082711-A1.					
PD 01-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 368					
ID ADB15663 standard; cDNA; 3732 BP.					
DE Human PRO polynucleotide #36.					
PN US2003087350-A1.					
PD 08-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 369					
ID ADA47449 standard; cDNA; 3732 BP.					
DE Human PRO polynucleotide #36.					
PN US2003073215-A1.					
PD 17-APR-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 370					
ID ADA67244 standard; cDNA; 3732 BP.					
DE Human PRO polynucleotide #36.					
PN US2003068795-A1.					
PD 10-APR-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 371					
ID ADB30251 standard; cDNA; 3732 BP.					
DE cDNA encoding human PRO polypeptide #36.					
PN US2003068794-A1.					
PD 10-APR-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 372					
ID ADA85547 standard; cDNA; 3732 BP.					
DE Novel human secreted and transmembrane protein PRO1885 cDNA.					
PN US2003082693-A1.					
PD 01-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 373					
ID ADA96759 standard; cDNA; 3732 BP.					
DE Human PRO polynucleotide #36.					
PN US2003082705-A1.					
PD 01-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 374					
ID ADA79063 standard; cDNA; 3732 BP.					
DE Human PRO polynucleotide #36.					
PN US2003082763-A1.					
PD 01-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 375					
ID ADA87202 standard; cDNA; 3732 BP.					
DE Novel human secreted and transmembrane protein PRO1885 cDNA.					
PN US2003087345-A1.					
PD 08-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 376					
ID ADB16404 standard; cDNA; 3732 BP.					
DE Human PRO polynucleotide #36.					
PN US2003087349-A1.					
PD 08-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 377					
ID ADA91496 standard; cDNA; 3732 BP.					
DE Novel human secreted and transmembrane protein PRO1885 cDNA.					
PN US2003082694-A1.					
PD 01-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 378					
ID ADB14559 standard; cDNA; 3732 BP.					
DE Human PRO polynucleotide #36.					
PN US2003087351-A1.					
PD 08-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 379					
ID ADB18520 standard; cDNA; 3732 BP.					
DE Novel human secreted and transmembrane protein PRO1885 cDNA.					
PN US2003073211-A1.					
PD 17-APR-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 380					
ID ADA93735 standard; cDNA; 3732 BP.					
DE Human PRO polynucleotide #36.					
PN US2003077722-A1.					
PD 24-APR-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 381					
ID ADB19631 standard; cDNA; 3732 BP.					
DE Novel human secreted and transmembrane protein PRO1885 cDNA.					
PN US2003082691-A1.					
PD 01-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	
RESULT 382					
ID ADA85547 standard; cDNA; 3732 BP.					
DE Novel human secreted and transmembrane protein PRO1885 cDNA.					
PN US2003082693-A1.					
PD 01-MAY-2003.					
PA (GETH ) GENENTECH INC.					
Best Local Similarity: 45.40%				Mismatches: 50	
Query Match: 33.48%				Indels: 12	

Query Match: 33.48% Indels: 12  
RESULT 382  
ID ADB12943 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 383  
ID ACD98459 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003044945-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 384  
ID ADA74197 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003086798-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 385  
ID ADB24430 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide SEQ ID NO 71.  
PN US2003077113-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 386  
ID ADA81954 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082701-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 387  
ID ADA74917 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003073216-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 388  
ID ADA84995 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082695-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 389  
ID ADA84443 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082708-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 390  
ID ADB29699 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003073214-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 391  
ID ADA80227 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082761-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 392  
ID ADA75469 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082703-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 393  
ID ADA46694 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003073210-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 394  
ID ADB24990 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide SEQ ID NO 71.  
PN US2003077115-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 395  
ID ADA93166 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US200307721-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 396  
ID ADB26516 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003092147-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 397  
ID ADB30803 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003096386-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 398  
ID ADA60731 standard; cDNA; 3732 BP.  
DE Homo sapiens.  
PN US2003049817-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 399  
ID ADB23878 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide SEQ ID NO 71.  
PN US2003077114-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 400  
ID ADB23878 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide SEQ ID NO 71.  
PN US2003077114-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

ID ADA96207 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082690-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 401  
ID ADA80779 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082702-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 402  
ID ADA95655 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082759-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 403  
ID ADB25964 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003082760-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 404  
ID ADB21449 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082765-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 405  
ID ADA77228 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003068797-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 406  
ID ADB17968 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003077710-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 407  
ID ADA86651 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082709-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 408  
ID ADA87754 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003082700-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 409  
ID ADA46142 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003054516-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 410  
ID ADB28172 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003082699-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 411  
ID ADB28724 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003082706-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 412  
ID ADA76676 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003059909-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 413  
ID ADA88306 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003073213-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 414  
ID ADA97311 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003082686-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 415  
ID ADB27068 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003022239-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 416  
ID ADB22001 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087344-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 417  
ID ADA66692 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003068793-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 418  
ID ADB22553 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003077711-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 419  
ID ADA46142 standard; cDNA; 3732 BP.

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PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 419
ID ADB23326 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077112-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 420
ID ADA92048 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 421
ID ADB15111 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 422
ID ADB38363 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 423
ID ADB37811 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 424
ID ADB66283 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 425
ID ADB89363 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 426
ID ADB90095 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 427
ID ADB39196 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 428
ID ADB46819 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 429
ID ADB86426 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 430
ID ADB77031 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 431
ID ADB34188 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077117-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 432
ID ADB35292 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077119-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 433
ID ADB33636 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077116-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 434
ID ADB34740 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US2003077118-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 435
ID ADB35844 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide SEQ ID NO 71.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 436
ID ADB46239 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
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Query Match: 33.48% Indels: 12  
RESULT 437  
ID ADC50112 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 438  
ID ADC71659 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 439  
ID ADC59638 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 440  
ID ADC52645 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID71.  
PN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 441  
ID ADC66999 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID71.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 442  
ID ADC60190 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 443  
ID ADC50665 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 444  
ID ADC65192 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 445  
ID ADC54290 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID71.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 446  
ID ADC53251 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID71.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 447  
ID ADC58774 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID71.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 448  
ID ADC55652 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID71.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 449  
ID ADC58222 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein cDNA Seq ID71.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 450  
ID ADD02896 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 451  
ID ADC89888 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 452  
ID ADC69307 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 453  
ID ADC48196 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 454  
ID ADD09725 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 455  
ID ADC50112 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

ID ADD04300 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 456  
ID ADC80256 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 457  
ID ADD10763 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 458  
ID ADC47644 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 459  
ID ADC75704 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 460  
ID ADD09173 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003194775-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 461  
ID ADD40886 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 462  
ID ADD52025 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 463  
ID ADD52765 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 464  
ID ADD53317 standard; cDNA; 3732 BP.

DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 465  
ID ADD51473 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 466  
ID ADD02272 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 467  
ID ADD01706 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 468  
ID ADD53888 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 469  
ID ADD92205 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 470  
ID ADD91101 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 471  
ID ADE03715 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 472  
ID ADE32012 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 473  
ID ADE21944 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.

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PN US2003199056-A1.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 474
ID ADD79168 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 475
ID ADE41704 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 476
ID ADE17521 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 477
ID ADD91653 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 478
ID ADE33116 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 479
ID ADE33668 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 480
ID ADD79720 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 481
ID ADD92757 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 482
ID ADE19177 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 483
ID ADE18625 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 484
ID ADE42821 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 485
ID ADD95610 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 486
ID ADE22496 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 487
ID ADD78614 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 488
ID ADE32564 standard; cDNA; 3732 BP.
DE Novel human secreted and transmembrane protein PRO1885 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 489
ID ADE42256 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 490
ID ADD80272 standard; cDNA; 3732 BP.
DE cDNA encoding human PRO polypeptide #36.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Best Local Similarity: 45.40% Mismatches: 50
Query Match: 33.48% Indels: 12
RESULT 491
ID ADD89300 standard; cDNA; 3732 BP.
DE Human PRO polynucleotide #36.
PN US2003199028-A1.
PD 23-OCT-2003.
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PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 492  
ID ADE40584 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 493  
ID ADE04383 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 494  
ID ADE92512 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 495  
ID ADG21221 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 496  
ID ADG22862 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 497  
ID ADF97197 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 498  
ID ADG80261 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 499  
ID ADG79709 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 500  
ID ADH55001 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 501  
ID ADH55553 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 502  
ID ADI64721 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 503  
ID ADH81634 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 504  
ID ADH81082 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 505  
ID ACD3888 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 506  
ID ACA67029 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003004311-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 507  
ID ADM82251 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 508  
ID ADNI5650 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 509  
ID ADNI6279 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50

Query Match: 33.48% Indels: 12  
RESULT 510  
ID ADN15098 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 511  
ID ADN14546 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 512  
ID ADI63772 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 513  
ID ADI63220 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 514  
ID ADC80808 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 515  
ID ADD76256 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 516  
ID ADD87620 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 517  
ID ADD86024 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 518  
ID ADE75472 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12

RESULT 519  
ID ADE23048 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 520  
ID ADE23600 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 521  
ID ADE24243 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 522  
ID ADD87068 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 523  
ID ADE88934 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 524  
ID ADE18073 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 525  
ID ADE88382 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 526  
ID ADE94402 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 527  
ID ADE90813 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 528

ID ADE94954 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 529  
ID ADE91064 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 530  
ID ADF34645 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 531  
ID ADE91960 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 532  
ID ADE90261 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 533  
ID ADE91408 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003199058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 534  
ID ADG01987 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 535  
ID ADG21773 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 536  
ID ADG19843 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 537  
ID ADF97749 standard; cDNA; 3732 BP.

DE Human PRO polynucleotide #36.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 538  
ID ADG23966 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 539  
ID ADF98320 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 540  
ID ADG03151 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 541  
ID ADF98872 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 542  
ID ADG16457 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 543  
ID ADG04916 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 544  
ID ADG19183 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 545  
ID ADG13020 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 546  
ID ADG08077 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.

PN US2003207424-A1.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 547  
ID ADG15247 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 548  
ID ADF96645 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 549  
ID ADG05830 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 550  
ID ADG23414 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 551  
ID ADG03703 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 552  
ID ADG24604 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 553  
ID ADG06901 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 554  
ID ADG07453 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 555  
ID ADG54948 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003194778-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 556  
ID ADG60612 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 557  
ID ADG61716 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 558  
ID ADG81917 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 559  
ID ADG57156 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 560  
ID ADG56604 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 561  
ID ADG55500 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 562  
ID ADG58260 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 563  
ID ADG70626 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 564  
ID ADG57708 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207363-A1.  
PD 06-NOV-2003.





RESULT 583  
ID AD114406 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207383-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 584  
ID AD118001 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207349-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 585  
ID ADJ63282 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 586  
ID ADJ77177 standard; cDNA; 3732 BP.  
DE Human PRO polynucleotide #36.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 587  
ID ADJ65299 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 588  
ID ADM27435 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 589  
ID ADM42159 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 590  
ID ADM28021 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 591  
ID ADI95503 standard; cDNA; 3732 BP.  
DE cDNA encoding human PRO polypeptide #36.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 592

ID ADI96055 standard; cDNA; 3732 BP.  
DE Novel human secreted and transmembrane protein PRO1885 cDNA.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 45.40% Mismatches: 50  
Query Match: 33.48% Indels: 12  
RESULT 593  
ID AAC84368 standard; cDNA; 2638 BP.  
DE Mouse Zace2-5 protein encoding cDNA.  
PN WO200070032-A1.  
PD 23-NOV-2000.  
PA (ZYMO ) ZYMOGENETICS INC.  
Best Local Similarity: 40.91% Mismatches: 52  
Query Match: 32.76% Indels: 30  
RESULT 594  
ID AAC84370 standard; cDNA; 2638 BP.  
DE Mouse Zace2-10 protein encoding cDNA.  
PN WO200070032-A1.  
PD 23-NOV-2000.  
PA (ZYMO ) ZYMOGENETICS INC.  
Best Local Similarity: 40.91% Mismatches: 52  
Query Match: 32.76% Indels: 30  
RESULT 595  
ID ABX93337 standard; cDNA; 2638 BP.  
DE cDNA encoding mouse zinc metalloproteinase mZace-10.  
PN US2002177211-A1.  
PD 28-NOV-2002.  
PA (ZYMO ) ZYMOGENETICS INC.  
Best Local Similarity: 40.91% Mismatches: 52  
Query Match: 32.76% Indels: 30  
RESULT 596  
ID ABX93335 standard; cDNA; 2638 BP.  
DE cDNA encoding mouse zinc metalloproteinase mZace-5.  
PN US2002177211-A1.  
PD 28-NOV-2002.  
PA (ZYMO ) ZYMOGENETICS INC.  
Best Local Similarity: 40.91% Mismatches: 52  
Query Match: 32.76% Indels: 30  
RESULT 597  
ID ADH51358 standard; DNA; 2739 BP.  
DE Mouse angiotensin-converting enzyme homologue ACE2 DNA.  
PN WO2004000367-A1.  
PD 31-DEC-2003.  
PA (UYHE-) UNIV HEALTH NETWORK.  
Best Local Similarity: 40.91% Mismatches: 52  
Query Match: 32.76% Indels: 30  
RESULT 598  
ID AAS14890 standard; cDNA; 2911 BP.  
DE Human cDNA encoding novel human protein NHP #11.  
PN WO200174896-A1.  
PD 11-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 47.17% Mismatches: 46  
Query Match: 32.58% Indels: 6  
RESULT 599  
ID AAS14880 standard; cDNA; 2920 BP.  
DE Human cDNA encoding novel human protein NHP #1.  
PN WO200174896-A1.  
PD 11-OCT-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 47.17% Mismatches: 46  
Query Match: 32.58% Indels: 6  
RESULT 600  
ID ADA03339 standard; DNA; 2920 BP.  
DE Human angiotensin converting enzyme 2 gene.  
PN WO200298448-A1.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 47.17% Mismatches: 46  
Query Match: 32.58% Indels: 6  
RESULT 601  
ID ACC79021 standard; cDNA; 2920 BP.

DE Human ACE-2 protein encoding cDNA SEQ ID NO:137.  
PN WO200298906-A1.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 47.17% Mismatches: 46  
Query Match: 32.58% Indels: 6  
RESULT 602  
ID ABA71751 standard; DNA; 213 BP.  
DE Human foetal liver single exon nucleic acid probe #20056.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 30.40% Indels: 0  
RESULT 603  
ID RA152077 standard; DNA; 213 BP.  
DE Probe #20763 used to measure gene expression in human placenta sample.  
PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 30.40% Indels: 0  
RESULT 604  
ID ABA37840 standard; DNA; 213 BP.  
DE Probe #16306 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 30.40% Indels: 0  
RESULT 605  
ID AAK46169 standard; DNA; 213 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 20726.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 30.40% Indels: 0  
RESULT 606  
ID AAK20115 standard; DNA; 213 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 20106.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 30.40% Indels: 0  
RESULT 607  
ID ABS45886 standard; DNA; 213 BP.  
DE Human liver single exon probe, SEQ ID No 20876.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 30.40% Indels: 0  
RESULT 608  
ID ABS20478 standard; DNA; 213 BP.  
DE Human genome-derived single exon probe ORF from lung SEQ ID No 20469.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 30.40% Indels: 0  
RESULT 609  
ID ABA59231 standard; DNA; 464 BP.  
DE Human foetal liver single exon nucleic acid probe #7536.  
PN WO200157277-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 29.40% Indels: 0  
RESULT 610  
ID RA139012 standard; DNA; 464 BP.  
DE Probe #7698 used to measure gene expression in human placenta sample.

PN WO200157272-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 29.40% Indels: 0  
RESULT 611  
ID ABA27979 standard; DNA; 464 BP.  
DE Probe #6445 for gene expression analysis in human heart cell sample.  
PN WO200157274-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 29.40% Indels: 0  
RESULT 612  
ID AAK33216 standard; DNA; 464 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 7773.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 29.40% Indels: 0  
RESULT 613  
ID AAK07438 standard; DNA; 464 BP.  
DE Human brain expressed single exon probe SEQ ID NO: 7429.  
PN WO200157275-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 29.40% Indels: 0  
RESULT 614  
ID ABS32964 standard; DNA; 464 BP.  
DE Human liver single exon probe, SEQ ID No 7954.  
PN WO200157273-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 29.40% Indels: 0  
RESULT 615  
ID ABS08046 standard; DNA; 464 BP.  
DE Human genome-derived single exon probe from lung SEQ ID No 8037.  
PN WO200186003-A2.  
PD 15-NOV-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 29.40% Indels: 0  
RESULT 616  
ID ACN43791 standard; cDNA; 3072 BP.  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:2666.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 40.00% Mismatches: 40  
Query Match: 25.77% Indels: 31  
RESULT 617  
ID AAC66136 standard; DNA; 862 BP.  
DE Human kidney disease associated gene SEQ ID 6.  
PN WO200061622-A2.  
PD 19-OCT-2000.  
PA (INCY-) INCYTE PHARM INC.  
Best Local Similarity: 98.28% Mismatches: 0  
Query Match: 25.50% Indels: 1  
RESULT 618  
ID AAC84367 standard; DNA; 2415 BP.  
DE Human Zace2 protein encoding degenerate sequence.  
PN WO200070032-A1.  
PD 23-NOV-2000.  
PA (ZYMO) ZYMOGENETICS INC.  
Best Local Similarity: 39.88% Mismatches: 70  
Query Match: 25.23% Indels: 8  
RESULT 619  
ID ABX93334 standard; DNA; 2415 BP.  
DE Degenerate DNA sequence encoding human zinc metalloproteinase Zace2.  
PN US2002177211-A1.

PD 28-NOV-2002.	PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.		
Best Local Similarity: 39.88%	Best Local Similarity: 56.67%	Mismatches: 6	
Query Match: 25.23%	Query Match: 8.89%	Indels: 0	
RESULT 620	RESULT 629		
ID AAZ59466 standard; DNA; 2262 BP.	ID ABA18993 standard; DNA; 4069 BP.		
DE Human MPROT15 coding sequence #2.	DE Human nervous system related polynucleotide SEQ ID NO 11324.		
PN JP11318472-A.	PN WO200159063-A2.		
PD 24-NOV-1999.	PD 16-AUG-2001.		
PA (SMIK ) SMITHKLINE BEECHAM PLC.	PA (HUMA-) HUMAN GENOME SCI INC.		
Best Local Similarity: 35.91%	Best Local Similarity: 24.77%	Mismatches: 87	
Query Match: 23.77%	Query Match: 8.53%	Indels: 42	
RESULT 621	RESULT 630		
ID ABQ57861 standard; cDNA; 561 BP.	ID ABL55857 standard; DNA; 34337 BP.		
DE Human colon cancer related nucleotide sequence SEQ ID NO:1556.	DE Human GABA transporter protein gene.		
PN WO200229086-A2.	PN US2002031800-A1.		
PD 11-APR-2002.	PD 14-MAR-2002.		
PA (FARB ) BAYER CORP.	PA (LIZZ/) LI Z.		
Best Local Similarity: 23.73%	PA (CHAT/) CHATURVEDI K.		
Query Match: 23.73%	PA (ZHUS/) ZHU S.		
RESULT 622	PA (WOOD/) WOODAGE T.		
ID AAC84369 standard; DNA; 2415 BP.	PA (GUEG/) GUEGLER K.		
DE Mouse Zace2-5 protein encoding degenerate sequence.	PA (WEBS/) WEBSTER M.		
PN WO200070032-A1.	PA (DPRA/) DI FRANCESCO V.		
PD 23-NOV-2000.	PA (BEAS/) BEASLEY E M.		
PA (ZYMO ) ZYMOGENETICS INC.	Best Local Similarity: 24.77%	Mismatches: 87	
Best Local Similarity: 33.33%	Query Match: 8.53%	Indels: 42	
Query Match: 23.50%	RESULT 631		
RESULT 623	ID ADG88376 standard; DNA; 34337 BP.		
ID ABX93336 standard; DNA; 2415 BP.	DE Human transporter gene.		
DE Degenerate DNA sequence encoding mouse zinc metalloproteinase mZace-5.	PN US2003157649-A1.		
PN US2002177211-A1.	PD 21-AUG-2003.		
PA (ZYMO ) ZYMOGENETICS INC.	PA (APPL-) APPLERA CORP.		
Best Local Similarity: 33.33%	Best Local Similarity: 24.77%	Mismatches: 87	
Query Match: 23.50%	Query Match: 8.53%	Indels: 42	
RESULT 624	RESULT 632		
ID AAS42515 standard; cDNA; 3474 BP.	ID ABL28081 standard; DNA; 2790 BP.		
DE Human cDNA encoding an mddt protein, clone LI:347572.1:2000MAY01.	DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35716.		
PN WO200162922-A2.	PN WO200171042-A2.		
PD 30-AUG-2001.	PD 27-SEP-2001.		
PA (INCY-) INCYTE GENOMICS INC.	PA (PEKE ) PE CORP NY.		
Best Local Similarity: 42.39%	Best Local Similarity: 28.82%	Mismatches: 66	
Query Match: 21.60%	Query Match: 8.48%	Indels: 33	
RESULT 625	RESULT 633		
ID ABK30270 standard; cDNA; 2350 BP.	ID ADP24566 standard; cDNA; 3857 BP.		
DE Human G-protein-coupled protease #40.	DE PRO polypeptide encoding cDNA SEQ ID NO:1744.		
PN US631427-B1.	PN WO2004041170-A2.		
PD 18-DEC-2001.	PD 21-MAY-2004.		
PA (MILL-) MILLENNIUM PHARM INC.	PA (GETH ) GENENTECH INC.		
Best Local Similarity: 43.57%	Best Local Similarity: 21.32%	Mismatches: 64	
Query Match: 21.19%	Query Match: 8.44%	Indels: 54	
RESULT 626	RESULT 634		
ID ABS51330 standard; cDNA; 3666 BP.	ID ABL34973 standard; cDNA; 3134 BP.		
DE cDNA encoding human secretory protein #28.	DE Murine cDNA isolated from skin cells SEQ ID NO: 478.		
PN WO200257304-A2.	PN WO200190357-A1.		
PD 25-JUL-2002.	PD 29-NOV-2001.		
PA (INCY-) INCYTE GENOMICS INC.	PA (GENE-) GENESIS RES & DEV CORP LTD.		
Best Local Similarity: 29.76%	Best Local Similarity: 20.39%	Mismatches: 70	
Query Match: 9.66%	Query Match: 8.30%	Indels: 57	
RESULT 627	RESULT 635		
ID ABN36017 standard; DNA; 60 BP.	ID ABL34985 standard; cDNA; 3380 BP.		
DE Human spliced transcript detection oligonucleotide SEQ ID NO:8765.	DE Rat cDNA isolated from skin cells SEQ ID NO: 514.		
PN WO200210449-A2.	PN WO200190357-A1.		
PD 07-FEB-2002.	PD 29-NOV-2001.		
PA (COMP-) COMPUGEN INC.	PA (GENE-) GENESIS RES & DEV CORP LTD.		
Best Local Similarity: 100.00%	Best Local Similarity: 20.39%	Mismatches: 70	
Query Match: 9.26%	Query Match: 8.30%	Indels: 57	
RESULT 628	RESULT 636		
ID ADL45106 standard; DNA; 531 BP.	ID AAC91905 standard; cDNA; 3567 BP.		
DE Human ovarian cancer DNA marker #18996.	DE Murine A259 ORF.		
PN WO200170979-A2.	PN WO200073339-A1.		
PD 27-SEP-2001.	PD 07-DEC-2000.		
	PA (MILL-) MILLENNIUM PHARM INC.		
	Best Local Similarity: 20.49%	Mismatches: 70	

Query Match:	8.30%	Indels:	57	PA (DOHE-) DOHENY EYE INST.		Mismatches:	91
RESULT 637				Best Local Similarity:	21.40%	Indels:	66
ID AAC91904 standard; cDNA; 4858 BP.				Query Match:	8.17%		
DE Murine A259 coding sequence.				RESULT 647			
PN WO200073339-A1.				ID AAT61917 standard; cDNA; 3136 BP.			
PD 07-DEC-2000.				DE Full length rat cadherin-8 cDNA.			
PA (MILL-) MILLENNIUM PHARM INC.				PN US5597725-A.			
Best Local Similarity:	20.49%	Mismatches:	70	PD 28-JAN-1997.			
Query Match:	8.30%	Indels:	57	PA (DOHE-) DOHENY EYE INST.		Mismatches:	91
RESULT 638				Best Local Similarity:	21.40%	Indels:	66
ID AAS16874 standard; cDNA; 4858 BP.				Query Match:	8.17%		
DE Murine A259 cDNA.				RESULT 648			
PN WO200181414-A2.				ID ADP26917 standard; cDNA; 2545 BP.			
PD 01-NOV-2001.				DE Human cadherin 8 encoding cDNA SEQ ID NO:18.			
PA (MILL-) MILLENNIUM PHARM INC.				PN EP1428893-A2.			
Best Local Similarity:	20.49%	Mismatches:	70	PD 16-JUN-2004.			
Query Match:	8.30%	Indels:	57	PA (SPRE/) SPRECHER E.			
RESULT 639				PA (BERG/) BERGMAN R.			
ID ACA39448 standard; DNA; 2421 BP.				Best Local Similarity:	20.58%	Mismatches:	93
DE Prokaryotic essential gene #21105.				Query Match:	8.12%	Indels:	65
PN WO200271183-A2.				RESULT 649			
PD 03-OCT-2002.				ID AAT85402 standard; cDNA; 2550 BP.			
PA (ELIT-) ELITRA PHARM INC.				DE Human cadherin-8 coding sequence.			
Best Local Similarity:	27.46%	Mismatches:	60	PN US5646250-A.			
Query Match:	8.26%	Indels:	50	PD 08-JUL-1997.			
RESULT 640				PA (DOHE-) DOHENY EYE INST.		Mismatches:	93
ID ABL06502 standard; cDNA; 5149 BP.				Best Local Similarity:	20.58%	Indels:	65
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 13988.				Query Match:	8.12%		
PN WO200171042-A2.				RESULT 650			
PD 27-SEP-2001.				ID AAT61923 standard; cDNA; 2550 BP.			
PA (PEKE ) PE CORP NY.				DE Full length human cadherin-8 cDNA.			
Best Local Similarity:	17.80%	Mismatches:	83	PN US5597725-A.			
Query Match:	8.26%	Indels:	85	PD 28-JAN-1997.			
RESULT 641				PA (DOHE-) DOHENY EYE INST.		Mismatches:	93
ID AAD63505 standard; DNA; 38459 BP.				Best Local Similarity:	20.58%	Indels:	65
DE Mycoplasma genitalium gene involved in translation-part I.				Query Match:	8.12%		
PN US200313877-A1.				RESULT 651			
PD 24-JUL-2003.				ID AAI58397 standard; cDNA; 3146 BP.			
PA (EVAN/) EVANS G A.				DE Human polynucleotide SEQ ID NO 600.			
Best Local Similarity:	27.46%	Mismatches:	60	PN WO200153312-A1.			
Query Match:	8.26%	Indels:	50	PD 26-JUL-2001.			
RESULT 642				PA (HYSE-) HYSEQ INC.		Mismatches:	40
ID ACC69135 standard; DNA; 38459 BP.				Best Local Similarity:	20.24%	Indels:	59
DE M. genitalium translation part 1 gene cassette DNA SEQ ID NO:3.				Query Match:	8.12%		
PN WO2003025145-A2.				RESULT 652			
PD 27-MAR-2003.				ID ADQ8607 standard; cDNA; 3146 BP.			
PA (EGEA-) EGEA BIOSCIENCES INC.				DE DNA encoding human GPCR-like protein seqid 277.			
Best Local Similarity:	27.46%	Mismatches:	60	PN US6569662-B1.			
Query Match:	8.26%	Indels:	50	PD 27-MAY-2003.			
RESULT 643				PA (HYSE-) HYSEQ INC.		Mismatches:	40
ID ADN48940 standard; DNA; 38459 BP.				Best Local Similarity:	20.24%	Indels:	59
DE Mycoplasma genitalium functional gene fragment #3.				Query Match:	8.12%		
PN US2004063097-A1.				RESULT 653			
PD 01-APR-2004.				ID ADB48367 standard; cDNA; 3146 BP.			
PA (EVAN/) EVANS G A.				DE Novel human cDNA SEQ ID NO 277.			
Best Local Similarity:	27.46%	Mismatches:	60	PN US2003104529-A1.			
Query Match:	8.26%	Indels:	50	PD 05-JUN-2003.			
RESULT 644				PA (ZHOU/) ZHOU P.			
ID ADB52297 standard; DNA; 492 BP.				PA (TANG/) TANG Y T.			
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:2839.				PA (LIUC/) LIU C.			
PN WO2003065993-A2.				PA (ASUN/) ASUNDI V.			
PD 14-AUG-2003.				PA (DRMA/) DRMANAC R T.			
PA (GENE-) GENE LOGIC INC.				Best Local Similarity:	20.24%	Mismatches:	40
Best Local Similarity:	20.81%	Mismatches:	37	Query Match:	8.12%	Indels:	59
Query Match:	8.17%	Indels:	54	RESULT 654			
RESULT 646				ID ABL65914 standard; DNA; 3150 BP.			
ID AAR85406 standard; cDNA; 3136 BP.				DE Lung cancer related gene sequence SEQ ID NO:4251.			
DE Rat full length cadherin-8 coding sequence.				PN WO200194629-A2.			
PN US5646250-A.				PD 13-DEC-2001.			
PD 08-JUL-1997.				PA (AVAL-) AVALON PHARM.		Mismatches:	40
				Best Local Similarity:	20.24%	Indels:	59
				Query Match:	8.12%		
				RESULT 655			

ID ABL65987 standard; DNA; 3150 BP.  
DE Prostate cancer related gene sequence SEQ ID NO:7924.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Best Local Similarity: 20.24% Mismatches: 40  
Query Match: 8.12% Indels: 59  
RESULT 656  
ID ABL64453 standard; DNA; 3150 BP.  
DE Stomach cancer related gene sequence SEQ ID NO:2790.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Best Local Similarity: 20.24% Mismatches: 40  
Query Match: 8.12% Indels: 59  
RESULT 657  
ID AAI60183 standard; cDNA; 3196 BP.  
DE Human polynucleotide SEQ ID NO 4172.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 20.24% Mismatches: 40  
Query Match: 8.12% Indels: 59  
RESULT 658  
ID ABL6049 standard; DNA; 3617 BP.  
DE NOVX related polynucleotide SEQ ID No 65.  
PN WO200299062-A2.  
PD 12-DEC-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 20.24% Mismatches: 40  
Query Match: 8.12% Indels: 59  
RESULT 659  
ID ADO41699 standard; cDNA; 3617 BP.  
DE Novel human polypeptide NOV24b cDNA.  
PN US2004018555-A1.  
PD 29-JAN-2004.  
PA (ANDE/) ANDERSON D W.  
PA (ZERH/) ZERHUSEN B D.  
PA (LILL/) LI L.  
PA (ZHON/) ZHONG M.  
PA (CASM/) CASMAN S J.  
PA (GERL/) GERLACH V.  
PA (SHIM/) SHIMKETS R A.  
PA (GORM/) GORMAN L.  
PA (PENA/) PENA C E A.  
PA (KEKU/) KEKUDA R.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (LEIT/) LEITE M W.  
PA (RAST/) RASTELLI L.  
PA (MACD/) MACDOUGALL J R.  
PA (TAUP/) TAUPIER R J.  
PA (GUOX/) GUO X S.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (HJAL/) HJALT T.  
PA (VOSS/) VOSS E Z.  
PA (BOLD/) BOLDOG F L.  
PA (MALY/) MALYANKAR U M.  
PA (PADI/) PADIGARU M.  
PA (JIWV/) JI W.  
PA (SMIT/) SMITHSON G.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLET I.  
PA (ELLE/) ELLERMAN K.  
Best Local Similarity: 20.24% Mismatches: 40  
Query Match: 8.12% Indels: 59  
RESULT 660  
ID AAD33323 standard; cDNA; 3868 BP.  
DE Human INTG-1 protein encoding cDNA.  
PN WO200212339-A2.  
PD 14-FEB-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 20.24% Mismatches: 40  
Query Match: 8.12% Indels: 59  
RESULT 661  
ID ADG42064 standard; DNA; 2929 BP.  
DE Human CDH8 nucleic acid sequence.  
PN WO2003087408-A2.  
PD 23-OCT-2003.  
PA (UYED-) UNIV EDINBURGH.  
Best Local Similarity: 21.40% Mismatches: 91  
Query Match: 8.08% Indels: 66  
RESULT 662  
ID ADR41320 standard; cDNA; 5427 BP.  
DE Human CD-like molecule HFOYM21 cDNA, SEQ ID NO:119.  
PN WO200226930-A2.  
PD 04-APR-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 22.78% Mismatches: 68  
Query Match: 8.08% Indels: 36  
RESULT 663  
ID ABL6048 standard; DNA; 3617 BP.  
DE NOVX related polynucleotide SEQ ID No 63.  
PN WO200299062-A2.  
PD 12-DEC-2002.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 20.24% Mismatches: 40  
Query Match: 8.03% Indels: 59  
RESULT 664  
ID ADO41697 standard; cDNA; 3617 BP.  
DE Novel human polypeptide NOV24a cDNA.  
PN US2004018555-A1.  
PD 29-JAN-2004.  
PA (ANDE/) ANDERSON D W.  
PA (ZERH/) ZERHUSEN B D.  
PA (LILL/) LI L.  
PA (ZHON/) ZHONG M.  
PA (CASM/) CASMAN S J.  
PA (GERL/) GERLACH V.  
PA (SHIM/) SHIMKETS R A.  
PA (GORM/) GORMAN L.  
PA (PENA/) PENA C E A.  
PA (KEKU/) KEKUDA R.  
PA (PATT/) PATTURAJAN M.  
PA (SPYT/) SPYTEK K A.  
PA (LEIT/) LEITE M W.  
PA (RAST/) RASTELLI L.  
PA (MACD/) MACDOUGALL J R.  
PA (TAUP/) TAUPIER R J.  
PA (GUOX/) GUO X S.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (HJAL/) HJALT T.  
PA (VOSS/) VOSS E Z.  
PA (BOLD/) BOLDOG F L.  
PA (MALY/) MALYANKAR U M.  
PA (PADI/) PADIGARU M.  
PA (JIWV/) JI W.  
PA (SMIT/) SMITHSON G.  
PA (EDIN/) EDINGER S R.  
PA (MILL/) MILLET I.  
PA (ELLE/) ELLERMAN K.  
Best Local Similarity: 20.24% Mismatches: 40  
Query Match: 8.03% Indels: 59  
RESULT 665  
ID AAC86870 standard; cDNA; 3983 BP.  
DE DNA encoding a human alpha11 integrin chain.  
PN WO200075187-A1.  
PD 14-DEC-2000.  
PA (ACTI-) ACTIVE BIOTECH AB.  
Best Local Similarity: 22.60% Mismatches: 54  
Query Match: 8.03% Indels: 47  
RESULT 666  
ID ABN86522 standard; cDNA; 1177 BP.  
DE Nucleotide sequence of mouse CD44 cDNA.

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PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 21.62% Mismatches: 30
Query Match: 7.99% Indels: 34
RESULT 667
ID ABL06503 standard; cDNA; 2908 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 13991.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE ) PE CORP NY.
Best Local Similarity: 18.32% Mismatches: 77
Query Match: 7.94% Indels: 100
RESULT 668
ID ABL06523 standard; cDNA; 1089 BP.
DE Nucleotide sequence of hamster CD44 cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 23.85% Mismatches: 29
Query Match: 7.89% Indels: 34
RESULT 669
ID AAA08620 standard; cDNA; 4631 BP.
DE Human secreted protein gene #7 from clone HOHBY69.
PN WO200029435-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 21.55% Mismatches: 65
Query Match: 7.89% Indels: 38
RESULT 670
ID ADA27044 standard; cDNA; 4631 BP.
DE Human novel secreted protein gene 7 cDNA HOHBY69 #2.
PN US200305231-A1.
PD 20-MAR-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
PA (LIUD/) LIU D.
PA (CROC/) CROCKER P R.
Best Local Similarity: 22.16% Mismatches: 74
Query Match: 7.89% Indels: 28
RESULT 671
ID ADE86574 standard; cDNA; 4631 BP.
DE Novel human secreted protein cDNA #15.
PN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENN/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Best Local Similarity: 22.16% Mismatches: 74
Query Match: 7.89% Indels: 28
RESULT 672
ID AEN86507 standard; cDNA; 2747 BP.
DE Rat glycoprotein CD44 polypeptide encoding cDNA.
PN WO200238794-A2.
PD 16-MAY-2002.
PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
Best Local Similarity: 20.72% Mismatches: 30
Query Match: 7.80% Indels: 34
RESULT 673
ID ABK63681 standard; cDNA; 2747 BP.
DE Rat sequence differentially expressed in response to a hepatotoxin #1588.
PN WO200210453-A2.
PD 07-FEB-2002.
PA (GENE-) GENE LOGIC INC.
Best Local Similarity: 20.72% Mismatches: 30
Query Match: 7.80% Indels: 34
RESULT 674
ID AAQ14263 standard; cDNA; 3207 BP.
DE p-meta-1 metastasis-specific variant of CD44 glycoprotein.
PN DE4014510-A.
PD 14-NOV-1991.
PA (GESL ) KERNFORSCHUNGSZENT KARLSRUHE.
PA (UYKA-) UNIV KARLSRUHE.
PA (DEKR-) DEUT KREBSFORSCHUNGSLENT.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENT.
Best Local Similarity: 20.72% Mismatches: 30
Query Match: 7.80% Indels: 34
RESULT 675
ID AAD53012 standard; DNA; 5965 BP.
DE B4 DNA clone (CA125).
PN WO200292836-A2.
PD 21-NOV-2002.
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
Best Local Similarity: 19.28% Mismatches: 75
Query Match: 7.80% Indels: 90
RESULT 676
ID ABZ38842 standard; DNA; 1404 BP.
DE N. gonorrhoeae nucleotide sequence SEQ ID 2273.
PN WO200279243-A2.
PD 10-OCT-2002.
PA (CHIR-) CHIRON SPA.
Best Local Similarity: 24.12% Mismatches: 77
Query Match: 7.76% Indels: 43
RESULT 677
ID ABN72972 standard; DNA; 3447 BP.
DE Truncated nucleotide sequence with homology to 0772P.
PN WO200206317-A2.
PD 24-JAN-2002.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 678
ID ADA08609 standard; DNA; 3447 BP.
DE Human 0772P homology protein #1 DNA.
PN US2003091580-A1.
PD 15-MAY-2003.
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 679
ID ADF08952 standard; cDNA; 3447 BP.
DE cDNA encoding secreted ovarian carcinoma antigen seqid 456.
PN US2003124140-A1.
PD 03-JUL-2003.
PA (CORI-) CORIXA CORP.
Best Local Similarity: 21.35% Mismatches: 60
Query Match: 7.76% Indels: 61
RESULT 680
ID ADG46239 standard; cDNA; 3447 BP.
DE Human ovarian carcinoma polynucleotide #388.
PN US2003165504-A1.
PD 04-SEP-2003.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
Best Local Similarity: 21.35% Mismatches: 60

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Query Match:	7.76%	Indels:	61
RESULT 681			
ID AHI18639 standard; cDNA; 3557 BP.			
DE Human cDNA sequence SEQ ID NO:18864.			
PN EPI074617-A2.			
PA (HELI-) HELIX RES INST.			
PA 07-FEB-2001.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 682			
ID ABA83109 standard; DNA; 3557 BP.			
DE HOST-1 ovarian tumour marker gene, SEQ ID NO:55.			
PN WO200175177-A2.			
PA 11-OCT-2001.			
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 683			
ID ABN72973 standard; DNA; 3557 BP.			
DE Full nucleotide sequence with homology to 0772P.			
PN WO200206317-A2.			
PA (CORI-) CORIXA CORP.			
PA 24-JAN-2002.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 684			
ID ABN72975 standard; cDNA; 3557 BP.			
DE cDNA sequence for clone FLJ14303.			
PN WO200206317-A2.			
PA 24-JAN-2002.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 685			
ID ACP36017 standard; DNA; 3557 BP.			
DE DNA expressed by human ovarian cancer cells.			
PN WO200305256-A2.			
PA 24-JUL-2003.			
PA (IDEC-) IDEC PHARM CORP.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 686			
ID ADA08610 standard; DNA; 3557 BP.			
DE Human 0772P homology protein #2 DNA.			
PN US2003091580-A1.			
PA 15-MAY-2003.			
PA (MITC/) MITCHAM J L.			
PA (KING/) KING G E.			
PA (ALGA/) ALGATE P A.			
PA (FLIN/) FLING S P.			
PA (RETT/) RETTER M W.			
PA (FANG/) FANGER G R.			
PA (REED/) REED S G.			
PA (VEDV/) VEDVICK T S.			
PA (CART/) CARTER D.			
PA (HILL/) HILL P.			
PA (ALBO/) ALBONE E.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 687			
ID ADA08616 standard; cDNA; 3557 BP.			
DE Human cDNA clone FLJ14303.			
PN US2003091580-A1.			
PA 15-MAY-2003.			
PA (MITC/) MITCHAM J L.			
PA (KING/) KING G E.			
PA (ALGA/) ALGATE P A.			
PA (FLIN/) FLING S P.			
PA (RETT/) RETTER M W.			
PA (FANG/) FANGER G R.			
PA (REED/) REED S G.			
PA (VEDV/) VEDVICK T S.			
PA (CART/) CARTER D.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 688			
ID ADF08953 standard; cDNA; 3557 BP.			
DE cDNA encoding secreted ovarian carcinoma antigen seqid 457.			
PN US2003124140-A1.			
PA 03-JUL-2003.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 689			
ID ADF08959 standard; cDNA; 3557 BP.			
DE cDNA encoding secreted ovarian carcinoma antigen seqid 463.			
PN US2003124140-A1.			
PA 03-JUL-2003.			
PA (CORI-) CORIXA CORP.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 690			
ID ADG46240 standard; cDNA; 3557 BP.			
DE Human ovarian carcinoma polynucleotide #389.			
PN US2003165504-A1.			
PA 04-SEP-2003.			
PA (RETT/) RETTER M W.			
PA (FANG/) FANGER G R.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 691			
ID ADG08770 standard; cDNA; 3557 BP.			
DE Human ovarian cancer related EST SEQ ID NO:11.			
PN WO2003104429-A2.			
PA 18-DEC-2003.			
PA (IDEC-) IDEC PHARM CORP.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 692			
ID ADQ29638 standard; DNA; 3557 BP.			
DE Human colorectal cancer-associated protein coding sequence #60.			
PN EPI439393-A2.			
PA 21-JUL-2004.			
PA (FARB) BAYER HEALTHCARE LLC.			
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.			
Best Local Similarity: 21.35%		Mismatches:	60
Query Match: 7.76%		Indels:	61
RESULT 693			
ID ABZ11844 standard; cDNA; 4573 BP.			
DE Human polynucleotide SEQ ID NO 726.			
PN WO200270539-A2.			
PA 12-SEP-2002.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 22.28%		Mismatches:	66
Query Match: 7.76%		Indels:	50
RESULT 694			
ID ACC72807 standard; cDNA; 5264 BP.			
DE Human cancer related protein encoding cDNA SEQ ID NO:145.			
PN WO2003025138-A2.			
PA 27-MAR-2003.			
PA (EOSB-) EOS BIOTECHNOLOGY INC.			
Best Local Similarity: 22.28%		Mismatches:	66
Query Match: 7.76%		Indels:	50
RESULT 695			
ID ADM44362 standard; cDNA; 5323 BP.			
DE Novel human arginine-rich protein cDNA #726.			
PN US2004053250-A1.			
PA 18-MAR-2004.			
PA (TANG/) TANG Y T.			
PA (XUEA/) XUE A.			
PA (DRMA/) DRMANAC R T.			
Best Local Similarity: 22.28%		Mismatches:	66
Query Match: 7.76%		Indels:	50
RESULT 696			

ID ABE72534 standard; cDNA; 6833 BP.  
DE Human cDNA encoding 13 Cal25 repeats and the carboxy terminus.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Best Local Similarity: 21.35% Mismatches: 60  
Query Match: 7.76% Indels: 61  
RESULT 697  
ID ABE80091 standard; DNA; 8186 BP.  
DE Human chemically modified disease associated gene SEQ ID NO 108.  
PN WO200200927-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 22.41% Mismatches: 69  
Query Match: 7.76% Indels: 37  
RESULT 698  
ID ADL16194 standard; DNA; 4756 BP.  
DE Human protein tyrosine phosphatase gene #18.  
PN WO2003068984-A2.  
PD 21-AUG-2003.  
PA (COLD-) COLD SPRING HARBOR LAB.  
PA (CEPT-) CEPTYR INC.  
Best Local Similarity: 20.48% Mismatches: 77  
Query Match: 7.71% Indels: 20  
RESULT 699  
ID ADI32135 standard; cDNA; 4756 BP.  
DE Human cDNA #1461.  
PN US6607879-B1.  
PD 19-AUG-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 20.48% Mismatches: 77  
Query Match: 7.71% Indels: 20  
RESULT 700  
Best Local Similarity: 23.98% Mismatches: 53  
Query Match: 7.71% Indels: 70  
RESULT 701  
Best Local Similarity: 23.98% Mismatches: 53  
Query Match: 7.71% Indels: 70  
RESULT 702  
ID ADL85166 standard; DNA; 529 BP.  
DE DNA up-regulated in murine common lymphoid myeloid cells SeqID 1559.  
PN WO2003093445-A2.  
PD 13-NOV-2003.  
PA (STOW-) STOWERS INST MEDICAL RES.  
Best Local Similarity: 23.08% Mismatches: 31  
Query Match: 7.67% Indels: 19  
RESULT 703  
ID ADL85165 standard; DNA; 529 BP.  
DE DNA up-regulated in murine common lymphoid myeloid cells SeqID 1558.  
PN WO2003093445-A2.  
PD 13-NOV-2003.  
PA (STOW-) STOWERS INST MEDICAL RES.  
Best Local Similarity: 23.08% Mismatches: 31  
Query Match: 7.67% Indels: 19  
RESULT 704  
ID AAZ53929 standard; DNA; 1407 BP.  
DE Neisseria meningitidis ORF 595 partial DNA sequence SEQ ID NO:1807.  
PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Best Local Similarity: 23.74% Mismatches: 81  
Query Match: 7.67% Indels: 41  
RESULT 705  
ID AAC91902 standard; cDNA; 3567 BP.  
DE Human A259 ORF.  
PN WO200073339-A1.  
PD 07-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 22.54% Mismatches: 59  
Query Match: 7.67% Indels: 39  
RESULT 706  
ID AAS22772 standard; cDNA; 3967 BP.

DE Human cDNA encoding a novel human protein #338.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 22.54% Mismatches: 59  
Query Match: 7.67% Indels: 39  
RESULT 707  
ID ADE09822 standard; DNA; 3967 BP.  
DE Novel DNA-related contig nucleotide sequence #544.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 22.54% Mismatches: 59  
Query Match: 7.67% Indels: 39  
RESULT 708  
ID AAS22536 standard; cDNA; 3969 BP.  
DE Human cDNA encoding a novel human protein #102.  
PN WO200155437-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 22.54% Mismatches: 59  
Query Match: 7.67% Indels: 39  
RESULT 709  
ID AAC91901 standard; cDNA; 5042 BP.  
DE Human A259 coding sequence.  
PN WO200073339-A1.  
PD 07-DEC-2000.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 22.54% Mismatches: 59  
Query Match: 7.67% Indels: 39  
RESULT 710  
ID AAS16873 standard; cDNA; 5042 BP.  
DE Human A259 cDNA.  
PN WO200181414-A2.  
PD 01-NOV-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 22.54% Mismatches: 59  
Query Match: 7.67% Indels: 39  
RESULT 711  
ID ADQ24050 standard; DNA; 5117 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6870.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 22.54% Mismatches: 59  
Query Match: 7.67% Indels: 39  
RESULT 712  
ID ADO05745 standard; DNA; 38306 BP.  
DE Recombinant adenoviral vector polynucleotide sequence.  
PN EP1418185-A1.  
PD 12-MAY-2004.  
PA (AVET) AVENTIS PHARMA DEUT GMBH.  
Best Local Similarity: 19.03% Mismatches: 101  
Query Match: 7.67% Indels: 92  
RESULT 713  
ID AAT06027 standard; cDNA; 5117 BP.  
DE huDEP-1 cDNA.  
PN WO9530008-A1.  
PD 09-NOV-1995.  
PA (COLD-) COLD SPRING HARBOR LAB.  
Best Local Similarity: 26.37% Mismatches: 34  
Query Match: 7.58% Indels: 13  
RESULT 714  
ID ADL16192 standard; DNA; 5117 BP.  
DE Human protein tyrosine phosphatase gene #17.  
PN WO2003068984-A2.  
PD 21-AUG-2003.  
PA (COLD-) COLD SPRING HARBOR LAB.  
PA (CEPT-) CEPTYR INC.  
Best Local Similarity: 26.37% Mismatches: 34  
Query Match: 7.58% Indels: 13  
RESULT 715  
ID ADP74602 standard; DNA; 5117 BP.



DE Nucleotide sequence of human DEP-1.  
PN WO2004048549-A2.  
PA (DILL/) DILLON P J.  
PA (COLD-) COLD SPRING HARBOR LAB.  
Best Local Similarity: 26.37% Mismatches: 34  
Query Match: 7.58% Indels: 13  
RESULT 716  
ID ADC87424 standard; DNA; 34551 BP.  
DE Human GPCR gene SEQ ID NO:1877.  
PN EP1270724-A2.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
Best Local Similarity: 29.25% Mismatches: 41  
Query Match: 7.58% Indels: 19  
RESULT 717  
ID ABK63658 standard; cDNA; 5588 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #1565.  
PN WO200210453-A2.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 24.30% Mismatches: 50  
Query Match: 7.53% Indels: 13  
RESULT 718  
Best Local Similarity: 22.80% Mismatches: 63  
Query Match: 7.53% Indels: 55  
RESULT 719  
ID ABL65294 standard; DNA; 386 BP.  
DE Lung cancer related gene sequence SEQ ID NO:3631.  
PN WO200194629-A2.  
PA (AVAL-) AVALON PHARM.  
Best Local Similarity: 22.50% Mismatches: 51  
Query Match: 7.49% Indels: 47  
RESULT 720  
ID ADK58075 standard; DNA; 551 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #5458.  
PN WO2003020936-A1.  
PA (DOWC) DOW CHEM CO.  
PA (DOWC) DOW AGROSCIENTES LLC.  
Best Local Similarity: 22.12% Mismatches: 37  
Query Match: 7.49% Indels: 19  
RESULT 721  
ID AA253927 standard; DNA; 696 BP.  
DE Neisseria gonorrhoeae ORF 585 partial DNA sequence SEQ ID NO:1803.  
PN WO9957280-A2.  
PA (CHIR) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Best Local Similarity: 24.10% Mismatches: 73  
Query Match: 7.49% Indels: 43  
RESULT 722  
ID ADH84658 standard; DNA; 1590 BP.  
DE Enterococcus faecalis polynucleotide #2543.  
PN US6617156-B1.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Best Local Similarity: 24.71% Mismatches: 75  
Query Match: 7.49% Indels: 25  
RESULT 723  
ID AAX13278 standard; DNA; 13884 BP.  
DE Enterococcus faecalis genome contig SEQ ID NO:341.  
PN WO9850555-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 24.71% Mismatches: 75  
Query Match: 7.49% Indels: 25  
RESULT 724  
ID ABS99073 standard; DNA; 13884 BP.  
DE Enterococcus faecalis contig sequence #341.  
PN US2002120116-A1.

PD 29-AUG-2002.  
PA (KUNS/) KUNSCH C A.  
PA (DILL/) DILLON P J.  
PA (BARA/) BARASH S.  
Best Local Similarity: 24.71% Mismatches: 75  
Query Match: 7.49% Indels: 25  
RESULT 725  
ID ACN45042 standard; DNA; 95835 BP.  
DE Human genomic sequence hCG37223.  
PN WO2003073826-A2.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 19.25% Mismatches: 51  
Query Match: 7.49% Indels: 47  
RESULT 726  
ID ACA31993 standard; DNA; 1401 BP.  
DE Prokaryotic essential gene #13650.  
PN WO200271183-A2.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 24.35% Mismatches: 67  
Query Match: 7.44% Indels: 54  
RESULT 727  
ID AAH33739 standard; cDNA; 1929 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:795.  
PN WO200122920-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.10% Mismatches: 73  
Query Match: 7.44% Indels: 54  
RESULT 728  
ID ABL09031 standard; cDNA; 2339 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21575.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 29.85% Mismatches: 26  
Query Match: 7.44% Indels: 5  
RESULT 729  
ID ACC72077 standard; DNA; 4779 BP.  
DE Human NOV2b coding sequence.  
PN WO2003029423-A2.  
PD 19-SEP-2002.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Best Local Similarity: 21.43% Mismatches: 74  
Query Match: 7.44% Indels: 40  
RESULT 730  
ID ABX04161 standard; cDNA; 4986 BP.  
DE Human mRNA differentially expressed in mesenchymal cells #8.  
PN WO200271927-A2.  
PD 19-SEP-2002.  
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.  
Best Local Similarity: 21.43% Mismatches: 74  
Query Match: 7.44% Indels: 40  
RESULT 731  
ID ADQ19967 standard; DNA; 4986 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2787.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 21.43% Mismatches: 74  
Query Match: 7.44% Indels: 40  
RESULT 732  
ID AAA80612 standard; cDNA; 4995 BP.  
DE Human ITGAl1 secreted protein gene #7.  
PN WO200029435-A1.  
PD 25-MAY-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 21.43% Mismatches: 74  
Query Match: 7.44% Indels: 40  
RESULT 733  
ID ACC72076 standard; DNA; 4995 BP.  
DE Human NOV2a coding sequence.

PN WO2003029423-A2.  
 PD 10-APR-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 21.43% Mismatches: 74  
 Query Match: 7.44% Indels: 40  
 RESULT 734  
 ID ADA27036 standard; cDNA; 4995 BP.  
 DE Human novel secreted protein gene 7 cDNA HOHBY69 #1.  
 PN US200305231-A1.  
 PD 20-MAR-2003.  
 PA (NIJG/) NI J.  
 PA (YOUN/) YOUNG P E.  
 PA (KENN/) KENNY J J.  
 PA (OLSE/) OLSEN H S.  
 PA (MOOR/) MOORE P A.  
 PA (WEIY/) WEI Y.  
 PA (GREE/) GREENE J M.  
 PA (RUBE/) RUBEN S M.  
 PA (LIUD/) LIU D.  
 PA (CROC/) CROCKER P R.  
 Best Local Similarity: 21.43% Mismatches: 74  
 Query Match: 7.44% Indels: 40  
 RESULT 735  
 ID ADE86566 standard; cDNA; 4995 BP.  
 DE Novel human secreted protein cDNA #7.  
 PN US2003129685-A1.  
 PD 10-JUL-2003.  
 PA (NIJG/) NI J.  
 PA (YOUN/) YOUNG P E.  
 PA (KENN/) KENNY J J.  
 PA (OLSE/) OLSEN H S.  
 PA (MOOR/) MOORE P A.  
 PA (WEIY/) WEI Y.  
 PA (GREE/) GREENE J M.  
 PA (RUBE/) RUBEN S M.  
 Best Local Similarity: 21.43% Mismatches: 74  
 Query Match: 7.44% Indels: 40  
 RESULT 736  
 ID ABL09030 standard; cDNA; 5820 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21572.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Best Local Similarity: 29.85% Mismatches: 26  
 Query Match: 7.44% Indels: 5  
 RESULT 737  
 ID ADL16199 standard; DNA; 6314 BP.  
 DE Rat protein tyrosine phosphatase gene #4.  
 PN WO2003068984-A2.  
 PD 21-AUG-2003.  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 PA (CEPT-) CEPTYR INC.  
 Best Local Similarity: 26.67% Mismatches: 36  
 Query Match: 7.44% Indels: 10  
 RESULT 738  
 ID RAZ91916 standard; cDNA; 8827 BP.  
 DE Wild type (C57BL/6J) murine mahogany protein coding sequence.  
 PN WO200005373-A2.  
 PD 03-FEB-2000.  
 PA (MILL-) MILLENIUM PHARM INC.  
 Best Local Similarity: 20.00% Mismatches: 111  
 Query Match: 7.44% Indels: 52  
 RESULT 739  
 ID ABV94618 standard; cDNA; 910 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:258.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 23.90% Mismatches: 63  
 Query Match: 7.40% Indels: 35  
 RESULT 740  
 ID ADM18893 standard; cDNA; 910 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:258.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 23.90% Mismatches: 63  
 Query Match: 7.40% Indels: 35  
 RESULT 741  
 ID ACF71663 standard; DNA; 1092 BP.  
 DE Photorhabdus luminescens nucleotide sequence #10130.  
 PN WO200294867-A2.  
 PD 28-NOV-2002.  
 PA (INSP ) INST PASTEUR.  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 Best Local Similarity: 25.00% Mismatches: 54  
 Query Match: 7.40% Indels: 63  
 RESULT 742  
 ID ABV78128 standard; DNA; 3147 BP.  
 DE Human alpha V integrin DNA SEQ ID NO 12.  
 PN WO200255693-A2.  
 PD 18-JUL-2002.  
 PA (RIBO-) RIBOPHARMA AG.  
 Best Local Similarity: 23.66% Mismatches: 82  
 Query Match: 7.40% Indels: 51  
 RESULT 743  
 ID ABZ35704 standard; DNA; 3147 BP.  
 DE Human alpha V integrin encoding polynucleotide SEQ ID NO 12.  
 PN DE10100588-A1.  
 PD 18-JUL-2002.  
 PA (RIBO-) RIBOPHARMA AG.  
 Best Local Similarity: 23.66% Mismatches: 82  
 Query Match: 7.40% Indels: 51  
 RESULT 744  
 ID ABX09947 standard; DNA; 3147 BP.  
 DE Human alpha v integrin DNA fragment SEQ ID 12.  
 PN DE10100587-C1.  
 PD 21-NOV-2002.  
 PA (RIBO-) RIBOPHARMA AG.  
 Best Local Similarity: 23.66% Mismatches: 82  
 Query Match: 7.40% Indels: 51  
 RESULT 745  
 ID ABL91669 standard; DNA; 3147 BP.  
 DE Human polynucleotide SEQ ID NO 12.  
 PN DE10100586-C1.  
 PD 11-APR-2002.  
 PA (RIBO-) RIBOPHARMA AG.  
 Best Local Similarity: 23.66% Mismatches: 82  
 Query Match: 7.40% Indels: 51  
 RESULT 746  
 ID ABL69959 standard; DNA; 3269 BP.  
 DE Pancreas cancer related gene sequence SEQ ID NO:8296.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Best Local Similarity: 21.83% Mismatches: 64  
 Query Match: 7.40% Indels: 54  
 RESULT 747  
 ID ADP24568 standard; cDNA; 3269 BP.  
 DE PRO polypeptide encoding cDNA SEQ ID NO:1746.  
 PN WO2004041170-A2.  
 PD 21-MAY-2004.  
 PA (GETH ) GENENTECH INC.  
 Best Local Similarity: 21.83% Mismatches: 64  
 Query Match: 7.40% Indels: 54  
 RESULT 748  
 ID AAS83082 standard; cDNA; 5717 BP.  
 DE DNA encoding novel human diagnostic protein #18886.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 23.66% Mismatches: 82  
 Query Match: 7.40% Indels: 51  
 RESULT 749  
 ID ABX08833 standard; cDNA; 5717 BP.  
 DE Angiogenesis-associated human polynucleotide sequence #95.

PN WO200279492-A2.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Best Local Similarity: 23.66% Mismatches: 82  
Query Match: 7.40% Indels: 51  
RESULT 750  
ID ADI32007 standard; cDNA; 5717 BP.  
DE Human cDNA #1333.  
PN US6607879-B1.  
PD 19-AUG-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 23.66% Mismatches: 82  
Query Match: 7.40% Indels: 51  
RESULT 751  
ID ADM95952 standard; cDNA; 5717 BP.  
DE Human integrin alphaV subunit precursor cDNA.  
PN WO2004007530-A2.  
PD 22-JAN-2004.  
PA (BLOO-) CENT BLOOD RES INC.  
Best Local Similarity: 23.66% Mismatches: 82  
Query Match: 7.40% Indels: 51  
RESULT 752  
ID AAL62048 standard; cDNA; 6871 BP.  
DE Human cell adhesion and extracellular matrix protein (CADECM)-36 cDNA.  
PN WO2003047526-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 23.66% Mismatches: 82  
Query Match: 7.40% Indels: 51  
RESULT 753  
ID ABV25831 standard; cDNA; 6952 BP.  
DE Human prostate expression marker cDNA 25822.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 23.66% Mismatches: 82  
Query Match: 7.40% Indels: 51  
RESULT 754  
ID ADL45678 standard; DNA; 6954 BP.  
DE Human ovarian cancer DNA marker #19568.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 23.66% Mismatches: 82  
Query Match: 7.40% Indels: 51  
RESULT 755  
ID ACP65372 standard; DNA; 21520 BP.  
DE Phototaxidus luminescens nucleotide sequence #25.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP-) INST PASTEUR.  
PA (CNRS-) CNRS CENT NAT RECH SCI.  
Best Local Similarity: 25.00% Mismatches: 54  
Query Match: 7.40% Indels: 63  
RESULT 756  
ID ACN45170 standard; DNA; 133955 BP.  
DE Human genomic sequence hCG23504.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 21.56% Mismatches: 65  
Query Match: 7.40% Indels: 37  
RESULT 758  
ID AAS71946 standard; cDNA; 853 BP.  
DE DNA encoding novel human diagnostic protein #7750.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 25.16% Mismatches: 62  
Query Match: 7.35% Indels: 28

RESULT 759  
ID ADK53982 standard; DNA; 484 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #1365.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DOWC-) DOW CHEM CO.  
PA (DOWC-) DOW AGROSCIENCES LLC.  
Best Local Similarity: 22.12% Mismatches: 37  
Query Match: 7.30% Indels: 19  
RESULT 760  
ID ABX72616 standard; cDNA; 1422 BP.  
DE Human cDNA encoding the CAL25 protein carboxy terminus.  
PN WO200283866-A2.  
PD 24-OCT-2002.  
PA (UYAR-) UNIV ARKANSAS.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 761  
ID ABN72979 standard; cDNA; 1636 BP.  
DE Clone 0772P partial cDNA sequence #4.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 762  
ID ADA08620 standard; cDNA; 1636 BP.  
DE Human 0772P partial cDNA clone #4.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC-) MITCHAM J L.  
PA (KING-) KING G E.  
PA (ALGA-) ALGATE P A.  
PA (FLIN-) FLING S P.  
PA (RETT-) RETTER M W.  
PA (FANG-) FANGER G R.  
PA (REED-) REED S G.  
PA (VEDV-) VEDVICK T S.  
PA (CART-) CARTER D.  
PA (HILL-) HILL P.  
PA (ALBO-) ALBONE E.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 763  
ID ADF08963 standard; cDNA; 1636 BP.  
DE cDNA encoding secreted ovarian carcinoma antigen seqid 467.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 764  
ID AAD20618 standard; cDNA; 1704 BP.  
DE Human ovarian cancer antigen-encoding gene 1 cDNA clone HIPAZ30.  
PN WO200170804-A1.  
PD 27-SEP-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 765  
ID ADH41325 standard; DNA; 1721 BP.  
DE Human ovarian specific gene (OSG) sequence #1.  
PN US2003096238-A1.  
PD 22-MAY-2003.  
PA (SALC-) SALCEDA S.  
PA (CAFF-) CAFFERKEY R.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 766  
ID ABZ35214 standard; cDNA; 2166 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 326.  
PN WO200274979-A2.  
PD 26-SEP-2002.

PA (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.  
Best Local Similarity: 18.94% Mismatches: 68  
Query Match: 7.30% Indels: 104  
RESULT 767  
ID AEX05223 standard; cDNA; 3546 BP.  
DE Human novel polynucleotide #238.  
PN WO200274961-A1.  
PD 26-SEP-2002  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 768  
ID ADR08401 standard; cDNA; 3613 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1907.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 769  
ID ADR08234 standard; cDNA; 4184 BP.  
DE Full length human cDNA useful for treating neurological disease Seq 1740.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 770  
ID ADH41327 standard; DNA; 4494 BP.  
DE Human ovarian specific gene (OSG) sequence #2.  
PN US22003096238-A1.  
PD 22-MAY-2003  
PA (SALC/) SALCEDA S.  
PA (CAFF/) CAFFERKEY R.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 771  
ID RAZ22904 standard; DNA; 15893 BP.  
DE Nucleotide sequence of wild type measles virus Montefiore strain.  
PN WO9949017-A2.  
PD 30-SEP-1999.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Best Local Similarity: 25.00% Mismatches: 55  
Query Match: 7.30% Indels: 57  
RESULT 772  
ID AAV18267 standard; DNA; 15894 BP.  
DE Measles virus Montefiore isolate wild-type L protein genomic DNA.  
PN WO9813501-A2.  
PD 02-APR-1998.  
PA (AMCY ) AMERICAN CYANAMID CO.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Best Local Similarity: 25.00% Mismatches: 55  
Query Match: 7.30% Indels: 57  
RESULT 773  
ID RAV18266 standard; DNA; 15894 BP.  
DE Measles virus 1983 isolate wild-type L protein genomic DNA.  
PN WO9813501-A2.  
PD 02-APR-1998.  
PA (AMCY ) AMERICAN CYANAMID CO.  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
Best Local Similarity: 25.58% Mismatches: 55  
Query Match: 7.30% Indels: 57  
RESULT 774  
ID RAZ22903 standard; DNA; 15894 BP.  
DE Nucleotide sequence of wild type measles virus 1983 strain.  
PN WO9949017-A2.  
PD 30-SEP-1999.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Best Local Similarity: 25.58% Mismatches: 55  
Query Match: 7.30% Indels: 57  
RESULT 775  
ID ADP84154 standard; cDNA; 66765 BP.  
DE Human CA125 cDNA SeqID 4.

PN WO2004045553-A2.  
PD 03-JUN-2004.  
PA (UYAR-) UNIV ARKANSAS.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 776  
ID ADR72872 standard; DNA; 66765 BP.  
DE Human ovarian cancer-related tumour marker CA125 DNA.  
PN WO2004075713-A2.  
PD 10-SEP-2004.  
PA (MOUN ) MOUNT SINAI HOSPITAL.  
Best Local Similarity: 20.77% Mismatches: 68  
Query Match: 7.30% Indels: 63  
RESULT 777  
ID ADG34281 standard; DNA; 762 BP.  
DE Neurokinin B antibody encoding DNA SEQ ID NO:4.  
PN WO2003102136-A2.  
PD 11-DEC-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.23% Mismatches: 56  
Query Match: 7.26% Indels: 53  
RESULT 778  
ID ABL04091 standard; cDNA; 1349 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6755.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 30.68% Mismatches: 36  
Query Match: 7.26% Indels: 9  
RESULT 779  
ID AAC46959 standard; DNA; 2219 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52039.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Best Local Similarity: 22.73% Mismatches: 69  
Query Match: 7.26% Indels: 32  
RESULT 780  
ID ADT05389 standard; DNA; 3711 BP.  
DE Haemophilus influenzae (NTHI) contig DNA sequence - SEQ ID 425.  
PN WO2004078949-A2.  
PD 16-SEP-2004.  
PA (CHIL-) CHILDRENS HOSPITAL INC.  
Best Local Similarity: 21.94% Mismatches: 60  
Query Match: 7.26% Indels: 61  
RESULT 781  
ID ADC00087 standard; DNA; 86248 BP.  
DE Enterohaemorrhagic E. coli 0157:H7-specific nucleic acid SEQ ID NO: 132.  
PN JP2002355074-A.  
PD 10-DEC-2002.  
PA (UYTS-) UNIV TSUKUBA.  
Best Local Similarity: 22.05% Mismatches: 88  
Query Match: 7.26% Indels: 32  
RESULT 782  
ID ACD19044 standard; DNA; 87563 BP.  
DE E. coli 0157 unique DNA sequence OZID\_57.  
PN US2003023075-A1.  
PD 30-JAN-2003.  
PA (BLAT/) BLATTNER F R.  
PA (BURL/) BURLAND V D.  
PA (PERN/) PERNA N T.  
PA (PLUN/) PLUNKETT G.  
PA (WELC/) WELCH R.  
Best Local Similarity: 22.05% Mismatches: 88  
Query Match: 7.26% Indels: 32  
RESULT 783  
ID ADN12161 standard; DNA; 172281 BP.  
DE Epstein-Barr virus genome B95-8.  
PN WO2004027036-A2.  
PD 01-APR-2004.  
PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.  
Best Local Similarity: 26.17% Mismatches: 59  
Query Match: 7.26% Indels: 32  
RESULT 784

ID ADT05738 standard; DNA; 308766 BP.  
 DE Haemophilus influenzae (NTHI) DNA sequence - SEQ ID 774.  
 PN WO2004078949-A2.  
 PD 16-SEP-2004.  
 PA (CHIL-) CHILDRENS HOSPITAL INC.  
 Best Local Similarity: 21.94% Mismatches: 60  
 Query Match: 7.26% Indels: 61  
 RESULT 785  
 ID AAS83081 standard; cDNA; 649 BP.  
 DE DNA encoding novel human diagnostic protein #18885.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 22.11% Mismatches: 69  
 Query Match: 7.21% Indels: 57  
 RESULT 786  
 ID ABV94552 standard; cDNA; 906 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:113.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 25.00% Mismatches: 59  
 Query Match: 7.21% Indels: 68  
 RESULT 787  
 ID ADM18748 standard; cDNA; 906 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:113.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 25.00% Mismatches: 59  
 Query Match: 7.21% Indels: 68  
 RESULT 788  
 ID ADS45602 standard; cDNA; 1065 BP.  
 DE Bacterial polynucleotide #345.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 23.24% Mismatches: 54  
 Query Match: 7.21% Indels: 63  
 RESULT 789  
 ID ACA36349 standard; DNA; 2292 BP.  
 DE Prokaryotic essential gene #18006.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 30.93% Mismatches: 31  
 Query Match: 7.21% Indels: 20  
 RESULT 790  
 ID ADF85455 standard; cDNA; 2306 BP.  
 DE Human adenoma marker cDNA, SEQ ID NO:20.  
 PN WO2003025214-A1.  
 PD 27-MAR-2003.  
 PA (MEDI-) MEDIMOLECULAR PTY LTD.  
 Best Local Similarity: 18.69% Mismatches: 47  
 Query Match: 7.21% Indels: 79  
 RESULT 791  
 ID ADM30753 standard; DNA; 3559 BP.  
 DE Human cancer linked gene referred to as H53701\_T\_1 SeqID 1.  
 PN WO2003075854-A2.  
 PD 18-SEP-2003.  
 PA (AVAL-) AVALON PHARM.  
 Best Local Similarity: 20.83% Mismatches: 61  
 Query Match: 7.21% Indels: 61  
 RESULT 792  
 ID ADN96165 standard; cDNA; 3879 BP.  
 DE Human NOVX polynucleotide #110.  
 PN US2004067490-A1.  
 PD 08-APR-2004.  
 PA (ZHON/) ZHONG M.

PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (SPYT/) SPYTEK K A.  
 PA (KEKU/) KEKUDA R.  
 PA (TAUP/) TAUPIER R J.  
 PA (ANDE/) ANDERSON D M.  
 PA (VERN/) VERNET C A M.  
 PA (CATT/) CATTERTON E.  
 PA (MILL/) MILLER C E.  
 PA (SHEN/) SHENOY S G.  
 PA (PATT/) PATTURAJAN M.  
 PA (PENA/) PENNA C E A.  
 PA (TCHE/) TCHERNEV V T.  
 PA (PADI/) PADIGARU M.  
 PA (GUSE/) GUSEV V Y.  
 PA (MALY/) MALYANKAR U M.  
 PA (BURG/) BURGESS C E.  
 PA (GERL/) GERLACH V.  
 PA (CASM/) CASHMAN S J.  
 PA (RIEG/) RIEGER D K.  
 PA (GROS/) GROSSE W M.  
 PA (SMIT/) SMITHSON G.  
 PA (PEYM/) PEYMAN J A.  
 PA (STAR/) STARLING G.  
 PA (ROTH/) ROTHENBERG M E.  
 PA (LARO/) LAROCHELLE W J.  
 PA (SHIM/) SHIMKETS R A.  
 PA (CRAB/) CRABTREE J.  
 PA (RAST/) RASTELLI L.  
 PA (VOSS/) VOSS E Z.  
 PA (BOLD/) BOLDOG F L.  
 PA (EDIN/) EDINGER S R.  
 PA (MILL/) MILLET I.  
 PA (MACD/) MACDOUGALL J R.  
 PA (ELLE/) ELLERMAN K.  
 PA (CHAP/) CHAPOVAL A.  
 Best Local Similarity: 31.82% Mismatches: 24  
 Query Match: 7.21% Indels: 19  
 RESULT 793  
 ID ABS76477 standard; cDNA; 5797 BP.  
 DE cDNA encoding human ovarian cancer markers M461 and M612.  
 PN WO200271928-A2.  
 PD 19-SEP-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 20.83% Mismatches: 61  
 Query Match: 7.21% Indels: 61  
 RESULT 794  
 Best Local Similarity: 30.93% Mismatches: 31  
 Query Match: 7.21% Indels: 20  
 RESULT 795  
 ID ADL08116 standard; DNA; 160361 BP.  
 DE Human gene associated with low HDL-C FABP-3.  
 PN US2004043389-A1.  
 PD 04-MAR-2004.  
 PA (VITI-) VITIVITY INC.  
 Best Local Similarity: 25.49% Mismatches: 33  
 Query Match: 7.21% Indels: 19  
 RESULT 796  
 ID AEN53251 standard; DNA; 65 BP.  
 DE Mouse spliced transcript detection oligonucleotide SEQ ID NO:25999.  
 PN WO200210449-A2.  
 PD 07-FEB-2002.  
 PA (COMP-) COMPUGEN INC.  
 Best Local Similarity: 75.00% Mismatches: 4  
 Query Match: 7.17% Indels: 0  
 RESULT 797  
 ID ABR74900 standard; DNA; 1512 BP.  
 DE Bacillus licheniformis genomic sequence tag (GST) #2191.  
 PN WO200229113-A2.  
 PD 11-APR-2002.  
 PA (NOVO) NOVOZYMES BIOTECH INC.  
 PA (NOVO) NOVOZYMES AS.  
 Best Local Similarity: 24.82% Mismatches: 45

Query Match: 7.17% Indels: 40  
RESULT 798  
ID ABL02681 standard; cDNA; 1695 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2525.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 25.33% Mismatches: 72  
Query Match: 7.17% Indels: 20  
RESULT 799  
ID AAS60896 standard; cDNA; 2664 BP.  
DE Human cancer agent-resistance marker #555.  
PN WO200179556-A2.  
PD 25-OCT-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 21.89% Mismatches: 78  
Query Match: 7.17% Indels: 45  
RESULT 800  
ID AAH17743 standard; cDNA; 2932 BP.  
DE Human cDNA sequence SEQ ID NO:17362.  
PN EF1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 21.89% Mismatches: 78  
Query Match: 7.17% Indels: 45  
RESULT 801  
ID ABL02680 standard; cDNA; 3750 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 2522.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 25.33% Mismatches: 72  
Query Match: 7.17% Indels: 20  
RESULT 802  
ID AAS77136 standard; cDNA; 3900 BP.  
DE DNA encoding novel human diagnostic protein #12940.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 21.84% Mismatches: 60  
Query Match: 7.17% Indels: 40  
RESULT 803  
ID ACC47353 standard; cDNA; 4603 BP.  
DE Human prostate selective polynucleotide Pr498.  
PN WO2003014298-A2.  
PD 20-FEB-2003.  
PA (ORIG-) ORIGENE TECHNOLOGIES INC.  
Best Local Similarity: 21.89% Mismatches: 78  
Query Match: 7.17% Indels: 45  
RESULT 804  
ID AAD35224 standard; cDNA; 5205 BP.  
DE Human TRNFR-9 cDNA.  
PN WO200226950-A2.  
PD 04-APR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 21.89% Mismatches: 78  
Query Match: 7.17% Indels: 45  
RESULT 805  
ID ABL30223 standard; DNA; 7630 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 42142.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 24.53% Mismatches: 30  
Query Match: 7.17% Indels: 30  
RESULT 806  
Best Local Similarity: 20.34% Mismatches: 68  
Query Match: 7.17% Indels: 46  
RESULT 807  
Best Local Similarity: 20.35% Mismatches: 79  
Query Match: 7.17% Indels: 67  
RESULT 808  
Best Local Similarity: 20.35% Mismatches: 79

Query Match: 7.17% Indels: 67  
RESULT 809  
ID ACN3996 standard; DNA; 254087 BP.  
DE Mouse genomic sequence mCG12572.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 22.86% Mismatches: 46  
Query Match: 7.17% Indels: 34  
RESULT 810  
ID ABL89941 standard; cDNA; 809 BP.  
DE Human polynucleotide SEQ ID NO 503.  
PN WO200190304-A2.  
PD 29-NOV-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 21.32% Mismatches: 54  
Query Match: 7.12% Indels: 68  
RESULT 811  
ID ABN73046 standard; cDNA; 1060 BP.  
DE cDNA sequence for the 3' constant region of 0772P.  
PN WO200206317-A2.  
PD 24-JAN-2002.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 20.83% Mismatches: 61  
Query Match: 7.12% Indels: 61  
RESULT 812  
ID ADA08721 standard; cDNA; 1060 BP.  
DE Human O772P variable region repeat cDNA #57.  
PN US2003091580-A1.  
PD 15-MAY-2003.  
PA (MITC/) MITCHAM J L.  
PA (KING/) KING G E.  
PA (ALGA/) ALGATE P A.  
PA (FLIN/) FLING S P.  
PA (RETT/) RETTER M W.  
PA (FANG/) FANGER G R.  
PA (REED/) REED S G.  
PA (VEDV/) VEDVICK T S.  
PA (CART/) CARTER D.  
PA (HILL/) HILL P.  
PA (ALBO/) ALBONE E.  
Best Local Similarity: 20.83% Mismatches: 61  
Query Match: 7.12% Indels: 61  
RESULT 813  
ID ADF09064 standard; cDNA; 1060 BP.  
DE cDNA encoding secreted ovarian carcinoma antigen seqid 568.  
PN US2003124140-A1.  
PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 20.83% Mismatches: 61  
Query Match: 7.12% Indels: 61  
RESULT 814  
ID ADN74328 standard; cDNA; 1173 BP.  
DE Thale cress cDNA repressed in E2Fa/Dpa expressing plants SeqID 2223.  
PN WO2004035798-A2.  
PD 29-APR-2004.  
PA (CROP-) CROPDDESIGN NV.  
Best Local Similarity: 33.02% Mismatches: 19  
Query Match: 7.12% Indels: 36  
RESULT 815  
ID AAC76608 standard; cDNA; 1405 BP.  
DE Human ORFX ORF2163 polynucleotide sequence SEQ ID NO:4325.  
PN WO200058473-A2.  
PD 05-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 22.09% Mismatches: 41  
Query Match: 7.12% Indels: 61  
RESULT 816  
ID AAA70076 standard; cDNA; 1761 BP.  
DE Human ovarian carcinoma antigen O772P polynucleotide SEQ ID NO:387.  
PN WO200036107-A2.  
PD 22-JUN-2000.  
PA (CORI-) CORIXA CORP.

Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 817  
 ID ABL34974 standard; cDNA; 1761 BP.  
 DE Rat cDNA isolated from skin cells SEQ ID NO: 479.  
 PN WO200190357-A1.  
 PD 29-NOV-2001.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 Best Local Similarity: 20.39% Mismatches: 70  
 Query Match: 7.12% Indels: 58  
 RESULT 823  
 ID ADI57683 standard; cDNA; 2194 BP.  
 DE Human breast specific nucleic acid (BSNA) #54.  
 PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 23.42% Mismatches: 56  
 Query Match: 7.12% Indels: 11  
 RESULT 822  
 ID ABL34974 standard; cDNA; 2100 BP.  
 DE Rat cDNA isolated from skin cells SEQ ID NO: 479.  
 PN WO200190357-A1.  
 PD 29-NOV-2001.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 Best Local Similarity: 20.39% Mismatches: 70  
 Query Match: 7.12% Indels: 58  
 RESULT 823  
 ID ADI57683 standard; cDNA; 2194 BP.  
 DE Human breast specific nucleic acid (BSNA) #54.  
 PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 23.42% Mismatches: 56  
 Query Match: 7.12% Indels: 11  
 RESULT 824  
 ID AAA70075 standard; cDNA; 2608 BP.  
 DE Human ovarian carcinoma antigen O772P polynucleotide SEQ ID NO:386.  
 PN WO200036107-A2.

PD 22-JUN-2000.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 825  
 ID ABL72969 standard; cDNA; 2608 BP.  
 DE cDNA sequence of O772P clone, 21003.  
 PN WO200206317-A2.  
 PD 24-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 826  
 ID ADA08540 standard; cDNA; 1761 BP.  
 DE Human ovarian carcinoma antigen polynucleotide O772P cDNA #3.  
 PN US2003091580-A1.  
 PD 15-MAY-2003.  
 PA (MITC/) MITCHAM J L.  
 PA (KING/) KING G E.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 PA (RETT/) RETTER M W.  
 PA (FANG/) FANGER G R.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (HILL/) HILL P.  
 PA (ALBO/) ALBONE E.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 819  
 ID ADF08883 standard; cDNA; 1761 BP.  
 DE cDNA encoding secreted ovarian carcinoma antigen seqid 387.  
 PN US2003124140-A1.  
 PD 03-JUL-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 820  
 ID ADG46170 standard; cDNA; 1761 BP.  
 DE Human ovarian carcinoma polynucleotide #386.  
 PN US2003165504-A1.  
 PD 04-SEP-2003.  
 PA (RETT/) RETTER M W.  
 PA (FANG/) FANGER G R.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 821  
 ID ADI57681 standard; cDNA; 2094 BP.  
 DE Human breast specific nucleic acid (BSNA) #52.  
 PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 23.42% Mismatches: 56  
 Query Match: 7.12% Indels: 11  
 RESULT 822  
 ID ABL34974 standard; cDNA; 2100 BP.  
 DE Rat cDNA isolated from skin cells SEQ ID NO: 479.  
 PN WO200190357-A1.  
 PD 29-NOV-2001.  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 Best Local Similarity: 20.39% Mismatches: 70  
 Query Match: 7.12% Indels: 58  
 RESULT 823  
 ID ADI57683 standard; cDNA; 2194 BP.  
 DE Human breast specific nucleic acid (BSNA) #54.  
 PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 23.42% Mismatches: 56  
 Query Match: 7.12% Indels: 11  
 RESULT 824  
 ID AAA70075 standard; cDNA; 2608 BP.  
 DE Human ovarian carcinoma antigen O772P polynucleotide SEQ ID NO:386.  
 PN WO200036107-A2.

DE Hypothetical nucleotide sequence for clone 0772P.  
 PN WO200206317-A2.  
 PD 24-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 833  
 ID ADA09060 standard; DNA; 2996 BP.  
 DE Human ovarian carcinoma antigen polynucleotide 0772P.  
 PN US2003091580-A1.  
 PD 15-MAY-2003.  
 PA (MITC/) MITCHAM J L.  
 PA (KING/) KING G E.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 PA (RETT/) RETTER M W.  
 PA (FANG/) FANGER G R.  
 PA (REED/) REED S G.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (HILL/) HILL P.  
 PA (ALBO/) ALBONE E.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 834  
 ID ADA08615 standard; cDNA; 2996 BP.  
 DE Human O772P hypothetical cDNA sequence.  
 PN US2003091580-A1.  
 PD 15-MAY-2003.  
 PA (MITC/) MITCHAM J L.  
 PA (KING/) KING G E.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 PA (RETT/) RETTER M W.  
 PA (FANG/) FANGER G R.  
 PA (REED/) REED S G.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (HILL/) HILL P.  
 PA (ALBO/) ALBONE E.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 835  
 ID ADF08807 standard; cDNA; 2996 BP.  
 DE cDNA encoding secreted ovarian carcinoma antigen seqid 311.  
 PN US2003124140-A1.  
 PD 03-JUL-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 836  
 ID ADF08958 standard; cDNA; 2996 BP.  
 DE cDNA encoding secreted ovarian carcinoma antigen seqid 462.  
 PN US2003124140-A1.  
 PD 03-JUL-2003.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 837  
 ID ADG46555 standard; cDNA; 2996 BP.  
 DE Human ovarian carcinoma polynucleotide #311.  
 PN US2003165504-A1.  
 PD 04-SEP-2003.  
 PA (RETT/) RETTER M W.  
 PA (FANG/) FANGER G R.  
 Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 838  
 ID ADN40450 standard; cDNA; 2996 BP.  
 DE Human breast cancer associated cDNA sequence #202.  
 PN US2004101899-A1.  
 PD 27-MAY-2004.  
 PA (CORI-) CORIXA CORP.

Best Local Similarity: 21.50% Mismatches: 74  
 Query Match: 7.12% Indels: 49  
 RESULT 839  
 ID AAF59534 standard; cDNA; 3489 BP.  
 DE cDNA encoding a mouse Prp-binding protein, OB-cadherin-1.  
 PN WO200100235-A1.  
 PD 04-JAN-2001.  
 PA (UYMC-) UNIV MCGILL.  
 PA (CAPR-) CAPRION PHARM INC.  
 Best Local Similarity: 22.34% Mismatches: 63  
 Query Match: 7.12% Indels: 51  
 RESULT 840  
 ID AAQ44391 standard; cDNA to mRNA; 3581 BP.  
 DE Sequence of murine OSF-4 cDNA.  
 PN EP595801-A2.  
 PD 09-MAR-1994.  
 PA (FARH) HOECHST JAPAN LTD.  
 Best Local Similarity: 22.34% Mismatches: 63  
 Query Match: 7.12% Indels: 51  
 RESULT 841  
 ID ABL23088 standard; DNA; 3755 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 20737.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEXE) PE CORP NY.  
 Best Local Similarity: 23.72% Mismatches: 77  
 Query Match: 7.12% Indels: 60  
 RESULT 842  
 ID ABL03155 standard; cDNA; 3862 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3947.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEXE) PE CORP NY.  
 Best Local Similarity: 24.52% Mismatches: 77  
 Query Match: 7.12% Indels: 49  
 RESULT 843  
 ID ABI99752 standard; cDNA; 4127 BP.  
 DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:825.  
 PN WO200188188-A2.  
 PD 22-NOV-2001.  
 PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.  
 Best Local Similarity: 22.34% Mismatches: 63  
 Query Match: 7.12% Indels: 51  
 RESULT 844  
 ID ADA08722 standard; cDNA; 10620 BP.  
 DE Human O772P variable region repeat cDNA #58.  
 PN US2003091580-A1.  
 PD 15-MAY-2003.  
 PA (MITC/) MITCHAM J L.  
 PA (KING/) KING G E.  
 PA (ALGA/) ALGATE P A.  
 PA (FLIN/) FLING S P.  
 PA (RETT/) RETTER M W.  
 PA (FANG/) FANGER G R.  
 PA (REED/) REED S G.  
 PA (VEDV/) VEDVICK T S.  
 PA (CART/) CARTER D.  
 PA (HILL/) HILL P.  
 PA (ALBO/) ALBONE E.  
 Best Local Similarity: 20.83% Mismatches: 61  
 Query Match: 7.12% Indels: 61  
 RESULT 845  
 ID ABN73047 standard; cDNA; 10622 BP.  
 DE cDNA sequence of 0772P and 3' constant and untranslated region.  
 PN WO200206317-A2.  
 PD 24-JAN-2002.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 20.83% Mismatches: 61  
 Query Match: 7.12% Indels: 61  
 RESULT 846  
 ID ADF09065 standard; cDNA; 10622 BP.  
 DE cDNA encoding secreted ovarian carcinoma antigen seqid 569.  
 PN US2003124140-A1.



PD 03-JUL-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 20.83% Mismatches: 61  
Query Match: 7.12% Indels: 61  
RESULT 847  
ID AAO90512 standard; DNA; 11288 BP.  
DE CEA clone HindIII-Sau3A fragment.  
PN WO9514100-A2.  
PD 26-MAY-1995.  
PA (WELL) WELLCOME FOUND LTD.  
Best Local Similarity: 43.33% Mismatches: 27  
Query Match: 7.12% Indels: 2  
RESULT 848  
ID AAS14778 standard; DNA; 11288 BP.  
DE Human carcinoembryonic antigen (CEA) genomic DNA.  
PN WO200174861-A2.  
PD 11-OCT-2001.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Best Local Similarity: 43.33% Mismatches: 27  
Query Match: 7.12% Indels: 2  
RESULT 849  
ID ABL15248 standard; cDNA; 11743 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 40226.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 26.25% Mismatches: 68  
Query Match: 7.12% Indels: 33  
RESULT 850  
ID ABL16702 standard; DNA; 12216 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 1579.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 22.86% Mismatches: 58  
Query Match: 7.12% Indels: 33  
RESULT 851  
ID ADL27165 standard; cDNA; 14450 BP.  
DE Human CDNA sequence for hCG23764.  
PN US2003216558-A1.  
PD 20-NOV-2003.  
PA (MORR) MORRIS D W.  
PA (ENGE) ENGELHARD E K.  
Best Local Similarity: 23.53% Mismatches: 64  
Query Match: 7.12% Indels: 51  
RESULT 852  
ID AAV52967 standard; DNA; 15056 BP.  
DE Carcinoembryonic antigen gene 5' flanking region.  
PN WO9839467-A2.  
PD 11-SEP-1998.  
PA (CALY-) CALYDON INC.  
Best Local Similarity: 43.33% Mismatches: 27  
Query Match: 7.12% Indels: 2  
RESULT 853  
ID AAZ99933 standard; DNA; 15056 BP.  
DE DNA sequence of comprising a carcinoembryonic antigen TRE.  
PN WO200015820-A1.  
PD 23-MAR-2000.  
PA (CALY-) CALYDON INC.  
Best Local Similarity: 43.33% Mismatches: 27  
Query Match: 7.12% Indels: 2  
RESULT 854  
ID AAA46851 standard; DNA; 15056 BP.  
DE Nucleotide sequence of a CEA-TRE.  
PN WO200039319-A2.  
PD 06-JUL-2000.  
PA (CALY-) CALYDON INC.  
Best Local Similarity: 43.33% Mismatches: 27  
Query Match: 7.12% Indels: 2  
RESULT 855  
ID AAH43620 standard; cDNA; 15056 BP.  
DE CEA-TRE.  
PN WO200173093-A2.

PD 04-OCT-2001.  
PA (CALY-) CALYDON INC.  
Best Local Similarity: 43.33% Mismatches: 27  
Query Match: 7.12% Indels: 2  
RESULT 856  
ID AAF87238 standard; DNA; 15056 BP.  
DE CEA-TRE fusion protein coding sequence.  
PN WO200172341-A2.  
PD 04-OCT-2001.  
PA (CALY-) CALYDON INC.  
Best Local Similarity: 43.33% Mismatches: 27  
Query Match: 7.12% Indels: 2  
RESULT 857  
ID ABK95982 standard; DNA; 15056 BP.  
DE Prostate-specific antigen transcriptional regulatory element (TRE).  
PN US2002068049-A1.  
PD 06-JUN-2002.  
PA (HEND) HENDERSON D R.  
PA (SCHU) SCHUUR E R.  
Best Local Similarity: 43.33% Mismatches: 27  
Query Match: 7.12% Indels: 2  
RESULT 858  
ID ACD07309 standard; DNA; 15056 BP.  
DE Human carcinoembryonic antigen (CEA) TRE.  
PN US2003044383-A1.  
PD 06-MAR-2003.  
PA (HEND) HENDERSON D R.  
PA (SCHU) SCHUUR E R.  
Best Local Similarity: 43.33% Mismatches: 27  
Query Match: 7.12% Indels: 2  
RESULT 859  
ID ACF62751 standard; DNA; 177380 BP.  
DE Cancer based on CYP3A5 related polynucleotide SEQ ID NO:683.  
PN WO2003013534-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
Best Local Similarity: 25.69% Mismatches: 38  
Query Match: 7.12% Indels: 47  
RESULT 860  
ID ADB20870 standard; DNA; 177380 BP.  
DE MRP1 based cancer related nucleic acid SEQ ID NO:683.  
PN WO2003013533-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
Best Local Similarity: 25.69% Mismatches: 38  
Query Match: 7.12% Indels: 47  
RESULT 861  
ID ADB87959 standard; DNA; 177380 BP.  
DE Human UGT1A1 gene sequence SEQ ID NO:683.  
PN WO2003013536-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
Best Local Similarity: 25.69% Mismatches: 38  
Query Match: 7.12% Indels: 47  
RESULT 862  
ID ADB96942 standard; DNA; 177380 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:683.  
PN WO2003013537-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
Best Local Similarity: 25.69% Mismatches: 38  
Query Match: 7.12% Indels: 47  
RESULT 863  
ID ADB92133 standard; DNA; 177380 BP.  
DE Human MDR1 related DNA sequence SEQ ID NO:683.  
PN WO2003013535-A2.  
PD 20-FEB-2003.  
PA (EPID-) EPIDAURUS BIOTECHNOLOGIE AG.  
Best Local Similarity: 25.69% Mismatches: 38  
Query Match: 7.12% Indels: 47  
RESULT 864  
ID AAT83807 standard; DNA; 825 BP.  
DE DNA encoding a surfactin synthetase.

PN WO9730070-A1.  
PD 21-AUG-1997.  
PA (SMIX ) SMITHKLINE BEECHAM CORP.  
Best Local Similarity: 27.78% Mismatches: 56  
Query Match: 7.08% Indels: 23  
RESULT 865  
ID ABV94556 standard; cDNA; 903 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:117.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 21.38% Mismatches: 58  
Query Match: 7.08% Indels: 38  
RESULT 866  
ID ADM18752 standard; cDNA; 903 BP.  
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:117.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 21.38% Mismatches: 58  
Query Match: 7.08% Indels: 38  
RESULT 867  
ID AAT36760 standard; DNA; 1599 BP.  
DE CD4:T-cell receptor eta chain chimaeric receptor DNA.  
PN WO9625953-A1.  
PD 29-AUG-1996.  
PA (GEHO ) GEN HOSPITAL CORP.  
Best Local Similarity: 23.88% Mismatches: 53  
Query Match: 7.08% Indels: 25  
RESULT 868  
ID ABQ99353 standard; cDNA; 1621 BP.  
DE Human coding sequence SEQ ID 86.  
PN WO200259260-A2.  
PD 01-AUG-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 20.96% Mismatches: 67  
Query Match: 7.08% Indels: 34  
RESULT 869  
ID ADQ22129 standard; DNA; 2012 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4949.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 20.50% Mismatches: 73  
Query Match: 7.08% Indels: 55  
RESULT 870  
ID ADG93388 standard; DNA; 2664 BP.  
DE Maize lipoxxygenase (LOX) DNA #10.  
PN US2003166855-A1.  
PD 04-SEP-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Best Local Similarity: 24.06% Mismatches: 53  
Query Match: 7.08% Indels: 24  
RESULT 871  
ID ADG93386 standard; DNA; 3080 BP.  
DE Maize lipoxxygenase (LOX) DNA #9.  
PN US2003166855-A1.  
PD 04-SEP-2003.  
PA (PION-) PIONEER HI-BRED INT INC.  
Best Local Similarity: 24.06% Mismatches: 53  
Query Match: 7.08% Indels: 24  
RESULT 872  
ID ABD33601 standard; DNA; 70019 BP.  
DE Murine cancer-associated (CA) gene MD07-122.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 27.62% Mismatches: 43  
Query Match: 7.08% Indels: 22  
RESULT 873  
ID ACN44044 standard; DNA; 134481 BP.  
DE Mouse genomic sequence mCG13084.  
PN WO2003073826-A2.

PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 26.21% Mismatches: 32  
Query Match: 7.08% Indels: 53  
RESULT 874  
ID ADI42109 standard; DNA; 583 BP.  
DE Plant transcription factor polynucleotide #317.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIAN/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HAAK/) HAAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PILG/) PILGRIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
Best Local Similarity: 25.81% Mismatches: 42  
Query Match: 7.03% Indels: 11  
RESULT 875  
ID ADO02651 standard; cDNA; 583 BP.  
DE Soybean orthologue of Thalecress transcription factor, cDNA #55.  
PN US2004045049-A1.  
PD 04-MAR-2004.  
PA (ZHAN/) ZHANG J.  
PA (FROM/) FROMM M E.  
PA (HEAR/) HEARD J E.  
PA (RIEC/) RIECHMANN J L.  
PA (ADAM/) ADAM L J.  
PA (BROU/) BROUN P E.  
PA (PINE/) PINEDA O.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J S.  
PA (YUGG/) YU G.  
PA (JIAN/) JIANG C.  
PA (SAMA/) SAMAHA R S.  
PA (PILG/) PILGRIM M L.  
PA (CREE/) CREELMAN R A.  
PA (DUBE/) DUBELL A N.  
PA (RATC/) RATCLIFFE O.  
PA (KUMI/) KUMIMOTO R.  
PA (SHER/) SHERMAN B K.  
Best Local Similarity: 25.81% Mismatches: 42  
Query Match: 7.03% Indels: 11  
RESULT 876  
ID AAK51735 standard; cDNA; 888 BP.  
DE Human polynucleotide SEQ ID NO 280.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 19.51% Mismatches: 46  
Query Match: 7.03% Indels: 31  
RESULT 877  
ID ABZ32399 standard; DNA; 945 BP.  
DE Candida albicans essential gene SEQ ID NO 6686.  
PN WO200253728-A2.  
PD 11-JUL-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 20.00% Mismatches: 67  
Query Match: 7.03% Indels: 59  
RESULT 878  
ID AAZ53928 standard; DNA; 1407 BP.  
DE Neisseria meningitidis ORF 585 partial DNA sequence SEQ ID NO:1805.  
PN WO9957280-A2.  
PD 11-NOV-1999.  
PA (CHIR ) CHIRON CORP.

PA (GENO-) INST GENOMIC RES.			
Best Local Similarity: 23.23%			
Query Match: 7.03%	81	Mismatches:	24
Indels:	41	Indels:	20
RESULT 879			
ID ADD69651 standard; cDNA; 1480 BP.			
DE Human REMAP cDNA - SEQ ID 80.			
PN WO2003048305-A2.			
PD 12-JUN-2003.			
PA (INCY-) INCYTE GENOMICS INC.			
Best Local Similarity: 23.56%	67	Mismatches:	56
Query Match: 7.03%	36	Indels:	57
RESULT 880			
ID AA294095 standard; cDNA; 2313 BP.			
DE Haematopoietic stem cell specific nucleic acid.			
PN WO200011168-A2.			
PD 02-MAR-2000.			
PA (UYPR-) UNIV PRINCETON.			
Best Local Similarity: 20.00%	49	Mismatches:	56
Query Match: 7.03%	78	Indels:	57
RESULT 881			
ID AA523202 standard; cDNA; 2653 BP.			
DE DNA encoding novel bone marrow polypeptide #103.			
PN WO200155442-A2.			
PD 02-AUG-2001.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 20.15%	74	Mismatches:	56
Query Match: 7.03%	102	Indels:	57
RESULT 882			
ID ADS11543 standard; DNA; 2653 BP.			
DE Human therapeutic contig DNA - SEQ ID 1780.			
PN WO2004080148-A2.			
PD 23-SEP-2004.			
PA (NUVE-) NUVELO INC.			
Best Local Similarity: 20.15%	74	Mismatches:	56
Query Match: 7.03%	102	Indels:	57
RESULT 883			
ID ADS11202 standard; DNA; 2653 BP.			
DE Human therapeutic contig DNA - SEQ ID 1439.			
PN WO2004080148-A2.			
PD 23-SEP-2004.			
PA (NUVE-) NUVELO INC.			
Best Local Similarity: 20.15%	74	Mismatches:	56
Query Match: 7.03%	102	Indels:	57
RESULT 884			
ID AA587573 standard; cDNA; 3097 BP.			
DE DNA encoding novel human diagnostic protein #23377.			
PN WO200175667-A2.			
PD 11-OCT-2001.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 21.70%	67	Mismatches:	56
Query Match: 7.03%	73	Indels:	57
RESULT 885			
ID AA579043 standard; cDNA; 3852 BP.			
DE DNA encoding novel human diagnostic protein #14847.			
PN WO200175067-A2.			
PD 11-OCT-2001.			
PA (HYSE-) HYSEQ INC.			
Best Local Similarity: 22.89%	48	Mismatches:	56
Query Match: 7.03%	54	Indels:	57
RESULT 886			
ID AA294129 standard; cDNA; 3857 BP.			
DE Haematopoietic stem cell specific nucleic acid.			
PN WO200011168-A2.			
PD 02-MAR-2000.			
PA (UYPR-) UNIV PRINCETON.			
Best Local Similarity: 20.00%	49	Mismatches:	56
Query Match: 7.03%	78	Indels:	57
RESULT 887			
ID ADF74188 standard; cDNA; 6957 BP.			
DE Human novel brain/hippocampus cDNA #6.			
PN JP2003009886-A.			
PD 14-JAN-2003.			
PA (KAZU-) ZH KAZUSA DNA KENKYUSHO.			
Best Local Similarity: 25.00%	56	Mismatches:	56
Query Match: 7.03%	57	Indels:	57
PA (PROT-) PROTEIN EXPRESS KK.			
Best Local Similarity: 29.76%	24	Mismatches:	56
Query Match: 7.03%	20	Indels:	57
RESULT 888			
ID AAQ40480 standard; cDNA; 15894 BP.			
DE Attenuated measles virus strain AIK-C.			
PN EP540135-A2.			
PD 05-MAY-1993.			
PA (KITA) KITASATO INST.			
Best Local Similarity: 25.00%	56	Mismatches:	56
Query Match: 7.03%	57	Indels:	57
RESULT 889			
ID AAV18271 standard; DNA; 15894 BP.			
DE Measles virus AIK-C vaccine L protein genomic DNA.			
PN WO9813501-A2.			
PD 02-APR-1998.			
PA (AMCY) AMERICAN CYANAMID CO.			
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.			
Best Local Similarity: 25.00%	56	Mismatches:	56
Query Match: 7.03%	57	Indels:	57
RESULT 890			
ID AAV18268 standard; DNA; 15894 BP.			
DE Measles virus Rubeovax vaccine L protein genomic DNA.			
PN WO9813501-A2.			
PD 02-APR-1998.			
PA (AMCY) AMERICAN CYANAMID CO.			
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.			
Best Local Similarity: 25.00%	56	Mismatches:	56
Query Match: 7.03%	57	Indels:	57
RESULT 891			
ID AAV18269 standard; DNA; 15894 BP.			
DE Measles virus Moraten vaccine L protein genomic DNA.			
PN WO9813501-A2.			
PD 02-APR-1998.			
PA (AMCY) AMERICAN CYANAMID CO.			
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.			
Best Local Similarity: 25.00%	56	Mismatches:	56
Query Match: 7.03%	57	Indels:	57
RESULT 892			
ID AAV18270 standard; DNA; 15894 BP.			
DE Measles virus Zagreb vaccine L protein genomic DNA.			
PN WO9813501-A2.			
PD 02-APR-1998.			
PA (AMCY) AMERICAN CYANAMID CO.			
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.			
Best Local Similarity: 25.00%	56	Mismatches:	56
Query Match: 7.03%	57	Indels:	57
RESULT 893			
ID AAV18264 standard; DNA; 15894 BP.			
DE Measles virus Edmonston isolate wild-type L protein genomic DNA.			
PN WO9813501-A2.			
PD 02-APR-1998.			
PA (AMCY) AMERICAN CYANAMID CO.			
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.			
Best Local Similarity: 25.00%	56	Mismatches:	56
Query Match: 7.03%	57	Indels:	57
RESULT 894			
ID AAV18265 standard; DNA; 15894 BP.			
DE Measles virus 1977 isolate wild-type L protein genomic DNA.			
PN WO9813501-A2.			
PD 02-APR-1998.			
PA (AMCY) AMERICAN CYANAMID CO.			
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.			
Best Local Similarity: 25.00%	56	Mismatches:	56
Query Match: 7.03%	57	Indels:	57
RESULT 895			
ID AA222907 standard; DNA; 15894 BP.			
DE Nucleotide sequence of Zagreb vaccine measles virus genome.			
PN WO9949017-A2.			
PD 30-SEP-1999.			
PA (AMCY) AMERICAN CYANAMID CO.			
Best Local Similarity: 25.00%	56	Mismatches:	56
Query Match: 7.03%	57	Indels:	57

RESULT 896  
ID AAZ22901 standard; DNA; 15894 BP.  
DE Nucleotide sequence of wild type measles virus Edmonston strain.  
PN WO9949017-A2.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Best Local Similarity: 25.00% Mismatches: 56  
Query Match: 7.03% Indels: 57  
RESULT 897  
ID AAZ22908 standard; DNA; 15894 BP.  
DE Nucleotide sequence of AIK-C vaccine measles virus genome.  
PN WO9949017-A2.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Best Local Similarity: 25.00% Mismatches: 56  
Query Match: 7.03% Indels: 57  
RESULT 898  
ID AAZ22902 standard; DNA; 15894 BP.  
DE Nucleotide sequence of wild type measles virus 1977 strain.  
PN WO9949017-A2.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Best Local Similarity: 25.00% Mismatches: 56  
Query Match: 7.03% Indels: 57  
RESULT 899  
ID AAZ22905 standard; DNA; 15894 BP.  
DE Nucleotide sequence of Rubioavax vaccine measles virus genome.  
PN WO9949017-A2.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Best Local Similarity: 25.00% Mismatches: 56  
Query Match: 7.03% Indels: 57  
RESULT 900  
ID AAZ22906 standard; DNA; 15895 BP.  
DE Nucleotide sequence of Moraten vaccine measles virus genome.  
PN WO9949017-A2.  
PA (AMCY ) AMERICAN CYANAMID CO.  
Best Local Similarity: 25.00% Mismatches: 56  
Query Match: 7.03% Indels: 57  
RESULT 901  
ID ADH43072 standard; cDNA; 18967 BP.  
DE Measles virus Schwarz antigenome cDNA sequence.  
PN WO2004000876-A1.  
PD 31-DEC-2003.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CENT NAT RECH SCI.  
Best Local Similarity: 25.00% Mismatches: 56  
Query Match: 7.03% Indels: 57  
RESULT 902  
ID ACA63261 standard; DNA; 18967 BP.  
DE PTM-MVSWchw plaemid containing measles virus Schwarz antigenome.  
PN WO2004001051-A2.  
PD 31-DEC-2003.  
PA (INSP ) INST PASTEUR.  
PA (CNRS ) CENT NAT RECH SCI.  
Best Local Similarity: 25.00% Mismatches: 56  
Query Match: 7.03% Indels: 57  
RESULT 903  
ID AAL56703 standard; DNA; 36462 BP.  
DE Chimpanzee adenovirus serotype Pan5 genomic DNA.  
PN WO2003046124-A2.  
PD 05-JUN-2003.  
PA (UYPE-) UNIV PENNSYLVANIA.  
PA (UYPE-) CENT NAT RECH SCI.  
Best Local Similarity: 22.66% Mismatches: 51  
Query Match: 7.03% Indels: 20  
RESULT 904  
ID AAA81457 standard; DNA; 49646 BP.  
DE N. meningitidis partial DNA sequence gnm\_5 SEQ ID NO:5.  
PN WO200022430-A2.  
PD 20-APR-2000.  
PA (CHIR ) CHIRON CORP.  
Best Local Similarity: 23.23% Mismatches: 81

Query Match: 7.03% Indels: 41  
RESULT 905  
Best Local Similarity: 23.23% Mismatches: 81  
Query Match: 7.03% Indels: 41  
RESULT 906  
ID AAF21607 standard; DNA; 349980 BP.  
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:108.  
PN WO200066791-A1.  
PD 09-NOV-2000.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Best Local Similarity: 23.23% Mismatches: 81  
Query Match: 7.03% Indels: 41  
RESULT 907  
ID AAF21608 standard; DNA; 349980 BP.  
DE Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.  
PN WO200066791-A1.  
PD 09-NOV-2000.  
PA (CHIR ) CHIRON CORP.  
PA (GENO-) INST GENOMIC RES.  
Best Local Similarity: 23.23% Mismatches: 81  
Query Match: 7.03% Indels: 41  
RESULT 908  
ID AAH73602 standard; DNA; 2979 BP.  
DE Human WT1-interacting protein coding sequence.  
PN WO200153484-A1.  
PD 26-JUL-2001.  
PA (SUGI/) SUGIYAMA H.  
Best Local Similarity: 23.98% Mismatches: 58  
Query Match: 6.99% Indels: 43  
RESULT 909  
ID ADC37608 standard; DNA; 2979 BP.  
DE Human nucleic acid associated protein NAAP-15 coding sequence.  
PN WO2003046151-A2.  
PD 05-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 23.98% Mismatches: 58  
Query Match: 6.99% Indels: 43  
RESULT 910  
ID ABL14505 standard; cDNA; 6030 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37997.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEXE ) PE CORP NY.  
Best Local Similarity: 20.64% Mismatches: 77  
Query Match: 6.99% Indels: 64  
RESULT 911  
Best Local Similarity: 30.09% Mismatches: 36  
Query Match: 6.99% Indels: 24  
RESULT 912  
Best Local Similarity: 24.32% Mismatches: 66  
Query Match: 6.99% Indels: 39  
RESULT 913  
ID ACN44200 standard; DNA; 211257 BP.  
DE Mouse genomic sequence mCG15870.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 24.58% Mismatches: 52  
Query Match: 6.99% Indels: 12  
RESULT 914  
ID ABQ81847 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1103.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST ) SOC PROD NESTLE SA.  
Best Local Similarity: 29.29% Mismatches: 31  
Query Match: 6.99% Indels: 16  
RESULT 915  
ID ABQ81847 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1103.  
PN EP1227152-A1.  
PD 31-JUL-2002.

PA (NEST ) SOC PROD NESTLE SA. Mismatches: 23  
Best Local Similarity: 24.27% Indels: 30  
Query Match: 6.99%  
RESULT 916  
ID ABQ81849 standard; DNA; 349980 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1105.  
PN EPI227152-A1.  
PD 31-JUL-2002.  
PA (NEST ) SOC PROD NESTLE SA. Mismatches: 27  
Best Local Similarity: 27.40% Indels: 8  
Query Match: 6.99%  
RESULT 917  
ID ABV94498 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:12.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC. Mismatches: 60  
Best Local Similarity: 22.64% Indels: 35  
Query Match: 6.94%  
RESULT 918  
ID ADM18647 standard; cDNA; 912 BP.  
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:12.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC. Mismatches: 60  
Best Local Similarity: 22.64% Indels: 35  
Query Match: 6.94%  
RESULT 919  
ID ADH83660 standard; DNA; 960 BP.  
DE Enterococcus faecalis polynucleotide #1545.  
PN US6617156-B1.  
PD 09-SEP-2003.  
PA (DOUC/) DOUCETTE-STAMM L A.  
PA (BUSH/) BUSH D.  
Best Local Similarity: 20.59% Mismatches: 55  
Query Match: 6.94% Indels: 53  
RESULT 920  
ID ABT1717379 standard; DNA; 1644 BP.  
DE Human IG gene related nucleic acid SEQ ID No 5.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC. Mismatches: 46  
Best Local Similarity: 25.43% Indels: 57  
Query Match: 6.94%  
RESULT 921  
ID AAD37441 standard; DNA; 1650 BP.  
DE Mouse nectin-3-human nectin 3alpha fusion protein encoding DNA.  
PN WO200228902-A2.  
PD 11-APR-2002.  
PA (IMMV ) IMMUNEX CORP. Mismatches: 46  
Best Local Similarity: 25.43% Indels: 57  
Query Match: 6.94%  
RESULT 922  
ID AAD37442 standard; DNA; 1650 BP.  
DE Human nectin-3alpha DNA.  
PN WO200228902-A2.  
PD 11-APR-2002.  
PA (IMMV ) IMMUNEX CORP. Mismatches: 46  
Best Local Similarity: 25.43% Indels: 57  
Query Match: 6.94%  
RESULT 923  
ID ABT17378 standard; DNA; 1650 BP.  
DE Human IG gene related nucleic acid SEQ ID No 4.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC. Mismatches: 46  
Best Local Similarity: 25.43% Indels: 57  
Query Match: 6.94%  
RESULT 924  
ID ADR66544 standard; DNA; 1650 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 56 #3.  
PN WO2004076614-A2.  
PD 10-SEP-2004.

PA (HINZ/) HINZMANN B. Mismatches: 46  
PA (DAHL/) DAHL E. Indels: 57  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Best Local Similarity: 25.43% Mismatches: 46  
Query Match: 6.94% Indels: 57  
RESULT 925  
ID ADR66202 standard; DNA; 1650 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 56 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ/) HINZMANN B. Mismatches: 46  
PA (DAHL/) DAHL E. Indels: 57  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Best Local Similarity: 25.43% Mismatches: 46  
Query Match: 6.94% Indels: 57  
RESULT 926  
ID AAS82539 standard; cDNA; 2155 BP.  
DE DNA encoding novel human diagnostic protein #18343.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC. Mismatches: 76  
Best Local Similarity: 21.81% Indels: 41  
Query Match: 6.94%  
RESULT 927  
ID AAD37440 standard; DNA; 3147 BP.  
DE Human deleted nectin-3alpha DNA.  
PN WO200228902-A2.  
PD 11-APR-2002.  
PA (IMMV ) IMMUNEX CORP. Mismatches: 46  
Best Local Similarity: 25.43% Indels: 57  
Query Match: 6.94%  
RESULT 928  
ID ABL03339 standard; cDNA; 3900 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4499.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY. Mismatches: 81  
Best Local Similarity: 23.56% Indels: 59  
Query Match: 6.94%  
RESULT 929  
ID ADN96169 standard; cDNA; 4031 BP.  
DE Human NOVX polynucleotide #112.  
PN US2004067490-A1.  
PD 08-APR-2004.  
PA (ZHON/) ZHONG M. Mismatches: 46  
PA (LILL/) LI L. Indels: 57  
PA (GORM/) GORMAN L.  
PA (SPYT/) SPYTEK K A.  
PA (KEKU/) KEKUDA R. J.  
PA (TAUP/) TAUFIER R. J.  
PA (ANDE/) ANDERSON D W.  
PA (VERN/) VERNET C A M.  
PA (CATT/) CATTERTON E.  
PA (MILL/) MILLER C E.  
PA (SHEN/) SHENOY S G.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENNA C E A.  
PA (TCHE/) TCHERNEV V T.  
PA (PADI/) PADIGARU M.  
PA (GUSE/) GUSEV V Y.  
PA (NALLY/) NALLYANKAR U M.  
PA (BURG/) BURGESS C E.  
PA (GERL/) GERLACH V.  
PA (CASM/) CASMAN S J.  
PA (RIEG/) RIEGER D K.  
PA (GROS/) GROSSE W M.  
PA (SMIT/) SMITHSON G.  
PA (PEYM/) PEYMAN J A.  
PA (STAR/) STARLING G.

PA (ROTH/) ROTHENBERG M E.  
 PA (LARO/) LAROCHELLE W J.  
 PA (SHIM/) SHIMKETS R A.  
 PA (CRAB/) CRASTREE J.  
 PA (RAST/) RASTELLI L.  
 PA (VOSS/) VOSS E Z.  
 PA (BOLD/) BOLDOG F L.  
 PA (EDIN/) EDINGER S R.  
 PA (MILL/) MILLET I.  
 PA (MACD/) MACDOUGALL J R.  
 PA (ELLE/) ELLERMAN K.  
 PA (CHAP/) CHAPOVAL A.  
 Best Local Similarity: 22.88%  
 Query Match: 6.94%  
 Mismatches: 48  
 Indels: 43

RESULT 930  
 ID AAQ13789 standard; DNA; 5363 BP.  
 DE Cellulose synthase catalytic subunit gene and related protein gene.  
 PN W09113988-A.  
 PD 19-SEP-1991.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 Best Local Similarity: 25.27%  
 Query Match: 6.94%  
 Mismatches: 69  
 Indels: 46

RESULT 931  
 ID ABS76476 standard; cDNA; 5793 BP.  
 DE cDNA encoding human ovarian cancer marker M460.  
 PN W0200271928-A2.  
 PD 19-SEP-2002.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 21.94%  
 Query Match: 6.94%  
 Mismatches: 59  
 Indels: 63

RESULT 932  
 ID ABZ11166 standard; cDNA; 6376 BP.  
 DE Human polynucleotide SEQ ID NO 48.  
 PN W0200270539-A2.  
 PD 12-SEP-2002.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 26.88%  
 Query Match: 6.94%  
 Mismatches: 61  
 Indels: 44

RESULT 933  
 ID ADM43684 standard; cDNA; 6376 BP.  
 DE Novel human arginine-rich protein cDNA #48.  
 PN US2004053250-A1.  
 PD 18-MAR-2004.  
 PA (TANG/) TANG Y T.  
 PA (XUEA/) XUE A.  
 PA (DRMA/) DRMANAC R T.  
 Best Local Similarity: 26.88%  
 Query Match: 6.94%  
 Mismatches: 61  
 Indels: 44

RESULT 934  
 ID ABL03338 standard; cDNA; 7572 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 4496.  
 PN W0200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE ) PE CORP NY.  
 Best Local Similarity: 23.56%  
 Query Match: 6.94%  
 Mismatches: 81  
 Indels: 59

RESULT 935  
 ID AAL56705 standard; DNA; 36535 BP.  
 DE Chimpanzee adenovirus serotype Pan7 genomic DNA.  
 PN W02003046124-A2.  
 PD 05-JUN-2003.  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 Best Local Similarity: 19.40%  
 Query Match: 6.94%  
 Mismatches: 75  
 Indels: 51

RESULT 936  
 ID AAL56705 standard; DNA; 36535 BP.  
 DE Chimpanzee adenovirus serotype Pan7 genomic DNA.  
 PN W02003046124-A2.  
 PD 05-JUN-2003.  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 Best Local Similarity: 22.55%  
 Query Match: 6.94%  
 Mismatches: 70  
 Indels: 87

RESULT 937  
 ID AAL56705 standard; DNA; 36535 BP.  
 DE Chimpanzee adenovirus serotype Pan7 genomic DNA.  
 PN W02003046124-A2.  
 PD 05-JUN-2003.  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 Best Local Similarity: 22.55%  
 Query Match: 6.94%  
 Mismatches: 70  
 Indels: 87

RESULT 938  
 ID AAL56705 standard; DNA; 36535 BP.  
 DE Chimpanzee adenovirus serotype Pan7 genomic DNA.  
 PN W02003046124-A2.  
 PD 05-JUN-2003.  
 PA (UYPE-) UNIV PENNSYLVANIA.  
 Best Local Similarity: 22.55%  
 Query Match: 6.94%  
 Mismatches: 70  
 Indels: 87

RESULT 939  
 ID ADN46845 standard; DNA; 2089378 BP.  
 DE Thermococcus kodakaraensis KOD1 genome DNA sequence SeqID723.  
 PN W02004022736-A1.  
 PD 18-MAR-2004.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Best Local Similarity: 22.55%  
 Query Match: 6.94%  
 Mismatches: 70  
 Indels: 87

RESULT 940  
 ID ADN46123 standard; DNA; 2089378 BP.  
 DE Thermococcus kodakaraensis KOD1 genome DNA sequence SeqID1.  
 PN W02004022736-A1.  
 PD 18-MAR-2004.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Best Local Similarity: 22.55%  
 Query Match: 6.94%  
 Mismatches: 70  
 Indels: 87

RESULT 941  
 ID ADN46464 standard; DNA; 2089378 BP.  
 DE Thermococcus kodakaraensis KOD1 DNA sequence SeqID342.  
 PN W02004022736-A1.  
 PD 18-MAR-2004.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Best Local Similarity: 22.55%  
 Query Match: 6.94%  
 Mismatches: 70  
 Indels: 87

RESULT 942  
 ID ADD16877 standard; DNA; 511 BP.  
 DE DNA (SeqID 945) that confers an altered visual phenotype in plants.  
 PN W02003020741-A1.  
 PD 13-MAR-2003.  
 PA (DOWC ) DOW CHEM CO.  
 Best Local Similarity: 23.77%  
 Query Match: 6.90%  
 Mismatches: 43  
 Indels: 30

RESULT 943  
 ID AAD56953 standard; cDNA; 730 BP.  
 DE Human mucin 1 transmembrane variant, MUC1/X cDNA.  
 PN W02003054154-A2.  
 PD 03-JUL-2003.  
 PA (ISIS-) ISIS PHARM INC.  
 Best Local Similarity: 24.02%  
 Query Match: 6.90%  
 Mismatches: 90  
 Indels: 18

RESULT 944  
 ID AAD56949 standard; cDNA; 981 BP.  
 DE Human mucin 1 transmembrane variant, MUC1-V cDNA.  
 PN W02003054154-A2.  
 PD 03-JUL-2003.  
 PA (ISIS-) ISIS PHARM INC.  
 Best Local Similarity: 26.27%  
 Query Match: 6.90%  
 Mismatches: 63  
 Indels: 8

RESULT 945  
 ID ADIS7684 standard; cDNA; 1183 BP.  
 DE Human breast specific nucleic acid (BSNA) #55.  
 PN W02003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 24.02%  
 Query Match: 6.90%  
 Mismatches: 90  
 Indels: 18

RESULT 946  
 ID ADIS7703 standard; cDNA; 1189 BP.  
 DE Human breast specific nucleic acid (BSNA) #74.  
 PN W02003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 21.54%  
 Query Match: 6.90%  
 Mismatches: 64  
 Indels: 15

RESULT 947  
 ID AAC34320 standard; DNA; 1327 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 74462.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 Best Local Similarity: 23.77%  
 Query Match: 6.90%  
 Mismatches: 43  
 Indels: 30

RESULT 948

ID AD157687 standard; cDNA; 1605 BP.  
 DE Human breast specific nucleic acid (BSNA) #58.  
 PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 26.27% Mismatches: 63  
 Query Match: 6.90% Indels: 8  
 RESULT 949

ID AD744101 standard; cDNA; 1608 BP.  
 DE Bacterial polynucleotide #18852.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 26.03% Mismatches: 36  
 Query Match: 6.90% Indels: 52  
 RESULT 950

ID AAS71120 standard; cDNA; 1687 BP.  
 DE DNA encoding novel human diagnostic protein #6924.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 23.33% Mismatches: 42  
 Query Match: 6.90% Indels: 49  
 RESULT 951

ID AAX99301 standard; cDNA; 1728 BP.  
 DE C. elegans CED-6 protein encoding nucleic acid.  
 PN WO9937770-A1.  
 PD 29-JUL-1999.  
 PA (COLD-) COLD SPRING HARBOR LAB.  
 PA (DEVG-) DEVGEN NV.  
 Best Local Similarity: 25.97% Mismatches: 49  
 Query Match: 6.90% Indels: 46  
 RESULT 952

ID ABK88194 standard; DNA; 1846 BP.  
 DE DNA encoding human 553 amino acid transporter protein.  
 PN JP2002171980-A.  
 PD 18-JUN-2002.  
 PA (TOHO) UNIV TOHOKU  
 Best Local Similarity: 26.15% Mismatches: 75  
 Query Match: 6.90% Indels: 58  
 RESULT 953

ID ABV97363 standard; cDNA; 295 BP.  
 DE Human pancreatic cancer expressed cDNA SEQ ID NO 2771.  
 PN WO200260317-A2.  
 PD 08-AUG-2002.  
 PA (CORI-) CORIXA CORP.  
 Best Local Similarity: 24.18% Mismatches: 51  
 Query Match: 6.85% Indels: 1  
 RESULT 954

ID ACN54849 standard; cDNA; 520 BP.  
 DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-K6-F8, SEQ:9630.  
 PN US2004123340-A1.  
 PD 24-JUN-2004.  
 PA (DEIK/) DEIKMAN J.  
 PA (PENG/) PENG P C C.  
 PA (FINC/) FINCHER K L.  
 PA (ZIEG/) ZIEGLER T E.  
 Best Local Similarity: 22.88% Mismatches: 48  
 Query Match: 6.85% Indels: 49  
 RESULT 955

ID AA121091 standard; DNA; 570 BP.  
 DE Probe #11024 for gene expression analysis in human cervical cell sample.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 19.23% Mismatches: 50  
 Query Match: 6.85% Indels: 29  
 RESULT 956

ID ABA66169 standard; DNA; 570 BP.

DE Human foetal liver single exon nucleic acid probe #14474.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 19.23% Mismatches: 50  
 Query Match: 6.85% Indels: 29  
 RESULT 957

ID AAI46353 standard; DNA; 570 BP.  
 DE Probe #15039 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 19.23% Mismatches: 50  
 Query Match: 6.85% Indels: 29  
 RESULT 958

ID ABA48285 standard; DNA; 570 BP.  
 DE Human breast cell single exon nucleic acid probe #6980.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 19.23% Mismatches: 50  
 Query Match: 6.85% Indels: 29  
 RESULT 959

ID ABA33236 standard; DNA; 570 BP.  
 DE Probe #11702 for gene expression analysis in human heart cell sample.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 19.23% Mismatches: 50  
 Query Match: 6.85% Indels: 29  
 RESULT 960

ID AAK40334 standard; DNA; 570 BP.  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 14891.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 19.23% Mismatches: 50  
 Query Match: 6.85% Indels: 29  
 RESULT 961

ID AAK14588 standard; DNA; 570 BP.  
 DE Human brain expressed single exon probe SEQ ID NO: 14579.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 19.23% Mismatches: 50  
 Query Match: 6.85% Indels: 29  
 RESULT 962

ID ABS39904 standard; DNA; 570 BP.  
 DE Human liver single exon probe, SEQ ID No 14894.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 19.23% Mismatches: 50  
 Query Match: 6.85% Indels: 29  
 RESULT 963

ID AAI06811 standard; DNA; 570 BP.  
 DE Probe #6802 used to measure gene expression in human breast sample.  
 PN WO200157270-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 19.23% Mismatches: 50  
 Query Match: 6.85% Indels: 29  
 RESULT 964

ID ABS14351 standard; DNA; 570 BP.  
 DE Human genome-derived single exon probe ORF from lung SEQ ID NO 14342.  
 PN WO200186003-A2.  
 PD 15-NOV-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC.  
 Best Local Similarity: 19.23% Mismatches: 50  
 Query Match: 6.85% Indels: 29  
 RESULT 965

ID AAI0681 standard; cDNA; 723 BP.  
 DE Mucin-derived protein MUC1/V cDNA.

PN WO9603502-A2.  
 PD 08-FEB-1996.  
 PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 966  
 ID RAT10682 standard; cDNA; 750 BP.  
 DE Mucin-derived protein MUC1/V/alt cDNA.  
 PN WO9603502-A2.  
 PD 08-FEB-1996.  
 PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 967  
 ID AAT10679 standard; cDNA; 768 BP.  
 DE Mucin-derived protein MUC1/Y cDNA.  
 PN WO9603502-A2.  
 PD 08-FEB-1996.  
 PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
 Best Local Similarity: 20.78% Mismatches: 77  
 Query Match: 6.85% Indels: 19  
 RESULT 968  
 ID ADA50574 standard; DNA; 768 BP.  
 DE Mucin 1 (MUC-1) splice variant #2 (MUC1Y) DNA, SEQ ID NO:29.  
 PN WO2003031569-A2.  
 PD 17-APR-2003.  
 PA (CENZ) CENTOCOR INC.  
 Best Local Similarity: 20.78% Mismatches: 77  
 Query Match: 6.85% Indels: 19  
 RESULT 969  
 ID AAT10680 standard; cDNA; 795 BP.  
 DE Mucin-derived protein MUC1/Y/alt cDNA.  
 PN WO9603502-A2.  
 PD 08-FEB-1996.  
 PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
 Best Local Similarity: 20.78% Mismatches: 77  
 Query Match: 6.85% Indels: 19  
 RESULT 970  
 ID AAA78516 standard; DNA; 808 BP.  
 DE Plant SDF polynucleotide sequence SEQ List 1 NO:290.  
 PN WO2000040695-A2.  
 PD 13-JUL-2000.  
 PA (CERE-) CERES INC.  
 Best Local Similarity: 27.74% Mismatches: 53  
 Query Match: 6.85% Indels: 22  
 RESULT 971  
 ID AAC48060 standard; DNA; 808 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 56120.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 972  
 ID AAT10677 standard; cDNA; 822 BP.  
 DE Mucin-derived protein MUC1/X cDNA.  
 PN WO9603502-A2.  
 PD 08-FEB-1996.  
 PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 973  
 ID AAT10678 standard; cDNA; 849 BP.  
 DE Mucin-derived protein MUC1/X/alt cDNA.  
 PN WO9603502-A2.  
 PD 08-FEB-1996.  
 PA (UYRA-) UNIV RAMOT APPL RES & IND DEV LTD.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 974  
 ID AAD57036 standard; cDNA; 859 BP.  
 DE Human mucin 1 transmembrane variant, MUC1/Z cDNA.  
 PN WO2003054154-A2.  
 PD 03-JUL-2003.

PA (ISIS-) ISIS PHARM INC.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 975  
 ID ADJ62779 standard; cDNA; 859 BP.  
 DE Human cDNA differentially expressed in response to docetaxel #49.  
 PN US2004018527-A1.  
 PD 29-JAN-2004.  
 PA (CHAN/) CHANG J C.  
 PA (OCON/) O'CONNELL P.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 976  
 ID ABV94488 standard; cDNA; 900 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:2.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 21.60% Mismatches: 57  
 Query Match: 6.85% Indels: 41  
 RESULT 977  
 ID ADM18637 standard; cDNA; 900 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:2.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 21.60% Mismatches: 57  
 Query Match: 6.85% Indels: 41  
 RESULT 978  
 ID ABV94501 standard; cDNA; 909 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:15.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 21.60% Mismatches: 57  
 Query Match: 6.85% Indels: 41  
 RESULT 979  
 ID ABV94573 standard; cDNA; 909 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:134.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 21.60% Mismatches: 57  
 Query Match: 6.85% Indels: 41  
 RESULT 980  
 ID ABV94563 standard; cDNA; 909 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:124.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 21.60% Mismatches: 57  
 Query Match: 6.85% Indels: 41  
 RESULT 981  
 ID ABV94540 standard; cDNA; 909 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:101.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 21.60% Mismatches: 57  
 Query Match: 6.85% Indels: 41  
 RESULT 982  
 ID ADM18736 standard; cDNA; 909 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:101.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN INC.  
 Best Local Similarity: 21.60% Mismatches: 57  
 Query Match: 6.85% Indels: 41  
 RESULT 983  
 ID ADM18650 standard; cDNA; 909 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:15.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.



PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Query Match: 21.60% Indels: 41  
 RESULT 984  
 ID ADM18769 standard; cDNA; 909 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:134.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Best Local Similarity: 21.60% Indels: 41  
 Query Match: 6.85%  
 RESULT 985  
 ID ADM18759 standard; cDNA; 909 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:124.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Best Local Similarity: 21.60% Indels: 41  
 Query Match: 6.85%  
 RESULT 986  
 ID ABV94579 standard; cDNA; 910 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:140.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Best Local Similarity: 21.60% Indels: 41  
 Query Match: 6.85%  
 RESULT 987  
 ID ABV94555 standard; cDNA; 910 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:116.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Best Local Similarity: 21.60% Indels: 41  
 Query Match: 6.85%  
 RESULT 988  
 ID ADM18751 standard; cDNA; 910 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:116.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Best Local Similarity: 21.60% Indels: 41  
 Query Match: 6.85%  
 RESULT 989  
 ID ADM18775 standard; cDNA; 910 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:140.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Best Local Similarity: 21.60% Indels: 41  
 Query Match: 6.85%  
 RESULT 990  
 ID ABV94571 standard; cDNA; 912 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:132.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Best Local Similarity: 21.60% Indels: 41  
 Query Match: 6.85%  
 RESULT 991  
 ID ABV94564 standard; cDNA; 912 BP.  
 DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:125.  
 PN WO200200717-A2.  
 PD 03-JAN-2002.  
 PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Best Local Similarity: 21.60% Indels: 41  
 Query Match: 6.85%  
 RESULT 992  
 ID ADM18760 standard; cDNA; 912 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:125.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Best Local Similarity: 21.60% Indels: 41  
 Query Match: 6.85%

Best Local Similarity: 21.60% Mismatches: 57  
 Query Match: 6.85% Indels: 41  
 RESULT 993  
 ID ADM18767 standard; cDNA; 912 BP.  
 DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:132.  
 PN WO2004029197-A2.  
 PD 08-APR-2004.  
 PA (MAXY-) MAXYGEN INC. Mismatches: 57  
 Best Local Similarity: 21.60% Indels: 41  
 Query Match: 6.85%  
 RESULT 994  
 ID AAI11883 standard; DNA; 962 BP.  
 DE Probe #1816 for gene expression analysis in human cervical cell sample.  
 PN WO200157278-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC. Mismatches: 50  
 Best Local Similarity: 19.23% Indels: 29  
 Query Match: 6.85%  
 RESULT 995  
 ID ABA53584 standard; DNA; 962 BP.  
 DE Human foetal liver single exon nucleic acid probe #1889.  
 PN WO200157277-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC. Mismatches: 50  
 Best Local Similarity: 19.23% Indels: 29  
 Query Match: 6.85%  
 RESULT 996  
 ID AAI33210 standard; DNA; 962 BP.  
 DE Probe #1896 used to measure gene expression in human placenta sample.  
 PN WO200157272-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC. Mismatches: 50  
 Best Local Similarity: 19.23% Indels: 29  
 Query Match: 6.85%  
 RESULT 997  
 ID ABA43165 standard; DNA; 962 BP.  
 DE Human breast cell single exon nucleic acid probe #1860.  
 PN WO200157271-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC. Mismatches: 50  
 Best Local Similarity: 19.23% Indels: 29  
 Query Match: 6.85%  
 RESULT 998  
 ID ABA23339 standard; DNA; 962 BP.  
 DE Probe #1805 for gene expression analysis in human heart cell sample.  
 PN WO200157274-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC. Mismatches: 50  
 Best Local Similarity: 19.23% Indels: 29  
 Query Match: 6.85%  
 RESULT 999  
 ID AAK27309 standard; DNA; 962 BP.  
 DE Human bone marrow expressed single exon probe SEQ ID NO: 1866.  
 PN WO200157276-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC. Mismatches: 50  
 Best Local Similarity: 19.23% Indels: 29  
 Query Match: 6.85%  
 RESULT 1000  
 ID AAK01850 standard; DNA; 962 BP.  
 DE Human brain expressed single exon probe SEQ ID NO: 1841.  
 PN WO200157275-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC. Mismatches: 50  
 Best Local Similarity: 19.23% Indels: 29  
 Query Match: 6.85%  
 RESULT 1001  
 ID ABS26883 standard; DNA; 962 BP.  
 DE Human liver single exon probe, SEQ ID No 1873.  
 PN WO200157273-A2.  
 PD 09-AUG-2001.  
 PA (MOLE-) MOLECULAR DYNAMICS INC. Mismatches: 50  
 Best Local Similarity: 19.23% Indels: 29  
 Query Match: 6.85%

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Query Match: 6.85% Indels: 29
RESULT 1002
ID AA101821 standard; DNA; 962 BP.
DE Probe #1812 used to measure gene expression in human breast sample.
PN WO200157270-A2.
PD 09-AUG-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 1003
ID ABS01829 standard; DNA; 962 BP.
DE Human genome-derived single exon probe from lung SEQ ID No 1820.
PN WO200186003-A2.
PD 15-NOV-2001.
PA (MOLE-) MOLECULAR DYNAMICS INC.
Best Local Similarity: 19.23% Mismatches: 50
Query Match: 6.85% Indels: 29
RESULT 1004
ID ACA20212 standard; DNA; 972 BP.
DE Prokaryotic essential gene #1869.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 27.54% Mismatches: 44
Query Match: 6.85% Indels: 35
RESULT 1005
ID ACF73847 standard; DNA; 1011 BP.
DE Staphylococcus aureus DNA #1527.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Best Local Similarity: 27.54% Mismatches: 44
Query Match: 6.85% Indels: 35
RESULT 1006
ID AAQ24679 standard; DNA; 1074 BP.
DE H23-ETA-T antigen C-terminal coding sequence.
PN WO9207000-A1.
PD 30-APR-1992.
PA (TRGE) TRANSGENE SA.
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1007
ID ADJ34831 standard; DNA; 1137 BP.
DE DNA encoding xylanase from an environmental sample seq id 47.
PN WO2003106654-A2.
PD 24-DEC-2003.
PA (DIVE-) DIVERSA CORP.
Best Local Similarity: 20.15% Mismatches: 87
Query Match: 6.85% Indels: 93
RESULT 1008
ID ADE43993 standard; DNA; 1164 BP.
DE Plasmid JNW389 gutted MUC-1 encoding DNA.
PN WO2003099193-A2.
PD 04-DEC-2003.
PA (GLAX) GLAXO GROUP LTD.
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1009
ID ADI57704 standard; cDNA; 1216 BP.
DE Human breast specific nucleic acid (BSNA) #75.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Best Local Similarity: 20.25% Mismatches: 77
Query Match: 6.85% Indels: 24
RESULT 1010
ID ADI57700 standard; cDNA; 1258 BP.
DE Human breast specific nucleic acid (BSNA) #71.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Best Local Similarity: 20.78% Mismatches: 77
Query Match: 6.85% Indels: 19
RESULT 1011
ID ADI57702 standard; cDNA; 1266 BP.
DE Human breast specific nucleic acid (BSNA) #73.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1012
ID ADI57695 standard; cDNA; 1285 BP.
DE Human breast specific nucleic acid (BSNA) #66.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Best Local Similarity: 21.39% Mismatches: 105
Query Match: 6.85% Indels: 21
RESULT 1013
ID ADR89849 standard; cDNA; 1290 BP.
DE Human mucin MUC-1 gene (7x VNTR removed), codon optimised.
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Best Local Similarity: 23.39% Mismatches: 63
Query Match: 6.85% Indels: 15
RESULT 1014
ID ADR89847 standard; cDNA; 1290 BP.
DE Human mucin MUC-1 gene (7x VNTR removed).
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1015
ID ADR89848 standard; cDNA; 1290 BP.
DE Human mucin MUC-1 gene (7x VNTR removed), codon optimised.
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Best Local Similarity: 24.18% Mismatches: 51
Query Match: 6.85% Indels: 1
RESULT 1016
ID ADI57680 standard; cDNA; 1312 BP.
DE Human breast specific nucleic acid (BSNA) #51.
PN WO2003106648-A2.
PD 24-DEC-2003.
PA (DIAD-) DIADEXUS INC.
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1017
ID AAT29190 standard; cDNA to mRNA; 1320 BP.
DE Glycoprotein 39 3' fragment.
PN JF07051065-A.
PD 28-FEB-1995.
PA (NIKO-) NIPPON KOTAI KENKYUSHO KK.
PA (UYRA-) UNIV KAGOSHIMA.
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
RESULT 1018
ID ADR89850 standard; cDNA; 1330 BP.
DE Human mucin MUC-1 gene (7x VNTR removed), codon optimised.
PN WO2004076665-A2.
PD 10-SEP-2004.
PA (GLAX) GLAXO GROUP LTD.
Best Local Similarity: 23.39% Mismatches: 63
Query Match: 6.85% Indels: 15
RESULT 1019
ID AAC77625 standard; cDNA; 1355 BP.
DE Human cancer associated gene sequence SEQ ID NO:19.
PN WO200055350-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 24.27% Mismatches: 57
Query Match: 6.85% Indels: 2
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RESULT 1020  
ID AAD00388 standard; DNA; 1371 BP.  
DE Human Mucin 1 (MUC-1) protein fragment encoding DNA #5.  
PN WO200025827-A2.  
PD 11-MAY-2000.  
PA (MENA ) MENARINI RICERCHE SPA.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1021  
ID ABL02275 standard; cDNA; 1391 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 1307.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE ) PE CORP NY.  
Best Local Similarity: 23.89% Mismatches: 67  
Query Match: 6.85% Indels: 40

RESULT 1022  
ID AAS16149 standard; cDNA; 1398 BP.  
DE Human leukocyte immunoglobulin receptor-like (LIR-like) cDNA #5.  
PN WO200155335-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 20.15% Mismatches: 74  
Query Match: 6.85% Indels: 102

RESULT 1023  
ID ABE43995 standard; DNA; 1404 BP.  
DE Plasmid JNW399 MUC-1 encoding DNA.  
PN WO200309193-A2.  
PD 04-DEC-2003.  
PA (GLAX ) GLAXO GROUP LTD.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1024  
ID ABL60159 standard; cDNA; 1428 BP.  
DE Human MUC1 encoding cDNA SEQ ID NO 2.  
PN WO200226765-A2.  
PD 04-APR-2002.  
PA (GENA-) GENAISSANCE PHARM INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1025  
ID ADO23125 standard; RNA; 1428 BP.  
DE Human MUC1 mucin glycoprotein RNA (coding sequence) SeqID 20.  
PN WO2004044160-A2.  
PD 27-MAY-2004.  
PA (DAND ) DANA FARBER CANCER INST INC.  
PA (ILEX-) ILEX PROD INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1026  
ID AAQ29276 standard; cDNA; 1452 BP.  
DE Encodes transmembrane form of H23-ETA antigen.  
PN WO9207000-A1.  
PD 30-APR-1992.  
PA (TRGE ) TRANSGENE SA.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1027  
ID AAS16150 standard; cDNA; 1455 BP.  
DE Human leukocyte immunoglobulin receptor-like (LIR-like) cDNA #6.  
PN WO200155335-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 20.15% Mismatches: 74  
Query Match: 6.85% Indels: 102

RESULT 1028  
ID AAL49724 standard; cDNA; 1455 BP.  
DE Human secreted LIR-like protein cDNA SEQ ID NO: 39.  
PN WO200266600-A2.  
PD 29-AUG-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 20.15% Mismatches: 74  
Query Match: 6.85% Indels: 102

RESULT 1029  
ID ADS10215 standard; DNA; 1455 BP.  
DE Human therapeutic DNA - SEQ ID 452.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Best Local Similarity: 20.15% Mismatches: 74  
Query Match: 6.85% Indels: 102

RESULT 1030  
ID ADF32627 standard; DNA; 1457 BP.  
DE Plasmid JNW358 MUC-1 nucleotide sequence.  
PN WO2003100060-A2.  
PD 04-DEC-2003.  
PA (GLAX ) GLAXO GROUP LTD.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1031  
ID ADS09841 standard; DNA; 1505 BP.  
DE Human therapeutic DNA - SEQ ID 78.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Best Local Similarity: 20.15% Mismatches: 74  
Query Match: 6.85% Indels: 102

RESULT 1032  
ID ADI57696 standard; cDNA; 1517 BP.  
DE Human breast specific nucleic acid (BSNA) #67.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 20.25% Mismatches: 77  
Query Match: 6.85% Indels: 24

RESULT 1033  
ID ADI57674 standard; cDNA; 1530 BP.  
DE Human breast specific nucleic acid (BSNA) #45.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 20.78% Mismatches: 77  
Query Match: 6.85% Indels: 19

RESULT 1034  
ID AAS00585 standard; DNA; 1572 BP.  
DE Human MUC1 DNA sequence.  
PN WO200118035-A2.  
PD 15-MAR-2001.  
PA (TRGE ) TRANSGENE SA.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1035  
ID ADK70370 standard; cDNA; 1614 BP.  
DE Respiratory disease differentially expressed cDNA #106.  
PN WO2003101283-A2.  
PD 11-DEC-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1036  
ID ADI57689 standard; cDNA; 1634 BP.  
DE Human breast specific nucleic acid (BSNA) #60.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1037  
ID ACA18749 standard; DNA; 1650 BP.  
DE Prokaryotic essential gene #406.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 20.29% Mismatches: 84  
Query Match: 6.85% Indels: 49

RESULT 1038  
ID ABS76475 standard; cDNA; 1721 BP.  
DE cDNA encoding human ovarian cancer marker OV45.  
PN WO200271928-A2.  
PD 19-SEP-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1039  
ID ABL68032 standard; DNA; 1721 BP.  
DE Ovary cancer related gene sequence SEQ ID NO:6369.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1040  
ID ABK09743 standard; cDNA; 1721 BP.  
DE Human ovarian tumour protein encoding cDNA #276.  
PN WO200190154-A2.  
PD 29-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1041  
ID ABV94067 standard; cDNA; 1721 BP.  
DE Breast carcinoma related nucleotide sequence SEQ ID NO:58.  
PN WO200246467-A2.  
PD 13-JUN-2002.  
PA (IPSO-) IPSOGEN.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1042  
ID ADA50566 standard; DNA; 1721 BP.  
DE Mucin 1 (MUC-1) encoding DNA, SEQ ID NO:21.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ-) CENTOCOR INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1043  
ID ACF12906 standard; cDNA; 1721 BP.  
DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:155.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1044  
ID AAD56938 standard; cDNA; 1721 BP.  
DE Human mucin 1 transmembrane cDNA.  
PN WO2003054154-A2.  
PD 03-JUL-2003.  
PA (ISIS-) ISIS PHARM INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1045  
ID ADK65926 standard; cDNA; 1721 BP.  
DE Human immunostimulating mucin MUC1 coding sequence.  
PN WO2004009632-A2.  
PD 23-JAN-2004.  
PA (NEMO-) NEMOD IMMUNOTHERAPIE AG.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1046  
ID ADR24914 standard; DNA; 1721 BP.  
DE Breast cancer prognosis marker #775.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1047  
ID AAD00394 standard; DNA; 1737 BP.  
DE Ubiquitin-E. coli LacI-human Mucin 1 fusion protein encoding DNA #5.  
PN WO200025827-A2.  
PD 11-MAY-2000.  
PA (MENA) MENARINI RICERCHE SPA.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1048  
ID ADI57669 standard; cDNA; 1738 BP.  
DE Human breast specific nucleic acid (BSNA) #40.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1049  
ID ADI57673 standard; cDNA; 1755 BP.  
DE Human breast specific nucleic acid (BSNA) #44.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1050  
ID ADE43991 standard; DNA; 1774 BP.  
DE Plasmid JMW283 MUC-1 encoding DNA.  
PN WO2003099193-A2.  
PD 04-DEC-2003.  
PA (GLAX) GLAXO GROUP LTD.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1051  
ID ADF32625 standard; DNA; 1774 BP.  
DE Plasmid JMW283 MUC-1 nucleotide sequence.  
PN WO2003100060-A2.  
PD 04-DEC-2003.  
PA (GLAX) GLAXO GROUP LTD.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1052  
ID ADI57679 standard; cDNA; 1798 BP.  
DE Human breast specific nucleic acid (BSNA) #50.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1053  
ID ADO23124 standard; RNA; 1799 BP.  
DE Human MUC1 mucin glycoprotein RNA SeqID 19.  
PN WO2004044160-A2.  
PD 27-MAY-2004.  
PA (DAND) DANA FARBER CANCER INST INC.  
PA (ILEX-) ILEX PROD INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1054  
ID ADR89853 standard; cDNA; 1800 BP.  
DE Human mucin MUC-1 gene coding sequence.  
PN WO2004076665-A2.  
PD 10-SEP-2004.  
PA (GLAX) GLAXO GROUP LTD.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1055  
ID ADI57699 standard; cDNA; 1803 BP.  
DE Human breast specific nucleic acid (BSNA) #70.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2

RESULT 1056  
ID ABL67539 standard; DNA; 1804 BP.  
DE Thyroid cancer related gene sequence SEQ ID NO:5876.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1057  
ID AAD56950 standard; cDNA; 1804 BP.  
DE Human mucin 1 transmembrane variant, MUC1-VI cDNA.  
PN WO2003054154-A2.  
PD 03-JUL-2003.  
PA (ISIS-) ISIS PHARM INC. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1058  
ID ADD14719 standard; cDNA; 1804 BP.  
DE Human src biomarker polynucleotide SEQ ID NO:113.  
PN WO2003062395-A2.  
PD 31-JUL-2003.  
PA (BRIM) BRISTOL-MYERS SQUIBB CO. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1059  
ID ADP13294 standard; DNA; 1804 BP.  
DE Renal cell carcinoma differentially expressed gene #30.  
PN WO2004048933-A2.  
PD 10-JUN-2004.  
PA (AMHP) WYETH.  
PA (TWIN) TWINE N C.  
PA (BURC) BURCZYNSKI M E.  
PA (TREP) TREPICCHIO W L.  
PA (DORN) DORNER A.  
PA (STOV) STOVER J A.  
PA (SLON) SLONI D K.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1060  
ID ADO28642 standard; cDNA; 1805 BP.  
DE Human MUC1 encoding cDNA SEQ ID NO:71.  
PN WO200404178-A2.  
PD 27-MAY-2004.  
PA (GETH) GENENTECH INC. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1061  
ID AQ083917 standard; cDNA; 1805 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #731.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1062  
ID ADQ86329 standard; cDNA; 1805 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #3201.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1063  
ID AQ085148 standard; cDNA; 1805 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #1962.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%

PA (ZHOU) ZHOU Y. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1064  
ID ADQ83237 standard; cDNA; 1805 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #51.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1065  
ID ADF32633 standard; DNA; 1818 BP.  
DE Plasmid JNW656 7x VNTR MUC-1 nucleotide sequence.  
PN WO2003100060-A2.  
PD 04-DEC-2003.  
PA (GLAX) GLAXO GROUP LTD. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1066  
ID ADR89851 standard; cDNA; 1818 BP.  
DE Human mucin MUC-1 gene (7x VNTR) expression cassette, codon optimised.  
PN WO2004076665-A2.  
PD 10-SEP-2004.  
PA (GLAX) GLAXO GROUP LTD. Mismatches: 63  
Best Local Similarity: 23.39% Indels: 15  
Query Match: 6.85%  
RESULT 1067  
ID ADR89846 standard; cDNA; 1818 BP.  
DE Human mucin MUC-1 gene coding sequence.  
PN WO2004076665-A2.  
PD 10-SEP-2004.  
PA (GLAX) GLAXO GROUP LTD. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1068  
ID ABZ35228 standard; cDNA; 1823 BP.  
DE Human gene expression profile polynucleotide SEQ ID NO 339.  
PN WO200274979-A2.  
PD 26-SEP-2002.  
PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1069  
ID ADP32631 standard; DNA; 1835 BP.  
DE Plasmid JNW321 2x VNTR MUC-1 nucleotide sequence.  
PN WO2003100060-A2.  
PD 04-DEC-2003.  
PA (GLAX) GLAXO GROUP LTD. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1070  
ID ADI57688 standard; cDNA; 1874 BP.  
DE Human breast specific nucleic acid (BSNA) #59.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1071  
ID ADI57677 standard; cDNA; 1882 BP.  
DE Human breast specific nucleic acid (BSNA) #48.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC. Mismatches: 57  
Best Local Similarity: 24.27% Indels: 2  
Query Match: 6.85%  
RESULT 1072  
ID ADI57672 standard; cDNA; 1918 BP.  
DE Human breast specific nucleic acid (BSNA) #43.  
PN WO2003106648-A2.

PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1073  
 ID ADI57678 standard; cDNA; 1930 BP.  
 DE Human breast specific nucleic acid (BSNA) #49.  
 PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1074  
 ID ADI57676 standard; cDNA; 1945 BP.  
 DE Human breast specific nucleic acid (BSNA) #47.  
 PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1075  
 ID ADI57698 standard; cDNA; 1949 BP.  
 DE Human breast specific nucleic acid (BSNA) #69.  
 PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1076  
 ID ADI57668 standard; cDNA; 1953 BP.  
 DE Human breast specific nucleic acid (BSNA) #39.  
 PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1077  
 ID ADH10475 standard; DNA; 1971 BP.  
 DE Human MUC-1-CPC fusion protein encoding DNA.  
 PN WO2003104272-A1.  
 PD 18-DEC-2003.  
 PA (GLAX ) GLAXOSMITHKLINE BIOLOGICALS SA.  
 PA (GLAX ) GLAXO GROUP LTD.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1078  
 ID ACN91439 standard; DNA; 2026 BP.  
 DE Breast cancer related marker, seq id 12589.  
 PN US2003099974-A1.  
 PD 29-MAY-2003.  
 PA (MILL-) MILLENNIUM PHARM INC.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1079  
 ID ADH10477 standard; DNA; 2037 BP.  
 DE CPC-MUC-1 fusion protein encoding DNA.  
 PN WO2003104272-A1.  
 PD 18-DEC-2003.  
 PA (GLAX ) GLAXOSMITHKLINE BIOLOGICALS SA.  
 PA (GLAX ) GLAXO GROUP LTD.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1080  
 ID ADI57701 standard; cDNA; 2045 BP.  
 DE Human breast specific nucleic acid (BSNA) #72.  
 PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1081  
 ID ADI57682 standard; cDNA; 2049 BP.  
 DE Human breast specific nucleic acid (BSNA) #53.

PN WO2003106648-A2.  
 PD 24-DEC-2003.  
 PA (DIAD-) DIADEXUS INC.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1082  
 ID ADF32629 standard; DNA; 2135 BP.  
 DE Plasmid JNW319 7x VNTR MUC-1 nucleotide sequence.  
 PN WO2003100060-A2.  
 PD 04-DEC-2003.  
 PA (GLAX ) GLAXO GROUP LTD.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1083  
 ID ADE53756 standard; cDNA; 2678 BP.  
 DE Human prostate cancer cDNA #103.  
 PN US2003190640-A1.  
 PD 09-OCT-2003.  
 PA (FARI/) FARIS M.  
 PA (PEAR/) PEARSON C I.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1084  
 ID ADE53756 standard; cDNA; 2678 BP.  
 DE Human prostate cancer cDNA #103.  
 PN US2003190640-A1.  
 PD 09-OCT-2003.  
 PA (FARI/) FARIS M.  
 PA (PEAR/) PEARSON C I.  
 Best Local Similarity: 20.62% Mismatches: 79  
 Query Match: 6.85% Indels: 21  
 RESULT 1085  
 ID ADC91583 standard; DNA; 2835 BP.  
 DE E. faecium DNA sequence SEQ ID 1210.  
 PN US6583275-B1.  
 PD 24-JUN-2003.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 21.26% Mismatches: 76  
 Query Match: 6.85% Indels: 25  
 RESULT 1086  
 ID ABL05460 standard; cDNA; 3187 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 10862.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEXE ) PE CORP NY.  
 Best Local Similarity: 25.93% Mismatches: 65  
 Query Match: 6.85% Indels: 52  
 RESULT 1087  
 ID ABL18139 standard; DNA; 3840 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 5890.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEXE ) PE CORP NY.  
 Best Local Similarity: 24.00% Mismatches: 49  
 Query Match: 6.85% Indels: 27  
 RESULT 1088  
 ID ABL67071 standard; DNA; 4139 BP.  
 DE Thyroid cancer related gene sequence SEQ ID NO:5408.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1089  
 ID ABL67544 standard; DNA; 4139 BP.  
 DE Thyroid cancer related gene sequence SEQ ID NO:5881.  
 PN WO200194629-A2.  
 PD 13-DEC-2001.  
 PA (AVAL-) AVALON PHARM.  
 Best Local Similarity: 24.27% Mismatches: 57  
 Query Match: 6.85% Indels: 2  
 RESULT 1090  
 ID ABL68884 standard; DNA; 4139 BP.

DE Kidney cancer related gene sequence SEQ ID NO:7221.  
PN WO200194629-A2.  
PD 13-DEC-2001.  
PA (AVAL-) AVALON PHARM.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1091  
ID ABR09797 standard; cDNA; 4139 BP.  
DE Human ovarian tumour protein encoding cDNA #330.  
PN WO200190154-A2.  
PD 29-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1092  
ID ABR95623 standard; DNA; 4139 BP.  
DE Gene #2121 used to diagnose liver cancer.  
PN WO200229103-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1093  
ID ACC50234 standard; cDNA; 4139 BP.  
DE Breast cancer associated cDNA sequence SEQ ID NO:310.  
PN WO2003004989-A2.  
PD 16-JAN-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1094  
ID ACF12907 standard; cDNA; 4139 BP.  
DE Human cervical cancer cell marker encoding cDNA SEQ ID NO:157.  
PN WO2002101075-A2.  
PD 19-DEC-2002.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1095  
ID ADH17156 standard; cDNA; 4139 BP.  
DE Human mucin 1 cDNA.  
PN WO2003097854-A2.  
PD 27-NOV-2003.  
PA (SUGE-) SUGEN INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1096  
ID ADQ29827 standard; DNA; 4139 BP.  
DE Human colorectal cancer-associated protein coding sequence #49.  
PN EPI439393-A2.  
PD 21-JUL-2004.  
PA (PARB-) BAYER HEALTHCARE LLC.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1097  
ID ADR44006 standard; DNA; 4139 BP.  
DE Human breast tumour associated gene clone-19 SEQ ID NO:16.  
PN WO2004074506-A2.  
PD 02-SEP-2004.  
PA (MERG-) MERGEN LTD.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1098  
ID ADI57666 standard; cDNA; 4144 BP.  
DE Human breast specific nucleic acid (BSNA) #37.  
PN WO2003106648-A2.  
PD 24-DEC-2003.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 24.27% Mismatches: 57  
Query Match: 6.85% Indels: 2  
RESULT 1099  
ID ADA69635 standard; DNA; 4425 BP.

DE Rice gene, SEQ ID 2958.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN-) SYNGENTA PARTICIPATIONS AG.  
Best Local Similarity: 27.59% Mismatches: 39  
Query Match: 6.85% Indels: 21  
RESULT 1100  
ID ADQ22765 standard; DNA; 5037 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5585.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 23.66% Mismatches: 20  
Query Match: 6.85% Indels: 35  
RESULT 1101  
ID ABL27091 standard; DNA; 5167 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32746.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Best Local Similarity: 24.06% Mismatches: 84  
Query Match: 6.85% Indels: 45  
RESULT 1102  
ID AAS57189 standard; cDNA; 5167 BP.  
DE cDNA encoding drosophila G-protein coupled receptor, GCPR #59.  
PN WO200170980-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Best Local Similarity: 24.06% Mismatches: 84  
Query Match: 6.85% Indels: 45  
RESULT 1103  
ID ADC35924 standard; cDNA; 5167 BP.  
DE Drosophila G protein coupled receptor cDNA seq id 60.  
PN US2003092124-A1.  
PD 15-MAY-2003.  
PA (APPL-) APPLERA CORP.  
Best Local Similarity: 24.06% Mismatches: 84  
Query Match: 6.85% Indels: 45  
RESULT 1104  
ID ABL28080 standard; DNA; 5350 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 35713.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Best Local Similarity: 25.93% Mismatches: 65  
Query Match: 6.85% Indels: 52  
RESULT 1105  
ID AAQ90511 standard; DNA; 14556 BP.  
DE CEA genomic clone.  
PN WO9514100-A2.  
PD 26-MAY-1995.  
PA (WELL-) WELLCOME FOUND LTD.  
Best Local Similarity: 46.94% Mismatches: 14  
Query Match: 6.85% Indels: 6  
RESULT 1106  
ID ADA02756 standard; DNA; 96594 BP.  
DE Human MORF carcinoma associated gene, SEQ ID NO:1274.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 21.86% Mismatches: 75  
Query Match: 6.85% Indels: 69  
RESULT 1107  
ID ADB72494 standard; DNA; 96594 BP.  
DE Human MORF gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 21.86% Mismatches: 75  
Query Match: 6.85% Indels: 69  
RESULT 1108  
ID ADC85236 standard; DNA; 96594 BP.  
DE Human Morf genomic sequence.

PN WO2003045230-A2.  
 PD 05-JUN-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 21.86% Mismatches: 75  
 Indels: 69  
 Query Match:  
 RESULT 1109  
 ID ADM74351 standard; DNA; 96594 BP.  
 DE Human carcinoma associated (CA) nucleic acid #10.  
 PN US2004072154-A1.  
 PD 15-APR-2004.  
 PA (MORR/) MORRIS D W.  
 PA (ENGE/) ENGELHARD E K.  
 Best Local Similarity: 21.86% Mismatches: 75  
 Indels: 69  
 Query Match:  
 RESULT 1110  
 ID ACN44734 standard; DNA; 102980 BP.  
 DE Human genomic sequence hCG27644.  
 PN WO2003073826-A2.  
 PD 12-SEP-2003.  
 PA (SAGR-) SAGRES DISCOVERY.  
 Best Local Similarity: 24.66% Mismatches: 68  
 Indels: 17  
 Query Match:  
 RESULT 1111  
 ID RAC04386 standard; CDNA; 414 BP.  
 DE Human secreted protein 5' EST, SEQ ID NO: 8461.  
 PN EP1033401-A2.  
 PD 06-SEP-2000.  
 PA (GEST) GENSET.  
 Best Local Similarity: 24.58% Mismatches: 31  
 Indels: 38  
 Query Match:  
 RESULT 1112  
 ID AAS52951 standard; DNA; 867 BP.  
 DE Enterococcus faecalis DNA for cellular proliferation protein #379.  
 PN WO200170955-A2.  
 PD 27-SEP-2001.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 29.52% Mismatches: 43  
 Indels: 15  
 Query Match:  
 RESULT 1113  
 ID ADC86988 standard; DNA; 1324 BP.  
 DE Human GPCR gene SEQ ID NO:1441.  
 PN EP1270724-A2.  
 PD 02-JAN-2003.  
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
 PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.  
 Best Local Similarity: 23.36% Mismatches: 69  
 Indels: 68  
 Query Match:  
 RESULT 1114  
 ID ADS04421 standard; DNA; 1647 BP.  
 DE Staphylococcus epidermis polynucleotide seqid 3716.  
 PN US2004147734-A1.  
 PD 29-JUL-2004.  
 PA (DOUC/) DOUCETTE-STAMM L.  
 PA (BUSH/) BUSH D.  
 Best Local Similarity: 32.69% Mismatches: 30  
 Indels: 26  
 Query Match:  
 RESULT 1115  
 ID AAS80665 standard; CDNA; 1863 BP.  
 DE DNA encoding novel human diagnostic protein #16469.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 19.42% Mismatches: 46  
 Indels: 34  
 Query Match:  
 RESULT 1116  
 ID AAD09561 standard; CDNA; 1986 BP.  
 DE Human transporter and ion channel-10 (TRICH-10) cDNA.  
 PN WO200146258-A2.  
 PD 28-JUN-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 23.26% Mismatches: 82  
 Indels: 52  
 Query Match:  
 RESULT 1117

ID ADO30284 standard; CDNA; 2048 BP.  
 DE Mouse GPCR MRGF polynucleotide, SEQ ID NO:1387.  
 PN WO2004040000-A2.  
 PD 13-MAY-2004.  
 PA (PRIM-) PRIMAL INC.  
 Best Local Similarity: 20.91% Mismatches: 76  
 Indels: 68  
 Query Match:  
 RESULT 1118  
 ID ADL27141 standard; CDNA; 3029 BP.  
 DE Human cDNA sequence for KCNJ9.  
 PN US2003216558-A1.  
 PD 20-NOV-2003.  
 PA (MORR/) MORRIS D W.  
 PA (ENGE/) ENGELHARD E K.  
 Best Local Similarity: 22.22% Mismatches: 82  
 Indels: 32  
 Query Match:  
 RESULT 1119  
 ID ABL13145 standard; CDNA; 3443 BP.  
 DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 33917.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PERE) PE CORP NY.  
 Best Local Similarity: 22.11% Mismatches: 58  
 Indels: 65  
 Query Match:  
 RESULT 1120  
 ID ADD49068 standard; DNA; 3462 BP.  
 DE Human NOV11a coding sequence, SEQ ID 41.  
 PN WO2003060149-A2.  
 PD 24-JUL-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 24.58% Mismatches: 47  
 Indels: 15  
 Query Match:  
 RESULT 1121  
 ID ADH71107 standard; DNA; 3462 BP.  
 DE Human gene of the invention NOV2a SEQ ID NO:3.  
 PN WO2003102155-A2.  
 PD 11-DEC-2003.  
 PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 24.58% Mismatches: 47  
 Indels: 15  
 Query Match:  
 RESULT 1122  
 ID AAT40235 standard; CDNA to mRNA; 3546 BP.  
 DE GPIa precursor cDNA for Br-a allele.  
 PN US5516634-A.  
 PD 14-MAY-1996.  
 PA (SANT/) SANTOSO S S.  
 PA (NEWM/) NEWMAN P J.  
 Best Local Similarity: 24.58% Mismatches: 47  
 Indels: 15  
 Query Match:  
 RESULT 1123  
 ID ADN96153 standard; CDNA; 3972 BP.  
 DE Human NOVX polynucleotide #104.  
 PN US2004067490-A1.  
 PD 08-APR-2004.  
 PA (ZHON/) ZHONG M.  
 PA (LILL/) LI L.  
 PA (GORM/) GORMAN L.  
 PA (SPYT/) SPYTEK K A.  
 PA (KEKU/) KEKUDA R.  
 PA (TAUP/) TAUPIER R J.  
 PA (ANDE/) ANDERSON D W.  
 PA (VERN/) VERNET C A M.  
 PA (CATT/) CATTERTON E.  
 PA (MILL/) MILLER C E.  
 PA (SHEN/) SHENOY S G.  
 PA (PATT/) PATTURAJAN M.  
 PA (PENA/) PENA C E A.  
 PA (TCHE/) TCHERNEV V T.  
 PA (PADI/) PADIGARU M.  
 PA (GUSE/) GUSEV V Y.  
 PA (MALY/) MALYANKAR U M.  
 PA (BURG/) BURGESS C E.  
 PA (GERL/) GERLACH V.



PA (CASM/) CASMAN S J.	ID ABA00829 standard; cDNA; 5361 BP.		
PA (RIEG/) RIEGER D K.	DE Alpha2 integrin coding sequence.		
PA (GROS/) GROSSE W M.	PN WO2002101070-A2.		
PA (SMIT/) SMITHSON G.	PD 19-DEC-2002.		
PA (PEYM/) PEYMAN J A.	PA (RIGE-) RIGEL PHARM INC.	Mismatches: 47	
PA (STAR/) STARLING G.	Best Local Similarity: 24.58%	Indels: 15	
PA (ROTH/) ROTHENBERG M E.	Query Match:		
PA (LARO/) LAROCHELLE W J.	RESULT 1130		
PA (SHIM/) SHIMKETS R A.	ID ABX08832 standard; cDNA; 5361 BP.		
PA (CRAB/) CRABTREE J.	DE Angiogenesis-associated human polynucleotide sequence #94.		
PA (RAST/) RASTELLI L.	PN WO200279492-A2.		
PA (VOSS/) VOSS E Z.	PD 10-OCT-2002.		
PA (BOLD/) BOLDOG F L.	PA (EOSB-) EOS BIOTECHNOLOGY INC.		
PA (EDIN/) EDINGER S R.	Best Local Similarity: 24.58%	Mismatches: 47	
PA (MILL/) MILLET I.	Query Match:	Indels: 15	
PA (MACD/) MACDOUGALL J R.	RESULT 1131		
PA (ELLE/) ELLERMAN K.	ID ADN39751 standard; cDNA; 5361 BP.		
PA (CHAP/) CHAPOVAL A.	DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO: C123.		
Best Local Similarity: 22.06%	PN WO2003042661-A2.		
Query Match: 6.81%	PD 22-MAY-2003.		
RESULT 1124	PA (EOSB-) EOS BIOTECHNOLOGY INC.		
ID ADS63543 standard; cDNA; 4140 BP.	Best Local Similarity: 24.58%	Mismatches: 47	
DE Bacterial polynucleotide #15530.	Query Match:	Indels: 15	
PN US2003233675-A1.	RESULT 1132		
PD 18-DEC-2003.	ID ADR46606 standard; DNA; 5361 BP.		
PA (CAOY/) CAO Y.	DE Cancer-associated protein coding sequence, SEQ ID 19.		
PA (HINK/) HINKLE G J.	PN WO2004073657-A2.		
PA (SLAT/) SLATER S C.	PD 02-SEP-2004.		
PA (CHEN/) CHEN X.	PA (PROT-) PROTEIN DESIGN LABS INC.		
PA (GOLD/) GOLDMAN B S.	Best Local Similarity: 24.58%	Mismatches: 47	
Best Local Similarity: 20.83%	Query Match:	Indels: 15	
Query Match: 6.81%	RESULT 1133		
RESULT 1125	ID ADI31992 standard; cDNA; 5373 BP.		
ID ADS63914 standard; cDNA; 4140 BP.	DE Human cDNA #1318.		
DE Bacterial polynucleotide #15901.	PN US6607879-B1.		
PN US2003233675-A1.	PD 19-AUG-2003.		
PD 18-DEC-2003.	PA (INCY-) INCYTE CORP.		
PA (CAOY/) CAO Y.	Best Local Similarity: 24.58%	Mismatches: 47	
PA (HINK/) HINKLE G J.	Query Match:	Indels: 15	
PA (SLAT/) SLATER S C.	RESULT 1134		
PA (CHEN/) CHEN X.	ID ADJ74578 standard; mRNA; 5373 BP.		
PA (GOLD/) GOLDMAN B S.	DE Human integrin alpha-2 subunit mRNA SEQ ID NO:2.		
Best Local Similarity: 20.83%	PN WO2004015104-A1.		
Query Match: 6.81%	PD 19-FEB-2004.		
RESULT 1126	PA (NAGO-) NAGOYA IND SCI RES INST.		
ID ADS64286 standard; cDNA; 4140 BP.	PA (GIFU-) GIFU INT INST BIOTECHNOLOGY.		
DE Bacterial polynucleotide #16273.	Best Local Similarity: 24.58%	Mismatches: 47	
PN US2003233675-A1.	Query Match:	Indels: 15	
PD 18-DEC-2003.	RESULT 1135		
PA (CAOY/) CAO Y.	ID ADO44024 standard; DNA; 5373 BP.		
PA (HINK/) HINKLE G J.	DE Nucleotide sequence of human polynucleotide #1.		
PA (SLAT/) SLATER S C.	PN WO2004029243-A1.		
PA (CHEN/) CHEN X.	PD 08-APR-2004.		
PA (GOLD/) GOLDMAN B S.	PA (NAGO-) NAGOYA IND SCI RES INST.		
Best Local Similarity: 20.83%	PA (GIFU-) GIFU INT INST BIOTECHNOLOGY.		
Query Match: 6.81%	Best Local Similarity: 24.58%	Mismatches: 47	
RESULT 1127	Query Match:	Indels: 15	
ID ABD32898 standard; cDNA; 4780 BP.	RESULT 1136		
DE Human cancer-associated cDNA HR18-037.1.	ID AAS93426 standard; cDNA; 5375 BP.		
PN WO2004074320-A2.	DE DNA encoding novel human diagnostic protein #29230.		
PD 02-SEP-2004.	PN WO200175067-A2.		
PA (SAGR-) SAGRES DISCOVERY INC.	PD 11-OCT-2001.		
Best Local Similarity: 24.58%	PA (HYSE-) HYSEQ INC.		
Query Match: 6.81%	Best Local Similarity: 24.58%	Mismatches: 47	
RESULT 1128	Query Match:	Indels: 15	
ID ACC81097 standard; mRNA; 5361 BP.	RESULT 1137		
DE Human VLA-2 receptor alpha 2 subunit mRNA.	ID ACN42598 standard; cDNA; 5622 BP.		
PN WO2003029277-A2.	DE Human diagnostic and therapeutic polynucleotide SEQ ID NO: 1473.		
PD 10-APR-2003.	PN WO2004023973-A2.		
PA (RIGE-) RIGEL PHARM INC.	PD 25-MAR-2004.		
Best Local Similarity: 24.58%	PA (INCY-) INCYTE CORP.		
Query Match: 6.81%	Best Local Similarity: 24.58%	Mismatches: 47	
RESULT 1129	Query Match:	Indels: 15	

RESULT 1138  
 ID AAS94779 standard; DNA; 5701 BP.  
 DE Human DNA sequence #34 expressed during foam cell differentiation.  
 PN WO200177389-A2.  
 PD 18-OCT-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 24.58% Mismatches: 47  
 Indels: 15  
 Query Match:  
 RESULT 1139  
 ID ABD32899 standard; cDNA; 7886 BP.  
 DE Human cancer-associated cDNA HR18-037.2.  
 PN WO2004074320-A2.  
 PD 02-SEP-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Best Local Similarity: 24.58% Mismatches: 47  
 Indels: 15  
 Query Match:  
 RESULT 1140  
 ID AAK84027 standard; DNA; 11872 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38839.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 35.96% Mismatches: 31  
 Indels: 13  
 Query Match:  
 RESULT 1141  
 ID AAK66893 standard; DNA; 11872 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:21705.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 35.96% Mismatches: 31  
 Indels: 13  
 Query Match:  
 RESULT 1142  
 ID AAZ35272 standard; DNA; 12571 BP.  
 DE Soybean retroelement Calypso 1-2.  
 PN WO9960842-A2.  
 PD 02-DEC-1999.  
 PA (WRIG/) WRIGHT D A.  
 PA (VOYT/) VOYTAS D F.  
 Best Local Similarity: 27.94% Mismatches: 29  
 Indels: 0  
 Query Match:  
 RESULT 1143  
 ID ADO59449 standard; DNA; 153740 BP.  
 DE Human cancer-associated (CA) gene sequence SEQ ID NO:85.  
 PN WO2004058288-A1.  
 PD 15-JUL-2004.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Best Local Similarity: 26.60% Mismatches: 37  
 Indels: 14  
 Query Match:  
 RESULT 1144  
 ID AAC48728 standard; DNA; 666 BP.  
 DE Arabidopsis thaliana DNA fragment SEQ ID NO: 58545.  
 PN EP1033405-A2.  
 PD 06-SEP-2000.  
 PA (SAGR-) SAGRES DISCOVERY INC.  
 Best Local Similarity: 26.40% Mismatches: 33  
 Indels: 39  
 Query Match:  
 RESULT 1145  
 ID AAZ09494 standard; DNA; 794 BP.  
 DE Rat olfactory 1h ion channel DNA fragment #4.  
 PN WO942574-A1.  
 PD 26-AUG-1999.  
 PA (KERJ ) FORSCHUNGSZENTRUM JUELICH GMBH.  
 Best Local Similarity: 23.35% Mismatches: 73  
 Indels: 69  
 Query Match:  
 RESULT 1146  
 ID ADM33294 standard; cDNA; 921 BP.  
 DE Human bitter taste receptor TAS2R41 encoding cDNA SEQ ID NO:8.  
 PN WO2004029087-A2.  
 PD 08-APR-2004.  
 PA (DEER-) DEUT INST ERNAERUNGFSORSCHUNG POTSDAM.  
 Best Local Similarity: 23.74% Mismatches: 68  
 Indels: 57  
 Query Match:  
 RESULT 1147

ID AAS18172 standard; cDNA; 924 BP.  
 DE Human T2R71 (hT2R71) cDNA.  
 PN WO200177676-A1.  
 PD 18-OCT-2001.  
 PA (SENO-) SENOMYX INC.  
 Best Local Similarity: 23.74% Mismatches: 68  
 Indels: 57  
 Query Match:  
 RESULT 1148  
 ID ABZ43209 standard; DNA; 924 BP.  
 DE Human GPCR polynucleotide SEQ ID NO 679.  
 PN WO200216548-A2.  
 PD 28-FEB-2002.  
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.  
 Best Local Similarity: 23.74% Mismatches: 68  
 Indels: 57  
 Query Match:  
 RESULT 1149  
 ID ADR29249 standard; DNA; 924 BP.  
 DE Taste receptor modulation-related human T2R71 gene sequence SeqID188.  
 PN WO2004069191-A2.  
 PD 19-AUG-2004.  
 PA (SENO-) SENOMYX INC.  
 Best Local Similarity: 23.74% Mismatches: 68  
 Indels: 57  
 Query Match:  
 RESULT 1150  
 ID ABK34698 standard; cDNA; 1239 BP.  
 DE Human cDNA for novel secreted protein, SEQ ID 467.  
 PN WO200177290-A2.  
 PD 18-OCT-2001.  
 PA (GEMY ) GENETICS INST INC.  
 Best Local Similarity: 21.24% Mismatches: 72  
 Indels: 45  
 Query Match:  
 RESULT 1151  
 ID ADI40346 standard; DNA; 1534 BP.  
 DE Human purified secretory polynucleotide (sptm), seq id 39.  
 PN WO2003062385-A2.  
 PD 31-JUL-2003.  
 PA (INCY-) INCYTE GENOMICS INC.  
 PA (JONE/) JONES A L.  
 PA (DAHL/) DAHL C R.  
 PA (GIET/) GIETZEN D.  
 PA (CHIN/) CHINN J.  
 PA (DUFO/) DUFOUR G E.  
 PA (JACK/) JACKSON J L.  
 PA (YUJY/) YU J Y.  
 PA (TUAS/) TUASON O.  
 PA (YAPP/) YAP P E.  
 PA (AMSH/) AMSHEY S R.  
 PA (DAMT/) DAM T C.  
 PA (LIUT/) LIU T F.  
 PA (GERS/) GERSTIN E H.  
 PA (PERA/) PERALTA C H.  
 PA (LEWI/) LEWIS S A.  
 PA (CHEN/) CHEN A J.  
 PA (MARW/) MARWAHA R.  
 PA (LANR/) LAN R Y.  
 PA (URAS/) URASHKA M E.  
 PA (KRIS/) KRISTNAM S R.  
 PA (KOLL/) KOLLURU V.  
 PA (PANE/) PANESAR I S.  
 Best Local Similarity: 25.95% Mismatches: 67  
 Indels: 12  
 Query Match:  
 RESULT 1152  
 ID AAH75169 standard; cDNA; 1561 BP.  
 DE Nucleotide sequence of a human enzyme.  
 PN WO200164896-A2.  
 PD 07-SEP-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 24.43% Mismatches: 63  
 Indels: 43  
 Query Match:  
 RESULT 1153  
 ID ADB52998 standard; DNA; 1711 BP.  
 DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3540.  
 PN WO2003065993-A2.

PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 24.35% Mismatches: 36  
Query Match: 6.76% Indels: 30  
RESULT 1154  
ID AB742063 standard; DNA: 1711 BP.  
DE Toxicity modelling related rat gene SEQ ID No 1765.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 24.35% Mismatches: 36  
Query Match: 6.76% Indels: 30  
RESULT 1155  
ID ABQ72565 standard; cDNA: 1725 BP.  
DE Human MDDT encoding cDNA SEQ ID NO 117.  
PN WO200240715-A2.  
PD 23-MAY-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 21.74% Mismatches: 37  
Query Match: 6.76% Indels: 47  
RESULT 1156  
ID AAS62254 standard; cDNA: 1727 BP.  
DE cDNA sequence #41 encoding novel human secreted protein.  
PN WO200177291-A2.  
PD 18-OCT-2001.  
PA (GEMY) GENETICS INST INC.  
Best Local Similarity: 21.74% Mismatches: 37  
Query Match: 6.76% Indels: 47  
RESULT 1157  
ID AQ87535 standard; cDNA: 2047 BP.  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #4413.  
PN WO2004060270-A2.  
PD 22-JUL-2004.  
PA (GETH) GENENTECH INC.  
Best Local Similarity: 24.43% Mismatches: 63  
Query Match: 6.76% Indels: 43  
PA (WUTD) WU T D.  
PA (ZHOU) ZHOU Y.  
Best Local Similarity: 24.43% Mismatches: 63  
Query Match: 6.76% Indels: 43  
RESULT 1158  
ID ADI31439 standard; cDNA: 2149 BP.  
DE Human cDNA #765.  
PN US6607879-B1.  
PD 19-AUG-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 22.09% Mismatches: 48  
Query Match: 6.76% Indels: 48  
RESULT 1159  
ID ADM91273 standard; DNA: 2545 BP.  
DE DNA homologue of a human DNA sequence encoding a protein SeqID 628.  
PN WO2004020595-A2.  
PD 11-MAR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
PA (RIKE-) RIKEN INST PHYSICAL & CHEM RES.  
PA (DNAF-) DNAFORM KK.  
Best Local Similarity: 27.71% Mismatches: 24  
Query Match: 6.76% Indels: 21  
RESULT 1160  
ID ADF90852 standard; DNA: 2829 BP.  
DE Human hepatic-fibrosis disease marker SEQ ID 314.  
PN JP2003259877-A.  
PD 16-SEP-2003.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Best Local Similarity: 24.43% Mismatches: 63  
Query Match: 6.76% Indels: 43  
RESULT 1161  
ID ADF90849 standard; DNA: 2829 BP.  
DE Human hepatic-fibrosis disease marker SEQ ID 311.  
PN JP2003259877-A.  
PD 16-SEP-2003.  
PA (SUMU) SUMITOMO SEIYAKU KK.  
Best Local Similarity: 24.43% Mismatches: 63  
Query Match: 6.76% Indels: 43  
RESULT 1162

ID ADA69512 standard; DNA: 3624 BP.  
DE Rice gene, SEQ ID 2835.  
PN WO2003000898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Best Local Similarity: 27.27% Mismatches: 30  
Query Match: 6.76% Indels: 15  
RESULT 1163  
ID AAK84138 standard; DNA: 17758 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:38950.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.95% Mismatches: 67  
Query Match: 6.76% Indels: 12  
RESULT 1164  
ID ABD33201 standard; DNA: 36312 BP.  
DE Murine cancer-associated (CA) gene MD07-031.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 19.37% Mismatches: 56  
Query Match: 6.76% Indels: 65  
RESULT 1165  
ID ABZ22473 standard; DNA: 36521 BP.  
DE Chimpanzee C68 adenovirus nucleotide sequence SEQ ID NO:33.  
PN WO2003000851-A2.  
PD 03-JAN-2003.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Best Local Similarity: 18.09% Mismatches: 77  
Query Match: 6.76% Indels: 49  
RESULT 1166  
ID ADQ97563 standard; DNA: 79084 BP.  
DE Human cancer associated sequence HD09-014, SEQ ID 540.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 32.00% Mismatches: 29  
Query Match: 6.76% Indels: 9  
RESULT 1167  
Best Local Similarity: 25.17% Mismatches: 59  
Query Match: 6.76% Indels: 26  
RESULT 1168  
ID ABK83461 standard; cDNA: 128600 BP.  
DE Human cDNA differentially expressed in granulocytic cells #32.  
PN WO200228999-A2.  
PD 11-APR-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 25.53% Mismatches: 27  
Query Match: 6.76% Indels: 29  
RESULT 1169  
ID ADM39522 standard; cDNA: 797 BP.  
DE Chicken cDNA encoding survival of motor neuron, SMN.  
PN US6646113-B1.  
PD 11-NOV-2003.  
PA (UYPE-) UNIV PENNSYLVANIA.  
Best Local Similarity: 24.24% Mismatches: 29  
Query Match: 6.72% Indels: 32  
RESULT 1170  
ID ABN67635 standard; DNA: 870 BP.  
DE Streptococcus polynucleotide SEQ ID NO 3183.  
PN WO200234771-A2.  
PD 02-MAY-2002.  
PA (CHIR-) CHIRON SPA.  
PA (GENO-) INST GENOMIC RES.  
Best Local Similarity: 24.16% Mismatches: 68  
Query Match: 6.72% Indels: 20  
RESULT 1171  
ID ABK13033 standard; cDNA: 895 BP.  
DE DNA encoding mouse B7-like protein, B7-L\_m2.  
PN WO200200710-A2.  
PD 03-JAN-2002.  
PA (AMGE-) AMGEN INC.

Best Local Similarity: 23.96% Mismatches: 71  
 Query Match: 6.72% Indels: 59  
 RESULT 1172  
 ID ADO05741 standard; cDNA; 1122 BP.  
 DE Human endothelial differentiation gene 2 (EDG2) coding sequence.  
 PN EF1418185-A1.  
 PD 12-MAY-2004.  
 PA (AVET ) AVENTIS PHARMA DEUT GMBH.  
 Best Local Similarity: 23.08% Mismatches: 42  
 Query Match: 6.72% Indels: 14  
 RESULT 1173  
 ID ADS47615 standard; cDNA; 1287 BP.  
 DE Bacterial polynucleotide #2358.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 22.44% Mismatches: 71  
 Query Match: 6.72% Indels: 61  
 RESULT 1174  
 ID ADO80507 standard; DNA; 1290 BP.  
 DE Schizosaccharomyces pombe metY DNA.  
 PN DE10239082-A1.  
 PD 04-MAR-2004.  
 PA (BADI ) BASF AG.  
 Best Local Similarity: 22.44% Mismatches: 71  
 Query Match: 6.72% Indels: 61  
 RESULT 1175  
 ID ABN67682 standard; DNA; 1482 BP.  
 DE Streptococcus polynucleotide SEQ ID NO 3277.  
 PN WO200234771-A2.  
 PD 02-MAY-2002.  
 PA (CHIR-) CHIRON SPA.  
 PA (GENO-) INST GENOMIC RES.  
 Best Local Similarity: 23.28% Mismatches: 57  
 Query Match: 6.72% Indels: 66  
 RESULT 1176  
 ID AAS87336 standard; cDNA; 1515 BP.  
 DE DNA encoding novel human diagnostic protein #23140.  
 PN WO200175067-A2.  
 PD 11-OCT-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 24.31% Mismatches: 58  
 Query Match: 6.72% Indels: 30  
 RESULT 1177  
 ID ADT48563 standard; cDNA; 1770 BP.  
 DE Bacterial polynucleotide #23314.  
 PN US2003233675-A1.  
 PD 18-DEC-2003.  
 PA (CAOY/) CAO Y.  
 PA (HINK/) HINKLE G J.  
 PA (SLAT/) SLATER S C.  
 PA (CHEN/) CHEN X.  
 PA (GOLD/) GOLDMAN B S.  
 Best Local Similarity: 23.65% Mismatches: 49  
 Query Match: 6.72% Indels: 88  
 RESULT 1178  
 ID ABA95063 standard; cDNA; 1919 BP.  
 DE Human speckled 110 splice variant (Sp110b) encoding cDNA.  
 PN WO200208383-A2.  
 PD 31-JAN-2002.  
 PA (GEHO ) GEN HOSPITAL CORP.  
 Best Local Similarity: 23.40% Mismatches: 46  
 Query Match: 6.72% Indels: 41  
 RESULT 1179  
 ID ADRI4348 standard; DNA; 1919 BP.  
 DE Human NF-kappaB pathway-associated gene SeqID349.  
 PN WO2004065577-A2.  
 PD 05-AUG-2004.  
 PA (BRIM ) BRISTOL-MYERS SQUIBB CO.

Best Local Similarity: 23.40% Mismatches: 46  
 Query Match: 6.72% Indels: 41  
 RESULT 1180  
 ID ACA20999 standard; DNA; 2304 BP.  
 DE Prokaryotic essential gene #2656.  
 PN WO200277183-A2.  
 PD 03-OCT-2002.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 23.58% Mismatches: 41  
 Query Match: 6.72% Indels: 29  
 RESULT 1181  
 ID AAZ58295 standard; DNA; 2862 BP.  
 DE Sorghum resistance gene homologue S6-1 coding region.  
 PN WO200004155-A2.  
 PD 27-JAN-2000.  
 PA (PURD ) PURDUE RES FOUND.  
 Best Local Similarity: 30.43% Mismatches: 28  
 Query Match: 6.72% Indels: 10  
 RESULT 1182  
 ID AAZ58294 standard; DNA; 2954 BP.  
 DE Sorghum resistance gene homologue S6-1 coding region.  
 PN WO200004155-A2.  
 PD 27-JAN-2000.  
 PA (PURD ) PURDUE RES FOUND.  
 Best Local Similarity: 30.43% Mismatches: 28  
 Query Match: 6.72% Indels: 10  
 RESULT 1183  
 ID ADHI8920 standard; cDNA; 3231 BP.  
 DE Human cell adhesion and extracellular matrix CADECM-16 cDNA - SEQ 47.  
 PN WO2003094843-A2.  
 PD 20-NOV-2003.  
 PA (INCY-) INCYTE CORP.  
 Best Local Similarity: 28.57% Mismatches: 21  
 Query Match: 6.72% Indels: 12  
 RESULT 1184  
 ID AAZ58293 standard; DNA; 6760 BP.  
 DE Sorghum resistance gene homologue S6-1.  
 PN WO200004155-A2.  
 PD 27-JAN-2000.  
 PA (PURD ) PURDUE RES FOUND.  
 Best Local Similarity: 30.43% Mismatches: 28  
 Query Match: 6.72% Indels: 10  
 RESULT 1185  
 ID ADR84309 standard; DNA; 8415 BP.  
 DE Aspergillus fumigatus essential gene genomic sequence #120.  
 PN WO2004067709-A2.  
 PD 12-AUG-2004.  
 PA (ELIT-) ELITRA PHARM INC.  
 Best Local Similarity: 20.00% Mismatches: 62  
 Query Match: 6.72% Indels: 89  
 RESULT 1186  
 ID AAK69113 standard; DNA; 10553 BP.  
 DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23925.  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 25.78% Mismatches: 40  
 Query Match: 6.72% Indels: 33  
 RESULT 1187  
 ID ABA16395 standard; DNA; 10553 BP.  
 DE Human nervous system related polynucleotide SEQ ID NO 8726.  
 PN WO200159063-A2.  
 PD 16-AUG-2001.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 25.78% Mismatches: 40  
 Query Match: 6.72% Indels: 33  
 RESULT 1188  
 ID AAF28534 standard; DNA; 39003 BP.  
 DE Genomic fragment #21.  
 PN WO200078968-A2.  
 PD 28-DEC-2000.  
 PA (INCY-) INCYTE GENOMICS INC.

Best Local Similarity: 19.57%	Mismatches: 81	Best Local Similarity: 30.23%	Mismatches: 25
Query Match: 6.72%	Indels: 64	Query Match: 6.67%	Indels: 48
RESULT 1189		RESULT 1200	
ID ACN44772 standard; DNA; 45152 BP.		ID AAH66699 standard; DNA; 804 BP.	
DE Mouse genomic sequence mCG3775.		DE C glutamicum coding sequence fragment SEQ ID NO: 1734.	
PN WO2003073826-A2.		PN EP1108790-A2.	
PD 12-SEP-2003.		PD 20-JUN-2001.	
PA (SAGR-) SAGRES DISCOVERY.		PA (KYOW) KYOWA HAKKO KOGYO KK.	
Best Local Similarity: 20.00%	Mismatches: 33	Best Local Similarity: 27.10%	Mismatches: 53
Query Match: 6.72%	Indels: 76	Query Match: 6.67%	Indels: 10
RESULT 1190		RESULT 1201	
ID ADQ97934 standard; DNA; 69648 BP.		ID ACA00849 standard; DNA; 804 BP.	
DE Human cancer associated sequence HD11-025, SEQ ID 911.		DE C. glutamicum derived ORF SEQ ID 840.	
PN WO2004060304-A2.		PN DE10128510-A1.	
PD 22-JUL-2004.		PD 19-DEC-2002.	
PA (SAGR-) SAGRES DISCOVERY INC.		PA (DEGS) DEGUSSA AG.	
Best Local Similarity: 23.26%	Mismatches: 64	Best Local Similarity: 27.10%	Mismatches: 53
Query Match: 6.72%	Indels: 43	Query Match: 6.67%	Indels: 10
RESULT 1191		RESULT 1202	
Best Local Similarity: 23.81%	Mismatches: 45	ID ADS46926 standard; cDNA; 825 BP.	
Query Match: 6.72%	Indels: 12	DE Bacterial polynucleotide #1669.	
RESULT 1192		PN US2003233675-A1.	
Best Local Similarity: 24.16%	Mismatches: 68	PD 18-DEC-2003.	
Query Match: 6.72%	Indels: 20	PA (CAOY) CAO Y.	
RESULT 1193		PA (HINK) HINKLE G J.	
Best Local Similarity: 25.17%	Mismatches: 42	PA (SLAT) SLATER S C.	
Query Match: 6.72%	Indels: 46	PA (CHEN) CHEN X.	
RESULT 1194		PA (GOLD) GOLDMAN B S.	
Best Local Similarity: 25.17%	Mismatches: 42	Best Local Similarity: 22.31%	Mismatches: 39
Query Match: 6.72%	Indels: 46	Query Match: 6.67%	Indels: 39
RESULT 1195		RESULT 1203	
ID ACN44850 standard; DNA; 142318 BP.		ID ABV94489 standard; cDNA; 900 BP.	
DE Human genomic sequence hCG33122.		DE Novel co-stimulatory molecule (NCSC) cDNA SEQ ID NO:3.	
PN WO2003073826-A2.		PD WO200200717-A2.	
PD 12-SEP-2003.		PD 03-JAN-2002.	
PA (SAGR-) SAGRES DISCOVERY.		PA (MAXY-) MAXYGEN INC.	
Best Local Similarity: 26.00%	Mismatches: 33	Best Local Similarity: 21.60%	Mismatches: 57
Query Match: 6.72%	Indels: 22	Query Match: 6.67%	Indels: 41
RESULT 1196		RESULT 1204	
ID ADS01853 standard; DNA; 375 BP.		ID ADM18638 standard; cDNA; 900 BP.	
DE Staphylococcus epidermis polynucleotide seqid 1148.		DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:3.	
PN US2004147734-A1.		PN WO2004029197-A2.	
PD 29-JUL-2004.		PD 08-APR-2004.	
PA (DOUC) DOUCETTE-STAMM L.		PA (MAXY-) MAXYGEN INC.	
PA (BUSH) BUSH D.		Best Local Similarity: 21.60%	Mismatches: 57
Best Local Similarity: 30.23%	Mismatches: 25	Query Match: 6.67%	Indels: 41
Query Match: 6.67%	Indels: 48	RESULT 1205	
RESULT 1197		ID ABV94548 standard; cDNA; 912 BP.	
ID ACH42016 standard; cDNA; 453 BP.		DE Novel co-stimulatory molecule (NCSC) cDNA SEQ ID NO:109.	
DE Human foetal brain cDNA #3383.		PN WO200200717-A2.	
PN US2003073623-A1.		PD 03-JAN-2002.	
PD 17-APR-2003.		PA (MAXY-) MAXYGEN INC.	
PA (DRMA) DRMANAC R T.		Best Local Similarity: 21.60%	Mismatches: 57
PA (LABA) LABAT I.		Query Match: 6.67%	Indels: 41
PA (STAC) STACHE-CRAIN B.		RESULT 1206	
PA (DICK) DICKSON M C.		ID ABV94561 standard; cDNA; 912 BP.	
PA (JONE) JONES L W.		DE Novel co-stimulatory molecule (NCSC) cDNA SEQ ID NO:122.	
Best Local Similarity: 28.12%	Mismatches: 20	DE WO200200717-A2.	
Query Match: 6.67%	Indels: 29	PD 03-JAN-2002.	
RESULT 1198		PA (MAXY-) MAXYGEN INC.	
ID ABL03163 standard; cDNA; 465 BP.		Best Local Similarity: 21.60%	Mismatches: 57
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3971.		Query Match: 6.67%	Indels: 41
PN WO200171042-A2.		RESULT 1207	
PD 27-SEP-2001.		ID ADM18744 standard; cDNA; 912 BP.	
PA (PEKE) PE CORP NY.		DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:109.	
Best Local Similarity: 34.85%	Mismatches: 24	DE WO2004029197-A2.	
Query Match: 6.67%	Indels: 7	PD 08-APR-2004.	
RESULT 1199		PA (MAXY-) MAXYGEN INC.	
ID ABN92099 standard; DNA; 753 BP.		Best Local Similarity: 21.60%	Mismatches: 57
DE Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:1562.		Query Match: 6.67%	Indels: 41
PN US6380370-B1.		RESULT 1208	
PD 30-APR-2002.		ID ADM18757 standard; cDNA; 912 BP.	
PA (GENO-) GENOME THERAPEUTICS CORP.		DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:122.	

PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 21.60% Mismatches: 57  
Query Match: 6.67% Indels: 41  
RESULT 1209  
ID ABV94560 standard; cDNA; 913 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:121.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 21.60% Mismatches: 57  
Query Match: 6.67% Indels: 41  
RESULT 1210  
ID ADM18756 standard; cDNA; 913 BP.  
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:121.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 21.60% Mismatches: 57  
Query Match: 6.67% Indels: 41  
RESULT 1211  
ID ADS01537 standard; DNA; 915 BP.  
DE Staphylococcus epidermis polynucleotide seqid 832.  
PN US2004147734-A1.  
PD 29-JUL-2004.  
PA (DOUC/) DOUCETTE-STAMM L.  
PA (BUSH/) BUSH D.  
Best Local Similarity: 30.23% Mismatches: 25  
Query Match: 6.67% Indels: 48  
RESULT 1212  
ID ADL65970 standard; DNA; 934 BP.  
DE C. Glutamicum RXA-associated DNA #164.  
PN DE10154177-A1.  
PD 08-MAY-2003.  
PA (BADI ) BASF AG.  
Best Local Similarity: 27.10% Mismatches: 53  
Query Match: 6.67% Indels: 10  
RESULT 1213  
ID ADM42775 standard; DNA; 942 BP.  
DE DNA encoding the murine carvone receptor car-c5 seqid 19.  
PN WO2003100057-A1.  
PD 04-DEC-2003.  
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.  
Best Local Similarity: 24.37% Mismatches: 79  
Query Match: 6.67% Indels: 38  
RESULT 1214  
ID AAS69112 standard; cDNA; 1002 BP.  
DE DNA encoding novel human diagnostic protein #4916.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 22.15% Mismatches: 60  
Query Match: 6.67% Indels: 30  
RESULT 1215  
ID ABX65804 standard; DNA; 1024 BP.  
DE Helicobacter pylori selected interacting domain (SID) DNA #403.  
PN WO200266501-A2.  
PD 29-AUG-2002.  
PA (HYBR-) HYBRIGENICS.  
PA (INSP ) INST PASTEUR.  
Best Local Similarity: 28.43% Mismatches: 42  
Query Match: 6.67% Indels: 16  
RESULT 1216  
ID ACD06271 standard; cDNA; 1034 BP.  
DE Human cDNA encoding protein NOV36j.  
PN WO2003023008-A2.  
PD 20-MAR-2003.  
PA (CURA-) CURAGEN CORP.  
Best Local Similarity: 21.86% Mismatches: 53  
Query Match: 6.67% Indels: 59  
RESULT 1217  
ID AAA56702 standard; DNA; 1046 BP.

DE EcorI/XbaI fragment from pscFv24-PDGFR DNA sequence SEQ ID NO:163.  
PN WO200023593-A2.  
PD 27-APR-2000.  
PA (FRAU ) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.  
Best Local Similarity: 18.42% Mismatches: 64  
Query Match: 6.67% Indels: 55  
RESULT 1218  
ID ABQ76938 standard; DNA; 1188 BP.  
DE Muvbeta-nucbeta-huCD3epsilon fusion construct DNA.  
PN DE10109854-A1.  
PD 12-SEP-2002.  
PA (STAN/) STANISLAWSKI T.  
Best Local Similarity: 24.14% Mismatches: 61  
Query Match: 6.67% Indels: 22  
RESULT 1219  
ID ADF00600 standard; DNA; 1209 BP.  
DE Bacterial polynucleotide #885.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
Best Local Similarity: 21.17% Mismatches: 37  
Query Match: 6.67% Indels: 39  
RESULT 1220  
ID AAS41209 standard; cDNA; 1270 BP.  
DE cDNA encoding novel human enzyme polypeptide #425.  
PN WO200155301-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 24.43% Mismatches: 64  
Query Match: 6.67% Indels: 43  
RESULT 1221  
ID ABA66628 standard; cDNA; 1270 BP.  
DE Human cDNA SEQ ID NO: 294.  
PN WO200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 24.43% Mismatches: 64  
Query Match: 6.67% Indels: 43  
RESULT 1222  
ID ABV83965 standard; cDNA; 1270 BP.  
DE Human polynucleotide SEQ ID NO 294.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Best Local Similarity: 24.43% Mismatches: 64  
Query Match: 6.67% Indels: 43  
RESULT 1223  
ID ACA29487 standard; DNA; 1272 BP.  
DE Prokaryotic essential gene #11144.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 31.25% Mismatches: 31  
Query Match: 6.67% Indels: 13  
RESULT 1224  
ID ADP98747 standard; DNA; 1353 BP.  
DE C. albicans specific gene, orf19.3956, DNA sequence.  
PN WO2004056965-A2.  
PD 08-JUL-2004.  
PA (ELIT-) ELITRA PHARM INC.  
PA (ELIT-) ELITRA CANADA LTD.  
Best Local Similarity: 28.03% Mismatches: 60  
Query Match: 6.67% Indels: 17  
RESULT 1225  
ID ACC61861 standard; DNA; 1398 BP.  
DE Gene sequence #SEQ ID 2504.  
PN EP1258494-A1.  
PD 20-NOV-2002.  
PA (CELL-) CELLZOME AG.  
Best Local Similarity: 20.00% Mismatches: 60  
Query Match: 6.67% Indels: 73

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RESULT 1226
ID ADK5005 standard; DNA; 1398 BP.
DE Disease treating protein complex-derived gene #1514.
PN EP1338608-A2.
PD 27-AUG-2003.
PA (CELL-) CELLZOME AG.
Best Local Similarity: 20.00%
Query Match: 6.67%
Mismatch: 60
Indels: 73
RESULT 1227
ID ACA53884 standard; DNA; 1488 BP.
DE Prokaryotic essential gene #35541.
PN WO20027183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Best Local Similarity: 23.95%
Query Match: 6.67%
Mismatch: 45
Indels: 62
RESULT 1228
ID ADS57032 standard; cDNA; 1494 BP.
DE Bacterial polynucleotide #9019.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Best Local Similarity: 19.23%
Query Match: 6.67%
Mismatch: 64
Indels: 17
RESULT 1229
ID AAH52763 standard; DNA; 1605 BP.
DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:919.
PN WO200134809-A2.
PD 17-MAY-2001.
PA (GLAX) GLAXO GROUP LTD.
Best Local Similarity: 30.23%
Query Match: 6.67%
Mismatch: 25
Indels: 48
RESULT 1230
ID AAX14344 standard; DNA; 1631 BP.
DE H. pylori GHP0 265 gene.
PN WO9843478-A1.
PD 08-OCT-1998.
PA (INMR) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
PA (HUMA-) HUMAN GENOME SCI INC.
Best Local Similarity: 28.43%
Query Match: 6.67%
Mismatch: 42
Indels: 16
RESULT 1231
ID ABV99336 standard; DNA; 1681 BP.
DE Human NOV3a coding sequence.
PN WO200272771-A2.
PD 19-SEP-2002.
PA (CURA-) CURAGEN CORP.
Best Local Similarity: 20.00%
Query Match: 6.67%
Mismatch: 48
Indels: 78
RESULT 1232
ID ACH95608 standard; DNA; 1689 BP.
DE Klebsiella pneumoniae polynucleotide seqid 1403.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Best Local Similarity: 19.81%
Query Match: 6.67%
Mismatch: 84
Indels: 49
RESULT 1233
ID ABK90489 standard; cDNA; 1822 BP.
DE Human transporter protein cDNA.
PN US2002082191-A1.
PD 27-JUN-2002.
PA (GUEG/) GUEGLER K.
PA (BRAN/) BRANDON R C.
PA (MERK/) MERKULOV G V.
PA (KETC/) KETCHUM K A.
PA (DFRA/) DI FRANCESCO V.
PA (BEAS/) BEASLEY E M.
Best Local Similarity: 20.00%
Mismatch: 48

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Query Match: 6.67%
RESULT 1234
ID AAV33673 standard; DNA; 1949 BP.
DE Candida parapsilosis IPC synthase encoding DNA.
PN EP872485-A2.
PD 21-OCT-1998.
PA (ELIL) LILLY & CO ELI.
Best Local Similarity: 22.12%
Query Match: 6.67%
Mismatch: 32
Indels: 22
RESULT 1235
ID AAH73591 standard; DNA; 1949 BP.
DE Candida parapsilosis IPC synthase gene.
PN US2001012615-A1.
PD 09-AUG-2001.
PA (HEID/) HEIDLER S A.
PA (RADD/) RADDING J A.
Best Local Similarity: 22.12%
Query Match: 6.67%
Mismatch: 32
Indels: 22
RESULT 1236
ID ACA62411 standard; DNA; 1949 BP.
DE C. parapsilosis inositolphosphoryl ceramide synthase gene.
PN US2003022343-A1.
PD 30-JAN-2003.
PA (HEID/) HEIDLER S A.
PA (RADD/) RADDING J A.
Best Local Similarity: 22.12%
Query Match: 6.67%
Mismatch: 32
Indels: 22
RESULT 1237
ID ACA62358 standard; DNA; 1949 BP.
DE Gene encoding C. parapsilosis inositolphosphoryl ceramide (IPC) synthase.
PN US2003022342-A1.
PD 30-JAN-2003.
PA (HEID/) HEIDLER S A.
PA (RADD/) RADDING J A.
Best Local Similarity: 22.12%
Query Match: 6.67%
Mismatch: 32
Indels: 22
RESULT 1238
ID AAS82555 standard; cDNA; 2182 BP.
DE DNA encoding novel human diagnostic protein #18359.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Best Local Similarity: 25.87%
Query Match: 6.67%
Mismatch: 66
Indels: 57
RESULT 1239
ID AAT85403 standard; cDNA; 2625 BP.
DE Human cadherin-11 coding sequence.
PN US646250-A.
PD 08-JUL-1997.
PA (DOHE-) DOHENY EYE INST.
Best Local Similarity: 20.74%
Query Match: 6.67%
Mismatch: 45
Indels: 36
RESULT 1240
ID AAF61925 standard; cDNA; 2625 BP.
DE Full length human cadherin-11 cDNA.
PN US5597725-A.
PD 28-JAN-1997.
PA (DOHE-) DOHENY EYE INST.
Best Local Similarity: 20.74%
Query Match: 6.67%
Mismatch: 45
Indels: 36
RESULT 1241
ID AAV83124 standard; cDNA; 2625 BP.
DE Cadherin-11 cDNA.
PN WO9849560-A1.
PD 05-NOV-1998.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Best Local Similarity: 20.74%
Query Match: 6.67%
Mismatch: 45
Indels: 36
RESULT 1242
ID AAF55586 standard; DNA; 2625 BP.
DE Nucleotide sequence of a human cadherin-11 polypeptide.
PN WO200117557-A1.
PD 15-MAR-2001.

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PA (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.  
Best Local Similarity: 20.74% Mismatches: 45  
Query Match: 6.67% Indels: 36  
RESULT 1243  
ID ADP18641 standard; cDNA; 2625 BP.  
DE Human TAT400 cDNA used to treat cancer SeqID 1.  
PN WO2004045516-A2.  
PD 03-JUN-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 20.74% Mismatches: 45  
Query Match: 6.67% Indels: 36  
RESULT 1244  
ID ADP26918 standard; cDNA; 2625 BP.  
DE Human OB-cadherin encoding cDNA SEQ ID NO:19.  
PN EP1428893-A2.  
PD 16-JUN-2004.  
PA (SPRE/) SPRECHER E.  
PA (BERG/) BERGMAN R.  
Best Local Similarity: 20.74% Mismatches: 45  
Query Match: 6.67% Indels: 36  
RESULT 1245  
ID ADR24809 standard; DNA; 2625 BP.  
DE Breast cancer prognosis marker #670.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSP-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Best Local Similarity: 20.74% Mismatches: 45  
Query Match: 6.67% Indels: 36  
RESULT 1246  
ID ABV23234 standard; cDNA; 2828 BP.  
DE Human prostate expression marker cDNA 23225.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 22.02% Mismatches: 40  
Query Match: 6.67% Indels: 61  
RESULT 1247  
ID ABV29077 standard; cDNA; 2828 BP.  
DE Human prostate expression marker cDNA 29068.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 22.02% Mismatches: 40  
Query Match: 6.67% Indels: 61  
RESULT 1248  
ID ABN59956 standard; cDNA; 2828 BP.  
DE Novel human coding sequence SEQ ID NO: 367.  
PN WO200222660-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 22.02% Mismatches: 40  
Query Match: 6.67% Indels: 61  
RESULT 1249  
ID ACN91315 standard; DNA; 2828 BP.  
DE Breast cancer related marker, seq id 12465.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 22.02% Mismatches: 40  
Query Match: 6.67% Indels: 61  
RESULT 1250  
ID AAH54530 standard; DNA; 2998 BP.  
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3894.  
PN WO200134809-A2.  
PD 17-MAY-2001.  
PA (GLAX ) GLAXO GROUP LTD.  
Best Local Similarity: 30.23% Mismatches: 25  
Query Match: 6.67% Indels: 48  
RESULT 1251  
ID AAH54434 standard; DNA; 3118 BP.  
DE S. epidermidis genomic polynucleotide sequence SEQ ID NO:3798.  
PN WO200134809-A2.

PD 17-MAY-2001.  
PA (GLAX ) GLAXO GROUP LTD.  
Best Local Similarity: 30.23% Mismatches: 25  
Query Match: 6.67% Indels: 48  
RESULT 1252  
ID ABX63597 standard; cDNA; 3403 BP.  
DE Human cDNA #597 differentially expressed in activated vascular tissue.  
PN US2002137081-A1.  
PD 26-SEP-2002.  
PA (BAND/) BANDMAN O.  
Best Local Similarity: 20.74% Mismatches: 45  
Query Match: 6.67% Indels: 36  
RESULT 1253  
ID ADJ56330 standard; cDNA; 3403 BP.  
DE Human cDNA differentially expressed in MYCN activated cells SeqID 136.  
PN US2003119009-A1.  
PD 26-JUN-2003.  
PA (STUA/) STUART S G.  
PA (NUCH/) NUCHTERN J G.  
PA (PLON/) PLON S E.  
PA (SHOH/) SHOHET J M.  
Best Local Similarity: 20.74% Mismatches: 45  
Query Match: 6.67% Indels: 36  
RESULT 1254  
ID AAA70202 standard; DNA; 3501 BP.  
DE Plasmodium falciparum chromosome 2 related DNA sequence SEQ ID NO:335.  
PN WO200025728-A2.  
PD 11-MAY-2000.  
PA (HOFF/) HOFFMAN S.  
PA (CARU/) CARUCCI D.  
PA (GARD/) GARDNER M.  
PA (VENT/) VENTER J C.  
Best Local Similarity: 22.07% Mismatches: 56  
Query Match: 6.67% Indels: 31  
RESULT 1255  
ID ADR48217 standard; cDNA; 3654 BP.  
DE Human cadherin 11 type 2 OB-cadherin encoding cDNA SEQ:5.  
PN WO2004074510-A1.  
PD 02-SEP-2004.  
PA (GARV-) GARVAN INST MEDICAL RES.  
Best Local Similarity: 20.74% Mismatches: 45  
Query Match: 6.67% Indels: 36  
RESULT 1256  
ID ADH17152 standard; cDNA; 3661 BP.  
DE Human OB-cadherin-1 cDNA.  
PN WO2003097854-A2.  
PD 27-NOV-2003.  
PA (SUGE-) SUGEN INC.  
Best Local Similarity: 20.74% Mismatches: 45  
Query Match: 6.67% Indels: 36  
RESULT 1257  
ID AAQ44392 standard; cDNA to mRNA; 3712 BP.  
DE Sequence of human OSP-4-1 cDNA.  
PN EP585801-A2.  
PD 09-MAR-1994.  
PA (FARH ) HOECHST JAPAN LTD.  
Best Local Similarity: 20.74% Mismatches: 45  
Query Match: 6.67% Indels: 36  
RESULT 1258  
ID ABA96103 standard; cDNA; 3767 BP.  
DE Human membrane transporter protein 58289 cDNA.  
PN WO200190146-A2.  
PD 29-NOV-2001.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 20.00% Mismatches: 48  
Query Match: 6.67% Indels: 78  
RESULT 1259  
ID ACN91063 standard; DNA; 3925 BP.  
DE Breast cancer related marker, seq id 12213.  
PN US2003099974-A1.  
PD 29-MAY-2003.  
PA (MILL-) MILLENNIUM PHARM INC.  
Best Local Similarity: 20.00% Mismatches: 48



Query Match: 6.67% Indels: 78  
RESULT 1260  
ID ABL03162 standard; cDNA; 5189 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 3968.  
PN WO200171042-A2.  
PA (PEKE ) PE CORP NY.  
PD 27-SEP-2001.  
Best Local Similarity: 34.85% Mismatches: 24  
Query Match: 6.67% Indels: 7  
RESULT 1261  
ID AAK69142 standard; DNA; 12997 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:23954.  
PN WO200157182-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PD 09-AUG-2001.  
Best Local Similarity: 25.00% Mismatches: 53  
Query Match: 6.67% Indels: 27  
RESULT 1262  
ID AA293705 standard; DNA; 18402 BP.  
DE CYP5B fatty acid desaturase gene.  
PN WO200021557-A1.  
PD 20-APR-2000.  
PA (MERI ) MERCK & CO INC.  
PD 21-NOV-2002.  
Best Local Similarity: 22.84% Mismatches: 55  
Query Match: 6.67% Indels: 45  
RESULT 1263  
ID ABX13172 standard; DNA; 65464 BP.  
DE Human gene encoding a Noelin-1-like secreted protein.  
PN US2002173459-A1.  
PD 21-NOV-2002.  
PA (PEKE ) PE CORP NY.  
PD 20-JUN-2001.  
Best Local Similarity: 30.10% Mismatches: 37  
Query Match: 6.67% Indels: 21  
RESULT 1264  
ID ABD32542 standard; DNA; 108845 BP.  
DE Mouse cancer-associated genomic DNA MD7-024.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
PD 17-AUG-2003.  
Best Local Similarity: 28.68% Mismatches: 33  
Query Match: 6.67% Indels: 50  
RESULT 1265  
Best Local Similarity: 21.78% Mismatches: 76  
Query Match: 6.67% Indels: 67  
RESULT 1266  
ID AAH68529 standard; DNA; 349980 BP.  
DE C glutamicum coding sequence fragment SEQ ID NO: 7064.  
PN EF108790-A2.  
PD 20-JUN-2001.  
PA (KYOW ) KYOWA HAKKO KOGYO KK.  
PD 17-APR-2003.  
Best Local Similarity: 27.10% Mismatches: 53  
Query Match: 6.67% Indels: 10  
RESULT 1267  
ID ACH32505 standard; cDNA; 452 BP.  
DE Human endothelial cell cDNA #638.  
PN US2003073623-A1.  
PD 17-APR-2003.  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.  
PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1268  
ID ADF03528 standard; DNA; 588 BP.  
DE Bacterial polynucleotide #3813.  
PN US6605709-B1.  
PD 12-AUG-2003.  
PA (GENO-) GENOME THERAPEUTICS CORP.  
PD 18-OCT-2001.  
Best Local Similarity: 21.21% Mismatches: 66  
Query Match: 6.62% Indels: 32  
RESULT 1269  
ID AAT03017 standard; cDNA to mRNA; 618 BP.  
DE Endothelial cell polypeptide coding sequence.  
PN EP682113-A2.  
PD 15-NOV-1995.  
PA (ONOV ) ONO PHARM CO LTD.  
PD 16-SEP-2004.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1270  
ID ADR59253 standard; cDNA; 794 BP.  
DE Cotton cDNA sequence, SEQ ID 34.  
PN US2004181830-A1.  
PD 16-SEP-2004.  
PA (KOVA/) KOVALIC D K.  
PA (ZHOU/) ZHOU Y.  
PA (CAOY/) CAO Y.  
Best Local Similarity: 26.00% Mismatches: 29  
Query Match: 6.62% Indels: 26  
RESULT 1271  
ID AAH33705 standard; cDNA; 813 BP.  
DE Human colon cancer antigen encoding cDNA SEQ ID NO:761.  
PN WO200122920-A2.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
PD 03-OCT-2002.  
Best Local Similarity: 21.76% Mismatches: 64  
Query Match: 6.62% Indels: 48  
RESULT 1272  
ID ACA33175 standard; DNA; 864 BP.  
DE Prokaryotic essential gene #14832.  
PN WO200271183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
PD 10-JUL-2003.  
Best Local Similarity: 29.52% Mismatches: 42  
Query Match: 6.62% Indels: 15  
RESULT 1273  
ID ADJ33272 standard; DNA; 867 BP.  
DE Enterococcus faecalis ORF1 encoding DNA SEQ ID NO:32.  
PN WO2003056295-A2.  
PD 10-JUL-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PD 06-NOV-2003.  
Best Local Similarity: 29.52% Mismatches: 42  
Query Match: 6.62% Indels: 15  
RESULT 1274  
ID ADF61795 standard; cDNA; 914 BP.  
DE Human D1-1 cDNA.  
PN WO2003091447-A2.  
PD 06-NOV-2003.  
PA (CALY ) CALIFORNIA INST OF TECHNOLOGY.  
PD 26-FEB-2004.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1275  
ID ADJ67700 standard; DNA; 935 BP.  
DE Kiflc DNA #16.  
PN US2004038222-A1.  
PD 26-FEB-2004.  
PA (DIET/) DIETRICH W F.  
PA (WATT/) WATERS J W.  
Best Local Similarity: 26.13% Mismatches: 32  
Query Match: 6.62% Indels: 28  
RESULT 1276  
ID AAT03018 standard; cDNA to mRNA; 983 BP.  
DE Endothelial cell polypeptide full length sequence.  
PN EP682113-A2.  
PD 15-NOV-1995.  
PA (ONOV ) ONO PHARM CO LTD.  
PD 16-SEP-2004.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1277  
ID ABK35835 standard; cDNA; 983 BP.  
DE cDNA sequence #226 encoding novel human secreted protein.  
PN WO200177289-A2.  
PD 18-OCT-2001.  
PA (GEMY ) GENETICS INST INC.  
PD 18-OCT-2001.  
Best Local Similarity: 19.12% Mismatches: 45

Query Match: 6.62% Indels: 42  
RESULT 1278  
ID ADE77092 standard; cDNA; 1002 BP.  
DE Human cDNA differentially expressed in a liver disorder #190.  
PN US2003108871-A1.  
PD 12-JUN-2003.  
PA (KASE/) KASER M R.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1279  
ID ACC69471 standard; cDNA; 1030 BP.  
DE Human malignant neoplasm related protein encoding cDNA SEQ ID NO:13.  
PN WO2003025135-A2.  
PD 27-MAR-2003.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1280  
ID AAF21798 standard; DNA; 1040 BP.  
DE Human breast and ovarian cancer associated antigen gene SEQ ID 185.  
PN WO200055173-A1.  
PD 21-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1281  
ID RAC69513 standard; DNA; 1047 BP.  
DE Human secreted protein gene 2 clone HEMFQ46.  
PN WO200061623-A1.  
PD 19-OCT-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1282  
ID AAK51736 standard; cDNA; 1070 BP.  
DE Human polynucleotide SEQ ID NO 281.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1283  
ID AAK52720 standard; cDNA; 1079 BP.  
DE Human polynucleotide SEQ ID NO 2249.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1284  
ID AAK52719 standard; cDNA; 1080 BP.  
DE Human polynucleotide SEQ ID NO 2248.  
PN WO200157190-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1285  
ID ADE53693 standard; cDNA; 1094 BP.  
DE Human prostate cancer cDNA #40.  
PN US2003190640-A1.  
PD 09-OCT-2003.  
PA (FARI/) PARIS M.  
PA (PEAR/) PEARSON C I.  
Best Local Similarity: 19.12% Mismatches: 45  
Query Match: 6.62% Indels: 42  
RESULT 1286  
ID ADA98577 standard; DNA; 1119 BP.  
DE Human secreted protein-related DNA sequence #170.  
PN WO2003004623-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76

Query Match: 6.62% Indels: 103  
RESULT 1287  
ID ADA44309 standard; DNA; 1119 BP.  
DE Human secreted protein DNA SEQ ID 502.  
PN WO2003000865-A2.  
PD 03-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1288  
ID ADC20693 standard; DNA; 1119 BP.  
DE Human secreted protein-related DNA sequence #111.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1289  
ID ADF10874 standard; DNA; 1119 BP.  
DE Human secreted protein encoding sequence #196.  
PN WO200295085-A2.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1290  
ID ADA98576 standard; DNA; 1121 BP.  
DE Human secreted protein-related DNA sequence #169.  
PN WO2003004623-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1291  
ID ADA44308 standard; DNA; 1121 BP.  
DE Human secreted protein DNA SEQ ID 501.  
PN WO2003000865-A2.  
PD 03-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1292  
ID ADC20692 standard; DNA; 1121 BP.  
DE Human secreted protein-related DNA sequence #110.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1293  
ID ADF10873 standard; DNA; 1121 BP.  
DE Human secreted protein encoding sequence #195.  
PN WO200295085-A2.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1294  
ID AAC59477 standard; cDNA; 1125 BP.  
DE Human secreted protein gene 29 SEQ ID NO:39.  
PN WO200056755-A1.  
PD 28-SEP-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1295  
ID ADA97977 standard; cDNA; 1125 BP.  
DE Human secreted protein cDNA sequence #71.  
PN WO2003004623-A2.  
PD 16-JAN-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103

RESULT 1296  
ID ADA43883 standard; cDNA; 1125 BP.  
DE Human secreted protein cDNA SEQ ID 71.  
PN WO2003000865-A2.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1297  
ID ADC20138 standard; DNA; 1125 BP.  
DE Human secreted protein coding sequence #77.  
PN WO200292787-A2.  
PD 21-NOV-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1298  
ID ADF10588 standard; DNA; 1125 BP.  
DE Human secreted protein encoding sequence #41.  
PN WO200299085-A2.  
PD 12-DEC-2002.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 20.66% Mismatches: 76  
Query Match: 6.62% Indels: 103  
RESULT 1299  
ID AAD45161 standard; DNA; 1478 BP.  
DE Flea chitinase DNA, nC1CHT1478.  
PN US6418977-B1.  
PD 09-JUL-2002.  
PA (HESK-) HESKA CORP.  
Best Local Similarity: 25.68% Mismatches: 63  
Query Match: 6.62% Indels: 22  
RESULT 1301  
ID ADR99937 standard; DNA; 1539 BP.  
DE Immune Response Associated Protein, IRAP-13, coding sequence, SEQ ID 45.  
PN WO2004081197-A2.  
PD 23-SEP-2004.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 20.90% Mismatches: 65  
Query Match: 6.62% Indels: 66  
RESULT 1302  
ID ABL27300 standard; DNA; 1592 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 33373.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Best Local Similarity: 21.74% Mismatches: 33  
Query Match: 6.62% Indels: 56  
RESULT 1303  
ID ADI42377 standard; DNA; 1637 BP.  
DE Plant transcription factor polynucleotide #512.  
PN US2004019927-A1.  
PD 29-JAN-2004.  
PA (SHER) SHERMAN B K.  
PA (RIEC) RIECHMANN J L.  
PA (JIAN) JIANG C.  
PA (HEAR) HEARD J E.  
PA (HAAR) HAAKE V.  
PA (CREE) CREELMAN R A.  
PA (RATC) RATCLIFFE O.  
PA (ADAM) ADAM L J.  
PA (REUB) REUBER T L.  
PA (KEDD) KEDDIE J.  
PA (BROU) BROUN P E.  
PA (PILG) PILGRIM M L.  
Mismatches: 48  
Indels: 19  
RESULT 1304  
ID AAQ96124 standard; DNA; 1727 BP.  
DE T-cell receptor eta DNA.  
PN WO9521528-A1.  
PD 17-AUG-1995.  
PA (GEHO) GEN HOSPITAL CORP.  
Best Local Similarity: 25.66% Mismatches: 53  
Query Match: 6.62% Indels: 36  
RESULT 1305  
ID ADR65967 standard; DNA; 1957 BP.  
DE Human prostatic carcinoma derived DNA SEQ ID 163 #1.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ) HINZMANN B.  
PA (DAHL) DAHL E.  
PA (ROSE) ROSENTHAL A.  
PA (HERM) HERMANN K.  
PA (PILA) PILARSKY C.  
Best Local Similarity: 23.23% Mismatches: 51  
Query Match: 6.62% Indels: 44  
RESULT 1306  
ID AAD27272 standard; cDNA; 2074 BP.  
DE Human transporter and ion channel-19 (TRICH-19) cDNA.  
PN WO200192304-A2.  
PD 06-DEC-2001.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 22.11% Mismatches: 52  
Query Match: 6.62% Indels: 72  
RESULT 1307  
ID AAV29911 standard; cDNA; 2103 BP.  
DE Mouse hedgehog interacting protein (HIP) cDNA.  
PN WO9812326-A1.  
PD 26-MAR-1998.  
PA (HARD) HARVARD COLLEGE.  
Best Local Similarity: 26.36% Mismatches: 45  
Query Match: 6.62% Indels: 16  
RESULT 1308  
ID ADE86235 standard; cDNA; 2103 BP.  
DE Mouse hedgehog interacting protein (HIP) cDNA sequence.  
PN US2003143595-A1.  
PD 31-JUL-2003.  
PA (MCMA) MCMAHON A P.  
PA (CHUA) CHUANG P.  
Best Local Similarity: 26.36% Mismatches: 45  
Query Match: 6.62% Indels: 16  
RESULT 1309  
ID AAH18175 standard; cDNA; 2122 BP.  
DE Human cDNA sequence SEQ ID NO:18074.  
PN EF1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 26.00% Mismatches: 54  
Query Match: 6.62% Indels: 39  
RESULT 1310  
ID ABK63725 standard; cDNA; 2171 BP.  
DE Rat sequence differentially expressed in response to a hepatotoxin #1632.  
PN WO200210453-A2.  
PD 07-FEB-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 23.53% Mismatches: 48  
Query Match: 6.62% Indels: 19  
RESULT 1311  
ID ABT17417 standard; DNA; 2171 BP.  
DE Human IG gene related nucleic acid SEQ ID No 43.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Best Local Similarity: 23.53% Mismatches: 48

Query Match: 6.62% Indels: 19  
RESULT 1312  
ID ADB52771 standard; DNA; 2171 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3313.  
PN WO2003085993-A2.  
PD 14-AUG-2003.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 23.53% Mismatches: 48  
Query Match: 6.62% Indels: 19  
RESULT 1313  
ID AET41948 standard; DNA; 2171 BP.  
DE Toxicity modelling related rat gene SEQ ID NO 1650.  
PN WO200295000-A2.  
PD 28-NOV-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 23.53% Mismatches: 48  
Query Match: 6.62% Indels: 19  
RESULT 1314  
ID AAX90848 standard; DNA; 2360 BP.  
DE cDNA clone cc359\_4.  
PN WO950405-A1.  
PD 07-OCT-1999.  
PA (GEMY ) GENETICS INST INC.  
Best Local Similarity: 20.77% Mismatches: 61  
Query Match: 6.62% Indels: 65  
RESULT 1315  
ID AAA37899 standard; DNA; 2669 BP.  
DE Mouse Hedgehog interacting protein coding sequence.  
PN WO200074706-A1.  
PD 14-DEC-2000.  
PA (LORA-) LORANTIS LTD.  
Best Local Similarity: 26.36% Mismatches: 45  
Query Match: 6.62% Indels: 16  
RESULT 1316  
ID ABS55985 standard; DNA; 2669 BP.  
DE Mouse hedgehog-interacting protein (HTP) DNA.  
PN WO200280952-A2.  
PD 17-OCT-2002.  
PA (LORA-) LORANTIS LTD.  
Best Local Similarity: 26.36% Mismatches: 45  
Query Match: 6.62% Indels: 16  
RESULT 1317  
ID ACN38684 standard; cDNA; 3617 BP.  
DE Tumour-associated antigenic target (TAT) cDNA DNA324988, SEQ ID NO:2351.  
PN WO2004030615-A2.  
PD 15-APR-2004.  
PA (GETH ) GENENTECH INC.  
Best Local Similarity: 21.76% Mismatches: 64  
Query Match: 6.62% Indels: 48  
RESULT 1318  
ID ADB84160 standard; DNA; 7800 BP.  
DE Gene expression estimation method-related DNA sequence #20.  
PN WO2003044227-A1.  
PD 30-MAY-2003.  
PA (NAAG-) NAT INST AGROBIOLOGICAL SCI.  
Best Local Similarity: 26.26% Mismatches: 29  
Query Match: 6.62% Indels: 27  
RESULT 1319  
ID ADJ33271 standard; DNA; 8347 BP.  
DE Enterococcus faecalis biosynthetic gene cluster SEQ ID NO:31.  
PN WO2003056295-A2.  
PD 10-JUL-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
Best Local Similarity: 29.52% Mismatches: 42  
Query Match: 6.62% Indels: 15  
RESULT 1320  
ID AAX13067 standard; DNA; 9767 BP.  
DE Enterococcus faecalis genome contig SEQ ID NO:130.  
PN WO9850555-A2.  
PD 12-NOV-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 21.99% Mismatches: 38  
Query Match: 6.62% Indels: 38

RESULT 1321  
ID ABS98862 standard; DNA; 9767 BP.  
DE Enterococcus faecalis contig sequence #130.  
PN US2002120116-A1.  
PD 29-AUG-2002.  
PA (KUNS/) KUNSCH C A.  
PA (DILL/) DILLON P J.  
PA (BARA/) BARASH S.  
Best Local Similarity: 21.99% Mismatches: 38  
Query Match: 6.62% Indels: 38  
RESULT 1322  
ID AAS59571 standard; DNA; 11808 BP.  
DE Propionibacterium acnes immunogenic protein encoding DNA #66.  
PN WO200181581-A2.  
PD 01-NOV-2001.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 20.28% Mismatches: 90  
Query Match: 6.62% Indels: 53  
RESULT 1323  
ID ACF64500 standard; DNA; 11808 BP.  
DE Propionibacterium acnes DNA contig sequence #66.  
PN WO2003033515-A1.  
PD 24-APR-2003.  
PA (CORI-) CORIXA CORP.  
Best Local Similarity: 20.28% Mismatches: 90  
Query Match: 6.62% Indels: 53  
RESULT 1324  
ID AAX13118 standard; DNA; 11879 BP.  
DE Enterococcus faecalis genome contig SEQ ID NO:181.  
PN WO9850555-A2.  
PD 12-NOV-1998.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 29.52% Mismatches: 42  
Query Match: 6.62% Indels: 15  
RESULT 1325  
ID ABS98913 standard; DNA; 11879 BP.  
DE Enterococcus faecalis contig sequence #181.  
PN US2002120116-A1.  
PD 29-AUG-2002.  
PA (KUNS/) KUNSCH C A.  
PA (DILL/) DILLON P J.  
PA (BARA/) BARASH S.  
Best Local Similarity: 29.52% Mismatches: 42  
Query Match: 6.62% Indels: 15  
RESULT 1326  
ID AAS46477 standard; DNA; 14112 BP.  
DE Tumour suppressor gene derived chemically modified sequence #199.  
PN WO200168912-A2.  
PD 20-SEP-2001.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 24.52% Mismatches: 62  
Query Match: 6.62% Indels: 32  
RESULT 1327  
ID ABL33442 standard; DNA; 14112 BP.  
DE Human immune system associated gene SEQ ID NO: 1415.  
PN WO200200928-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 24.52% Mismatches: 62  
Query Match: 6.62% Indels: 32  
RESULT 1328  
ID ABK31332 standard; DNA; 14112 BP.  
DE Signal transduction associated gene modified DNA #88.  
PN WO200200926-A2.  
PD 03-JAN-2002.  
PA (EPIG-) EPIGENOMICS AG.  
Best Local Similarity: 24.52% Mismatches: 62  
Query Match: 6.62% Indels: 32  
RESULT 1329  
ID ABQ66979 standard; DNA; 14112 BP.  
DE Human angiogenesis associated polynucleotide SEQ ID NO 9.  
PN WO200246454-A2.  
PD 13-JUN-2002.

PA (EPIC-) EPIGENOMICS AG.  
Best Local Similarity: 24.52% Mismatches: 62  
Query Match: 6.62% Indels: 32  
RESULT 1330  
ID AD097543 standard; DNA; 65590 BP.  
DE Human cancer associated sequence HD09-011, SEQ ID 520.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 30.91% Mismatches: 38  
Query Match: 6.62% Indels: 16  
RESULT 1331  
ID ABX14591 standard; DNA; 106323 BP.  
DE Human chloride intracellular channel isoform protein genomic DNA.  
PN US2002132292-A1.  
PD 19-SEP-2002.  
PA (WEIM/) WEI M.  
PA (YANC/) YAN C.  
PA (DPR/) DI FRANCESCO V.  
PA (BRAS/) BEASLEY E M.  
Best Local Similarity: 23.85% Mismatches: 48  
Query Match: 6.62% Indels: 31  
RESULT 1332  
ID AD58821 standard; DNA; 106323 BP.  
DE Human transporter gene.  
Best Local Similarity: 23.85% Mismatches: 48  
Query Match: 6.62% Indels: 31  
RESULT 1333  
Best Local Similarity: 29.20% Mismatches: 59  
Query Match: 6.62% Indels: 13  
RESULT 1334  
Best Local Similarity: 24.32% Mismatches: 60  
Query Match: 6.62% Indels: 24  
RESULT 1335  
Best Local Similarity: 24.32% Mismatches: 60  
Query Match: 6.62% Indels: 24  
RESULT 1336  
Best Local Similarity: 24.32% Mismatches: 60  
Query Match: 6.62% Indels: 24  
RESULT 1337  
Best Local Similarity: 22.22% Mismatches: 79  
Query Match: 6.62% Indels: 62  
RESULT 1338  
Best Local Similarity: 32.39% Mismatches: 22  
Query Match: 6.62% Indels: 14  
RESULT 1339  
Best Local Similarity: 32.39% Mismatches: 22  
Query Match: 6.62% Indels: 14  
RESULT 1340  
Best Local Similarity: 32.39% Mismatches: 22  
Query Match: 6.62% Indels: 14  
RESULT 1341  
Best Local Similarity: 32.39% Mismatches: 22  
Query Match: 6.62% Indels: 14  
RESULT 1342  
Best Local Similarity: 32.39% Mismatches: 22  
Query Match: 6.62% Indels: 14  
RESULT 1343  
Best Local Similarity: 32.39% Mismatches: 22  
Query Match: 6.62% Indels: 14  
RESULT 1344  
ID ABT10146 standard; cDNA; 140167 BP.  
DE Human breast cancer associated coding sequence SEQ ID NO: 280.  
PN WO200259271-A2.  
PD 01-AUG-2002.  
PA (GENE-) GENE LOGIC INC.  
Best Local Similarity: 27.27% Mismatches: 15  
Query Match: 6.62% Indels: 16  
RESULT 1345  
ID AAC81914 standard; DNA; 273254 BP.  
DE Chlamydia pneumoniae genome DNA.  
PN WO200027994-A2.  
PD 18-MAY-2000.

PA (REGC ) UNIV CALIFORNIA.  
Best Local Similarity: 29.20% Mismatches: 59  
Query Match: 6.62% Indels: 13  
RESULT 1346  
ID ABD32602 standard; DNA; 277616 BP.  
DE Human cancer-associated genomic DNA HD7-221.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 25.84% Mismatches: 33  
Query Match: 6.62% Indels: 84  
RESULT 1347  
ID ABK89296 standard; DNA; 326014 BP.  
DE Human gene for novel serine/threonine serine kinase.  
Best Local Similarity: 26.02% Mismatches: 48  
Query Match: 6.62% Indels: 20  
RESULT 1348  
ID ADQ94981 standard; DNA; 326014 BP.  
DE Human kinase genomic DNA.  
Best Local Similarity: 26.02% Mismatches: 48  
Query Match: 6.62% Indels: 20  
RESULT 1349  
ID AAX36693 standard; DNA; 486 BP.  
DE Mouse OHP106 protein coding sequence.  
PN WO9918205-A1.  
PD 15-APR-1999.  
PA (ONQY ) ONO PHARM CO LTD.  
Best Local Similarity: 23.01% Mismatches: 32  
Query Match: 6.58% Indels: 31  
RESULT 1350  
ID ADL67238 standard; DNA; 492 BP.  
DE Chimeric TCR related human DNA.  
PN US2004043401-A1.  
PD 04-MAR-2004.  
PA (SLOK ) SLOAN KETTERING INST CANCER RES.  
Best Local Similarity: 24.79% Mismatches: 43  
Query Match: 6.58% Indels: 24  
RESULT 1351  
ID ADI32056 standard; cDNA; 585 BP.  
DE Human cDNA #1382.  
PN US6607879-B1.  
PD 19-AUG-2003.  
PA (INCY-) INCYTE CORP.  
Best Local Similarity: 24.79% Mismatches: 43  
Query Match: 6.58% Indels: 24  
RESULT 1352  
ID ADA50578 standard; DNA; 759 BP.  
DE Mucin 1 (MUC-1) splice variant #4 (MUC1Y variant) DNA, SEQ ID NO:33.  
PN WO2003031569-A2.  
PD 17-APR-2003.  
PA (CENZ ) CENTOCOR INC.  
Best Local Similarity: 20.13% Mismatches: 77  
Query Match: 6.58% Indels: 19  
RESULT 1353  
ID AAD56945 standard; cDNA; 759 BP.  
DE Human mucin 1 transmembrane variant, MUC1/Y cDNA.  
PN WO2003054154-A2.  
PD 03-JUL-2003.  
PA (ISIS-) ISIS PHARM INC.  
Best Local Similarity: 20.13% Mismatches: 77  
Query Match: 6.58% Indels: 19  
RESULT 1354  
ID AAZ16180 standard; cDNA; 776 BP.  
DE Human gene expression product cDNA sequence SEQ ID NO:3650.  
PN WO9938972-A2.  
PD 05-AUG-1999.  
PA (CHIR ) CHIRON CORP.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 31.13% Mismatches: 29  
Query Match: 6.58% Indels: 31  
RESULT 1355  
ID AAZ09234 standard; DNA; 900 BP.  
DE Rabbit B7-1 DNA.

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PN WO9941368-A2.
PD 19-AUG-1999.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 21.25% Mismatches: 56
Query Match: 6.58% Indels: 41
RESULT 1356
ID ABV94626 standard; cDNA; 900 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:276.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 21.25% Mismatches: 56
Query Match: 6.58% Indels: 41
RESULT 1357
ID ADM18911 standard; cDNA; 900 BP.
DE Rabbit B7-1 encoding cDNA SEQ ID NO:276.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 21.25% Mismatches: 56
Query Match: 6.58% Indels: 41
RESULT 1358
ID ABV94622 standard; cDNA; 910 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:262.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 21.60% Mismatches: 58
Query Match: 6.58% Indels: 41
RESULT 1359
ID ADM18897 standard; cDNA; 910 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:262.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 21.60% Mismatches: 58
Query Match: 6.58% Indels: 41
RESULT 1360
ID ABV94546 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:107.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1361
ID ABV94553 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:114.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1362
ID ABV94557 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:118.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1363
ID ABV94500 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:14.
PN WO200200717-A2.
PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1364
ID ABV94545 standard; cDNA; 912 BP.
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:106.
PN WO200200717-A2.
PD 06-SEP-2000.
Best Local Similarity: 22.58% Mismatches: 45
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PD 03-JAN-2002.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1365
ID ADM18649 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:14.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1366
ID ADM18749 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:114.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1367
ID ADM18742 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:107.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1368
ID ADM18753 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:118.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1369
ID ADM18741 standard; cDNA; 912 BP.
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:106.
PN WO2004029197-A2.
PD 08-APR-2004.
PA (MAXY-) MAXYGEN INC.
Best Local Similarity: 24.64% Mismatches: 49
Query Match: 6.58% Indels: 35
RESULT 1370
ID AAX36694 standard; DNA; 996 BP.
DE Mouse CHP106 protein coding sequence.
PN WO9918205-A1.
PD 15-APR-1999.
PA (ONCY ) ONO PHARM CO LTD.
Best Local Similarity: 23.01% Mismatches: 32
Query Match: 6.58% Indels: 31
RESULT 1371
ID AAC40859 standard; DNA; 1072 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 29802.
PN EP1033405-A2.
PD 06-SEP-2000.
Best Local Similarity: 22.58% Mismatches: 45
Query Match: 6.58% Indels: 27
RESULT 1372
ID ABQ76937 standard; DNA; 1074 BP.
DE Muvalpha-hucalpa-huCD3epsilon fusion construct DNA.
PN DE10109854-A1.
PD 12-SEP-2002.
PA (STAN/) STANISLAWSKI T.
Best Local Similarity: 24.79% Mismatches: 43
Query Match: 6.58% Indels: 24
RESULT 1373
ID AAC9689 standard; DNA; 1174 BP.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 62075.
PN EP1033405-A2.
PD 06-SEP-2000.
Best Local Similarity: 22.58% Mismatches: 45
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Query Match: 6.58% Indels: 27  
RESULT 1374  
ID AAC39377 standard; DNA; 1175 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 24411.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Best Local Similarity: 22.58% Mismatches: 45  
Query Match: 6.58% Indels: 27  
RESULT 1375  
ID AAC49684 standard; DNA; 1233 BP.  
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 62055.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Best Local Similarity: 22.58% Mismatches: 45  
Query Match: 6.58% Indels: 27  
RESULT 1376  
ID ADA71366 standard; DNA; 1266 BP.  
DE Rice gene SEQ ID 4689.  
PN WO200300898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
Best Local Similarity: 27.83% Mismatches: 43  
Query Match: 6.58% Indels: 19  
RESULT 1377  
ID AAT97844 standard; DNA; 1350 BP.  
DE DNA of a single chain T-cell receptor specific for hemagglutinin antigen.  
PN WO9732603-A1.  
PD 12-SEP-1997.  
PA (SCRI) SCRIPPS RES INST.  
Best Local Similarity: 24.79% Mismatches: 43  
Query Match: 6.58% Indels: 24  
RESULT 1378  
ID AAL49722 standard; cDNA; 1398 BP.  
DE Human secreted LIR-like protein cDNA SEQ ID NO: 36.  
PN WO200266600-A2.  
PD 29-AUG-2002.  
PA (HYSE-) HYSEQ INC.  
Best Local Similarity: 20.15% Mismatches: 72  
Query Match: 6.58% Indels: 104  
RESULT 1379  
ID AAT90509 standard; DNA; 1422 BP.  
DE DNA encoding chimeric receptor hCTM01/CD8/zeta.  
PN WO9723613-A2.  
PD 03-JUL-1997.  
PA (CLLT) CELLTech THERAPEUTICS LTD.  
Best Local Similarity: 24.79% Mismatches: 43  
Query Match: 6.58% Indels: 24  
RESULT 1380  
ID AAT90510 standard; DNA; 1545 BP.  
DE DNA encoding chimeric receptor hCTM01/CD8/zeta-CD28.  
PN WO9723613-A2.  
PD 03-JUL-1997.  
PA (CLLT) CELLTech THERAPEUTICS LTD.  
Best Local Similarity: 24.79% Mismatches: 43  
Query Match: 6.58% Indels: 24  
RESULT 1381  
ID ACA24284 standard; DNA; 1587 BP.  
DE Prokaryotic essential gene #5941.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC.  
Best Local Similarity: 32.81% Mismatches: 29  
Query Match: 6.58% Indels: 3  
RESULT 1382  
ID ADG32711 standard; DNA; 1723 BP.  
DE Human DNA differentially expressed in patients with SLE SeqID35.  
PN WO2003090694-A2.  
PD 06-NOV-2003.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
Best Local Similarity: 24.79% Mismatches: 43  
Query Match: 6.58% Indels: 24  
RESULT 1383  
ID ADR24663 standard; DNA; 1723 BP.

DE Breast cancer prognosis marker #524.  
PN WO2004065545-A2.  
PD 05-AUG-2004.  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
Best Local Similarity: 24.79% Mismatches: 43  
Query Match: 6.58% Indels: 24  
RESULT 1384  
ID ABD33068 standard; cDNA; 1724 BP.  
DE Human cancer-associated cDNA HR23-013.2.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 24.79% Mismatches: 43  
Query Match: 6.58% Indels: 24  
RESULT 1385  
ID ADR20362 standard; DNA; 1944 BP.  
DE Recombinant pDAB2097 cosmid open reading frame 3 DNA SeqID 11.  
PN WO2004067750-A2.  
PD 12-AUG-2004.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Best Local Similarity: 32.73% Mismatches: 21  
Query Match: 6.58% Indels: 9  
RESULT 1386  
ID ADR21491 standard; DNA; 1944 BP.  
DE Xerorhabdus strain Xwi cosmid pDAB2097 ORF3 SEQ ID NO:11.  
PN WO2004067727-A2.  
PD 12-AUG-2004.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Best Local Similarity: 32.73% Mismatches: 21  
Query Match: 6.58% Indels: 9  
RESULT 1387  
ID ADR20372 standard; DNA; 1947 BP.  
DE Recombinant pDAB2097 cosmid DNA encoding an exochitinase SeqID 21.  
PN WO2004067750-A2.  
PD 12-AUG-2004.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Best Local Similarity: 32.73% Mismatches: 21  
Query Match: 6.58% Indels: 9  
RESULT 1388  
ID AAT90512 standard; DNA; 1956 BP.  
DE DNA encoding chimeric receptor hCTM01/G1/zeta.  
PN WO9723613-A2.  
PD 03-JUL-1997.  
PA (CLLT) CELLTech THERAPEUTICS LTD.  
Best Local Similarity: 24.79% Mismatches: 43  
Query Match: 6.58% Indels: 24  
RESULT 1389  
ID AAT90513 standard; DNA; 2079 BP.  
DE DNA encoding chimeric receptor hCTM01/G1/zeta-CD28.  
PN WO9723613-A2.  
PD 03-JUL-1997.  
PA (CLLT) CELLTech THERAPEUTICS LTD.  
Best Local Similarity: 24.79% Mismatches: 43  
Query Match: 6.58% Indels: 24  
RESULT 1390  
ID AAH16102 standard; cDNA; 2582 BP.  
DE Human cDNA sequence SEQ ID NO:14822.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 29.75% Mismatches: 42  
Query Match: 6.58% Indels: 28  
RESULT 1391  
ID ACF68678 standard; DNA; 2718 BP.  
DE Photorhabdus luminescens nucleotide sequence #7145.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Best Local Similarity: 22.05% Mismatches: 69  
Query Match: 6.58% Indels: 51  
RESULT 1392

ID AAV62748 standard; cDNA; 2911 BP.  
DE Human secreted protein clone er80\_1 cDNA.  
PN WO9846757-A2.  
PD 22-OCT-1998.  
PA (GEM) GENETICS INST INC.  
Best Local Similarity: 25.21% Mismatches: 46  
Query Match: 6.58% Indels: 15  
RESULT 1393  
ID ABQ92051 standard; cDNA; 2911 BP.  
DE Human polynucleotide SEQ ID NO 48.  
PN US2002065394-A1.  
PD 30-MAY-2002.  
PA (JACO) JACOBS K.  
PA (MCCO) MCCOY J M.  
PA (LAVA) LAVALLIE E R.  
PA (COLL) COLLINS-RACIE L A.  
PA (EVAN) EVANS C.  
PA (MERB) MERBERG D.  
PA (TREA) TREACY M.  
PA (SPAU) SPAULDING V.  
Best Local Similarity: 25.21% Mismatches: 46  
Query Match: 6.58% Indels: 15  
RESULT 1394  
ID AAD07726 standard; cDNA; 2913 BP.  
DE Human secreted protein-encoding gene 2 cDNA clone HWLEZ82, SEQ ID NO:32.  
PN WO200134800-A1.  
PD 17-MAY-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.21% Mismatches: 46  
Query Match: 6.58% Indels: 15  
RESULT 1395  
ID AAI99481 standard; DNA; 3178 BP.  
DE Human excretory related polynucleotide SEQ ID NO 1245.  
PN WO200155313-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 26.34% Mismatches: 62  
Query Match: 6.58% Indels: 44  
RESULT 1396  
ID AAI64126 standard; cDNA; 3178 BP.  
DE Human bladder related polynucleotide, SEQ ID NO: 159.  
PN WO200159064-A2.  
PD 16-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 26.34% Mismatches: 62  
Query Match: 6.58% Indels: 44  
RESULT 1397  
ID ADF71724 standard; DNA; 3178 BP.  
DE Human bladder associated antigen #37 genomic DNA #1.  
PN US2003199008-A1.  
PD 23-OCT-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 26.34% Mismatches: 62  
Query Match: 6.58% Indels: 44  
RESULT 1398  
ID ADS08282 standard; DNA; 7489 BP.  
DE Plasmid pBRT7Q containing the Qbeta genome.  
PN AU2004200867-A1.  
PD 25-MAR-2004.  
PA (DIAT-) DIATECH PTV LTD.  
Best Local Similarity: 24.66% Mismatches: 50  
Query Match: 6.58% Indels: 84  
RESULT 1399  
ID AAL06039 standard; DNA; 20987 BP.  
DE Human reproductive system related antigen DNA SEQ ID NO: 8727.  
PN WO200155320-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 23.58% Mismatches: 36  
Query Match: 6.58% Indels: 34  
RESULT 1400  
ID ABL98604 standard; DNA; 20987 BP.  
DE Human testicular antigen encoding DNA fragment SEQ ID NO: 3256.  
PN WO200155317-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 23.58% Mismatches: 36  
Query Match: 6.58% Indels: 34  
RESULT 1401  
ID ADR20357 standard; DNA; 39005 BP.  
DE Recombinant pDAB2097 cosmid containing 7 open reading frames Seq 6.  
PN WO2004067750-A2.  
PD 12-AUG-2004.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Best Local Similarity: 32.73% Mismatches: 21  
Query Match: 6.58% Indels: 9  
RESULT 1402  
ID ADR21486 standard; DNA; 39005 BP.  
DE Xenorhabdus strain Xwi cosmid pDAB2097 SEQ ID NO:6.  
PN WO2004067727-A2.  
PD 12-AUG-2004.  
PA (DOWC) DOW AGROSCIENCES LLC.  
Best Local Similarity: 32.73% Mismatches: 21  
Query Match: 6.58% Indels: 9  
RESULT 1403  
ID AAK85590 standard; DNA; 75384 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40402.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 27.69% Mismatches: 29  
Query Match: 6.58% Indels: 5  
RESULT 1404  
ID ADC85340 standard; DNA; 96597 BP.  
DE Human lmo2 coding sequence.  
PN WO2003045230-A2.  
PD 05-JUN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 29.41% Mismatches: 51  
Query Match: 6.58% Indels: 54  
RESULT 1405  
ID ADA02861 standard; DNA; 96598 BP.  
DE Mouse Itpr1 carcinoma associated gene, SEQ ID NO:1379.  
PN WO2003057146-A2.  
PD 17-JUL-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 29.41% Mismatches: 51  
Query Match: 6.58% Indels: 54  
RESULT 1406  
ID ADB72599 standard; DNA; 96598 BP.  
DE Mouse Itpr1 Gene.  
PN WO2003008583-A2.  
PD 30-JAN-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 29.41% Mismatches: 51  
Query Match: 6.58% Indels: 54  
RESULT 1407  
ID ADM74456 standard; DNA; 96598 BP.  
DE Murine carcinoma associated (CA) nucleic acid #64.  
PN US2004072154-A1.  
PD 15-APR-2004.  
PA (MORR-) MORRIS D W.  
PA (ENGE-) ENGELHARD E K.  
Best Local Similarity: 29.41% Mismatches: 51  
Query Match: 6.58% Indels: 54  
RESULT 1408  
ID ACF65381 standard; DNA; 249878 BP.  
DE Photorhabdus luminescens nucleotide sequence #34.  
PN WO200294867-A2.  
PD 28-NOV-2002.  
PA (INSP) INST PASTEUR.  
PA (CNRS) CNRS CENT NAT RECH SCI.  
Best Local Similarity: 22.05% Mismatches: 69  
Query Match: 6.58% Indels: 51



Query Match: 6.58% Indels: 51  
RESULT 1410  
ID AAK41226 standard; DNA; 349980 BP.  
DE Pyrococcus abyssi genomic fragment #5.  
PN FR2792651-A1.  
PD 27-OCT-2000.  
PA (GNRS) CNRS CENT NAT RECH SCI.  
PA (IPRE-) IPREMER INST FR RECH EXPL MER.  
Best Local Similarity: 23.27% Mismatches: 74  
Query Match: 6.58% Indels: 51  
RESULT 1411  
ID AAK30260 standard; DNA; 424 BP.  
DE Human bone marrow expressed single exon probe SEQ ID NO: 4817.  
PN WO200157276-A2.  
PD 09-AUG-2001.  
PA (MOLE-) MOLECULAR DYNAMICS INC.  
Best Local Similarity: 28.57% Mismatches: 45  
Query Match: 6.53% Indels: 37  
RESULT 1412  
ID ABV42919 standard; cDNA; 470 BP.  
DE Human prostate expression marker cDNA 42910.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 24.29% Mismatches: 49  
Query Match: 6.53% Indels: 34  
RESULT 1413  
ID ABV34052 standard; cDNA; 470 BP.  
DE Human prostate expression marker cDNA 34043.  
PN WO200160860-A2.  
PD 23-AUG-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 24.29% Mismatches: 49  
Query Match: 6.53% Indels: 34  
RESULT 1414  
ID AAD56948 standard; cDNA; 577 BP.  
DE Human mucin 1 transmembrane variant, MUC1-IV cDNA.  
PN WO2003054154-A2.  
PD 03-JUL-2003.  
PA (ISIS-) ISIS PHARM INC.  
Best Local Similarity: 27.00% Mismatches: 49  
Query Match: 6.53% Indels: 6  
RESULT 1415  
ID AAV07189 standard; cDNA; 591 BP.  
DE cDNA encoding a human phospholemman-like protein.  
PN WO9814572-A1.  
PD 09-APR-1998.  
PA (INCY-) INCYTE PHARM INC.  
Best Local Similarity: 22.22% Mismatches: 33  
Query Match: 6.53% Indels: 56  
RESULT 1416  
ID ACD92381 standard; cDNA; 630 BP.  
DE Human colon cancer cell expressed cDNA #793.  
PN US2002155438-A1.  
PD 24-OCT-2002.  
PA (SIMP/) SIMPSON A J G.  
PA (NETO/) NETO E D.  
PA (BREN/) BRENTANI R R.  
Best Local Similarity: 25.88% Mismatches: 43  
Query Match: 6.53% Indels: 6  
RESULT 1417  
ID ABS67307 standard; cDNA; 667 BP.  
DE Breast specific polynucleotide #43.  
PN WO200264741-A2.  
PD 22-AUG-2002.  
PA (DIAD-) DIADEXUS INC.  
Best Local Similarity: 31.65% Mismatches: 37  
Query Match: 6.53% Indels: 4  
RESULT 1418  
ID ADC75106 standard; cDNA; 730 BP.  
DE Poppy phytopathogen resistance-related contig cDNA - SEQ ID 30.  
PN WO2003020905-A2.  
PD 13-MAR-2003.

PA (DOWC) DOW CHEM CO.  
Best Local Similarity: 23.62% Mismatches: 42  
Query Match: 6.53% Indels: 25  
RESULT 1419  
ID AAK86322 standard; DNA; 783 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41134.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 19.89% Mismatches: 59  
Query Match: 6.53% Indels: 66  
RESULT 1420  
ID ADC76034 standard; DNA; 796 BP.  
DE DNA homologous to phytopathogen resistance-related cDNA - SEQ ID 958.  
PN WO2003020905-A2.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
Best Local Similarity: 20.13% Mismatches: 55  
Query Match: 6.53% Indels: 48  
RESULT 1421  
ID ADK59012 standard; DNA; 796 BP.  
DE Plant DNA sequence which confers altered metabolic characteristic #6395.  
PN WO2003020936-A1.  
PD 13-MAR-2003.  
PA (DOWC) DOW CHEM CO.  
Best Local Similarity: 20.13% Mismatches: 55  
Query Match: 6.53% Indels: 48  
RESULT 1422  
ID ADL46032 standard; DNA; 870 BP.  
DE Human ovarian cancer DNA marker #19922.  
PN WO200170979-A2.  
PD 27-SEP-2001.  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
Best Local Similarity: 28.57% Mismatches: 45  
Query Match: 6.53% Indels: 37  
RESULT 1423  
ID ABV75311 standard; cDNA; 981 BP.  
DE Murine OX2R full-length protein encoding cDNA.  
PN WO200288164-A1.  
PD 07-NOV-2002.  
PA (IMMV) IMMUNEX CORP.  
Best Local Similarity: 22.99% Mismatches: 81  
Query Match: 6.53% Indels: 27  
RESULT 1424  
ID AAK86971 standard; DNA; 999 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41783.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.00% Mismatches: 46  
Query Match: 6.53% Indels: 35  
RESULT 1425  
ID AAK86970 standard; DNA; 999 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41782.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Best Local Similarity: 25.00% Mismatches: 46  
Query Match: 6.53% Indels: 35  
RESULT 1426  
ID ADJ94242 standard; DNA; 1165 BP.  
DE Mouse IPC marker Ly-49Q coding sequence, SEQ ID 1.  
PN WO2004013325-A1.  
PD 12-FEB-2004.  
PA (GINK-) GINKGO BIOMEDICAL RES INST CO LTD.  
Best Local Similarity: 24.03% Mismatches: 50  
Query Match: 6.53% Indels: 20  
RESULT 1427  
ID AAS10874 standard; cDNA; 1245 BP.  
DE Human cDNA encoding NOV7 polypeptide.  
PN WO200149729-A2.  
PD 12-JUL-2001.

PA (CURA-) CURAGEN CORP.  
 Best Local Similarity: 28.57% Mismatches: 45  
 Query Match: 6.53% Indels: 37  
 RESULT 1428  
 ID ADS85090 standard; DNA; 1413 BP.  
 DE Mouse atopic dermatitis-related gene sequence SeqID92.  
 PN WO2004031386-A1.  
 PD 15-APR-2004.  
 PA (GENO-) GENOX RES INC.  
 Best Local Similarity: 20.00% Mismatches: 67  
 Query Match: 6.53% Indels: 56  
 RESULT 1429  
 ID AAZ97021 standard; cDNA; 1445 BP.  
 DE Human secreted protein gene 3 cDNA clone HWHGU54, SEQ ID NO:13.  
 PN WO996041-A1.  
 PD 23-DEC-1999.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 28.57% Mismatches: 45  
 Query Match: 6.53% Indels: 37  
 RESULT 1430  
 ID ADA40242 standard; cDNA; 1445 BP.  
 DE Human secreted protein encoding cDNA.  
 PN WO2002102993-A2.  
 PD 27-DEC-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 28.57% Mismatches: 45  
 Query Match: 6.53% Indels: 37  
 RESULT 1431  
 ID ACH66650 standard; cDNA; 1445 BP.  
 DE Novel human secreted protein #3 cDNA.  
 PN US2003065151-A1.  
 PD 03-APR-2003.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 28.57% Mismatches: 45  
 Query Match: 6.53% Indels: 37  
 RESULT 1432  
 ID ADA56404 standard; DNA; 1445 BP.  
 DE Gene encoding human secreted protein #583.  
 PN WO2002102994-A2.  
 PD 27-DEC-2002.  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 Best Local Similarity: 28.57% Mismatches: 45  
 Query Match: 6.53% Indels: 37  
 RESULT 1433  
 ID ADN05951 standard; cDNA; 1445 BP.  
 DE Antipsoriatic cDNA sequence #1210.  
 PN WO2004028479-A2.  
 PD 08-APR-2004.  
 PA (GETH-) GENENTECH INC.  
 Best Local Similarity: 28.57% Mismatches: 45  
 Query Match: 6.53% Indels: 37  
 RESULT 1434  
 ID AAC84169 standard; DNA; 1490 BP.  
 DE Mouse OX2R homologue 1 (OX2RH1) nucleotide sequence.  
 PN WO200070045-A1.  
 PD 23-NOV-2000.  
 PA (MEDI-) MEDICAL RES COUNCIL.  
 PA (SCHE-) SCHERING CORP.  
 Best Local Similarity: 22.99% Mismatches: 81  
 Query Match: 6.53% Indels: 27  
 RESULT 1435  
 ID AAD09549 standard; cDNA; 1497 BP.  
 DE Human protease protein-12 (PRTS-12) cDNA.  
 PN WO200146443-A2.  
 PD 28-JUN-2001.  
 PA (INCY-) INCYTE GENOMICS INC.  
 Best Local Similarity: 28.57% Mismatches: 45  
 Query Match: 6.53% Indels: 37  
 RESULT 1436  
 ID ABK73077 standard; DNA; 1512 BP.  
 DE Bacillus licheniformis genomic sequence tag (GST) #368.  
 PN WO200229113-A2.

PD 11-APR-2002.  
 PA (NOVO-) NOVOZYMES BIOTECH INC.  
 Best Local Similarity: 21.53% Mismatches: 53  
 Query Match: 6.53% Indels: 83  
 RESULT 1437  
 ID ADL02542 standard; DNA; 1533 BP.  
 DE DNA encoding a M. catarrhalis protein #228.  
 PN US6673910-B1.  
 PD 06-JAN-2004.  
 PA (GENO-) GENOME THERAPEUTICS CORP.  
 Best Local Similarity: 19.57% Mismatches: 81  
 Query Match: 6.53% Indels: 64  
 RESULT 1438  
 ID AAQ89706 standard; DNA; 1599 BP.  
 DE DNA encoding CD4:gamma peptide chimeric protein.  
 PN WO9215322-A1.  
 PD 17-SEP-1992.  
 PA (GEHO-) GEN HOSPITAL CORP.  
 Best Local Similarity: 25.66% Mismatches: 53  
 Query Match: 6.53% Indels: 36  
 RESULT 1439  
 ID AAT10803 standard; DNA; 1599 BP.  
 DE CD4:eta fusion protein coding sequence.  
 PN WO9603883-A1.  
 PD 15-FEB-1996.  
 PA (GEHO-) GEN HOSPITAL CORP.  
 Best Local Similarity: 25.66% Mismatches: 53  
 Query Match: 6.53% Indels: 36  
 RESULT 1440  
 ID AAV70157 standard; DNA; 1599 BP.  
 DE Chimeric receptor containing human eta polypeptide encoding DNA.  
 PN US5843728-A.  
 PD 01-DEC-1998.  
 PA (GEHO-) GEN HOSPITAL CORP.  
 Best Local Similarity: 25.66% Mismatches: 53  
 Query Match: 6.53% Indels: 36  
 RESULT 1441  
 ID AAL56192 standard; DNA; 1624 BP.  
 DE Murine inhibitory receptor CD200Ra coding sequence.  
 PN WO2003077947-A1.  
 PD 25-SEP-2003.  
 PA (SCHE-) SCHERING CORP.  
 Best Local Similarity: 22.99% Mismatches: 81  
 Query Match: 6.53% Indels: 27  
 RESULT 1442  
 ID AAK52031 standard; cDNA; 1646 BP.  
 DE Human polynucleotide SEQ ID NO 576.  
 PN WO200157190-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 28.57% Mismatches: 45  
 Query Match: 6.53% Indels: 37  
 RESULT 1443  
 ID ABL28927 standard; DNA; 1767 BP.  
 DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38254.  
 PN WO200171042-A2.  
 PD 27-SEP-2001.  
 PA (PEKE-) PE CORP NY.  
 Best Local Similarity: 25.83% Mismatches: 41  
 Query Match: 6.53% Indels: 30  
 RESULT 1444  
 ID ABA09076 standard; cDNA; 1778 BP.  
 DE Human secreted protein homologue-encoding cDNA, SEQ ID NO:852.  
 PN WO200157188-A2.  
 PD 09-AUG-2001.  
 PA (HYSE-) HYSEQ INC.  
 Best Local Similarity: 28.57% Mismatches: 45  
 Query Match: 6.53% Indels: 37  
 RESULT 1445  
 ID AAK53015 standard; cDNA; 1778 BP.  
 DE Human polynucleotide SEQ ID NO 2544.  
 PN WO200157190-A2.

PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC. Mismatches: 45  
Best Local Similarity: 28.57% Indels: 37  
Query Match:  
RESULT 1446  
ID AAF81799 standard; cDNA; 1799 BP.  
DE Human secreted protein gene 13 SEQ ID NO:23.  
PN WO200112775-A2.  
PD 22-FEB-2001.  
PA (HUMA-) HUMAN GENOME SCI INC. Mismatches: 33  
Best Local Similarity: 22.33% Indels: 24  
Query Match:  
RESULT 1447  
ID ADM03363 standard; cDNA; 1953 BP.  
DE Human cDNA of the invention SEQ ID NO:2048.  
PN EP1347046-A1.  
PD 24-SEP-2003.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY. Mismatches: 34  
Best Local Similarity: 25.33% Indels: 61  
Query Match:  
RESULT 1448  
ID AAC85823 standard; DNA; 1977 BP.  
DE HOAT4 DNA.  
PN WO200104283-A2.  
PD 18-JAN-2001.  
PA (META-) METABASIS THERAPEUTICS INC. Mismatches: 78  
Best Local Similarity: 25.93% Indels: 54  
Query Match:  
RESULT 1449  
ID AAC61892 standard; cDNA; 2027 BP.  
DE cDNA encoding a human secreted protein.  
PN WO200061755-A2.  
PD 19-OCT-2000.  
PA (CHIR) CHIRON CORP. Mismatches: 78  
Best Local Similarity: 25.93% Indels: 54  
Query Match:  
RESULT 1450  
ID ADS92515 standard; DNA; 2072 BP.  
DE B. licheniformis mutant protease gene SEQ ID NO:61.  
PN WO2003087149-A2.  
PD 23-OCT-2003.  
PA (NOVO) NOVOZYMES AS. Mismatches: 53  
Best Local Similarity: 21.53% Indels: 83  
Query Match:  
RESULT 1451  
ID ADA69794 standard; DNA; 2115 BP.  
DE Rice gene. SEQ ID 3117.  
PN WO200300898-A1.  
PD 03-JAN-2003.  
PA (SYGN) SYNGENTA PARTICIPATIONS AG. Mismatches: 60  
Best Local Similarity: 17.93% Indels: 62  
Query Match:  
RESULT 1452  
ID ADE82901 standard; DNA; 2342 BP.  
DE Human sulfate conjugate organic anion transporter hoAT7 gene.  
PN WO2003076617-A1.  
PD 18-SEP-2003.  
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP. Mismatches: 78  
Best Local Similarity: 25.93% Indels: 54  
Query Match:  
RESULT 1453  
ID ABL28926 standard; DNA; 3767 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 38251.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY. Mismatches: 41  
Best Local Similarity: 25.83% Indels: 30  
Query Match:  
RESULT 1454  
ID ADB53912 standard; DNA; 3774 BP.  
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4454.  
PN WO2003065993-A2.  
PD 14-AUG-2003.

PA (GENE-) GENE LOGIC INC. Mismatches: 37  
Best Local Similarity: 22.60% Indels: 50  
Query Match:  
RESULT 1455  
ID ABL20016 standard; DNA; 4417 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11521.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY. Mismatches: 66  
Best Local Similarity: 26.19% Indels: 37  
Query Match:  
RESULT 1456  
ID ADP10572 standard; DNA; 4633 BP.  
DE Reference mRNA sequences for marker probe #249.  
PN WO2004042346-A2.  
PD 21-MAY-2004.  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC. Mismatches: 31  
Best Local Similarity: 20.18% Indels: 34  
Query Match:  
RESULT 1457  
ID ABL24614 standard; DNA; 6888 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 25315.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY. Mismatches: 66  
Best Local Similarity: 26.19% Indels: 37  
Query Match:  
RESULT 1458  
ID ABL10730 standard; cDNA; 8436 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 26672.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY. Mismatches: 69  
Best Local Similarity: 25.61% Indels: 26  
Query Match:  
RESULT 1459  
ID ABL03974 standard; cDNA; 9576 BP.  
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 6404.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY. Mismatches: 63  
Best Local Similarity: 24.00% Indels: 29  
Query Match:  
RESULT 1460  
ID ABL18540 standard; DNA; 12727 BP.  
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 7093.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY. Mismatches: 63  
Best Local Similarity: 24.00% Indels: 29  
Query Match:  
RESULT 1461  
ID AAX99560 standard; DNA; 15016 BP.  
DE Nucleic acid sequence from U. urealyticum.  
PN WO9939007-A1.  
PD 05-AUG-1999.  
PA (UABR-) UAB RES FOUND. Mismatches: 42  
Best Local Similarity: 23.96% Indels: 8  
Query Match:  
RESULT 1462  
ID ACA52817 standard; DNA; 15018 BP.  
DE Prokaryotic essential gene #34474.  
PN WO200277183-A2.  
PD 03-OCT-2002.  
PA (ELIT-) ELITRA PHARM INC. Mismatches: 42  
Best Local Similarity: 23.96% Indels: 8  
Query Match:  
RESULT 1463  
ID AAK65305 standard; DNA; 22916 BP.  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:20117.  
PN WO200157182-A2.  
PD 09-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.

Best Local Similarity: 18.09% Mismatches: 68  
Query Match: 6.53% Indels: 66  
RESULT 1464  
ID ACN44860 standard; DNA; 48133 BP.  
DE Mouse genomic sequence MCG49939.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 35.42% Mismatches: 15  
Query Match: 6.53% Indels: 12  
RESULT 1465  
ID ACN44300 standard; DNA; 57137 BP.  
DE Mouse genomic sequence MCG17164.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 19.59% Mismatches: 88  
Query Match: 6.53% Indels: 78  
RESULT 1466  
ID ACN44706 standard; DNA; 59341 BP.  
DE Human genomic sequence hCG17286.  
PN WO2003073826-A2.  
PD 12-SEP-2003.  
PA (SAGR-) SAGRES DISCOVERY.  
Best Local Similarity: 20.11% Mismatches: 61  
Query Match: 6.53% Indels: 37  
RESULT 1467  
ID ADQ97703 standard; DNA; 103665 BP.  
DE Human cancer associated sequence HD10-031, SEQ ID 680.  
PN WO2004060304-A2.  
PD 22-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 24.60% Mismatches: 35  
Query Match: 6.53% Indels: 44  
RESULT 1468  
ID ABD32804 standard; DNA; 608916 BP.  
DE Mouse cancer-associated genomic DNA MD16-059.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 23.46% Mismatches: 59  
Query Match: 6.53% Indels: 49  
RESULT 1469  
Best Local Similarity: 23.46% Mismatches: 59  
Query Match: 6.53% Indels: 49  
RESULT 1470  
ID ABQ81850 standard; DNA; 156638 BP.  
DE Bifidobacterium longum NCC2705 related nucleotide sequence SEQ ID:1106.  
PN EP1227152-A1.  
PD 31-JUL-2002.  
PA (NEST ) SOC PROD NESTLE SA.  
Best Local Similarity: 23.15% Mismatches: 60  
Query Match: 6.53% Indels: 69  
RESULT 1471  
ID ABD33389 standard; DNA; 197526 BP.  
DE Human cancer-associated (CA) gene HD07-072.  
PN WO2004058146-A2.  
PD 15-JUL-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Best Local Similarity: 32.14% Mismatches: 19  
Query Match: 6.53% Indels: 8  
RESULT 1472  
ID ADL13693 standard; DNA; 231222 BP.  
DE Osteoarthritis-associated polymorphic nucleotide #225.  
PN WO2003054166-A2.  
PD 03-JUL-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Best Local Similarity: 24.29% Mismatches: 60  
Query Match: 6.53% Indels: 46  
RESULT 1473  
ID ABQ67392 standard; DNA; 321 BP.  
DE Listeria innocua DNA sequence #194.  
PN WO200228891-A2.

PD 11-APR-2002.  
PA (INSP ) INST PASTEUR.  
Best Local Similarity: 28.41% Mismatches: 33  
Query Match: 6.49% Indels: 13  
RESULT 1474  
ID AAC51744 standard; DNA; 424 BP.  
DE Zea mays DNA fragment SEQ ID NO: 69628.  
PN EP1033405-A2.  
PD 06-SEP-2000.  
Best Local Similarity: 22.56% Mismatches: 54  
Query Match: 6.49% Indels: 22  
RESULT 1475  
ID ADQ20718 standard; DNA; 468 BP.  
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 3538.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Best Local Similarity: 30.00% Mismatches: 16  
Query Match: 6.49% Indels: 7  
RESULT 1476  
ID ABV94493 standard; cDNA; 546 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:7.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1477  
ID ADJ66748 standard; DNA; 710 BP.  
DE Muc 16 Stump plasmid construct DNA sequence.  
PN WO2004005470-A2.  
PD 15-JAN-2004.  
PA (IMMU-) IMMUNOGEN INC.  
Best Local Similarity: 19.23% Mismatches: 60  
Query Match: 6.49% Indels: 77  
RESULT 1478  
ID AAH04390 standard; cDNA; 856 BP.  
DE Human cDNA clone (5'-primer) SEQ ID NO:1225.  
PN EP1074617-A2.  
PD 07-FEB-2001.  
PA (HELI-) HELIX RES INST.  
Best Local Similarity: 23.77% Mismatches: 48  
Query Match: 6.49% Indels: 17  
RESULT 1479  
ID ABV94567 standard; cDNA; 903 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:128.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1480  
ID ABV94504 standard; cDNA; 903 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:18.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1481  
ID ADM18763 standard; cDNA; 903 BP.  
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:128.  
PN WO2004029197-A2.  
PD 08-APR-2004.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1482  
ID ADM18653 standard; cDNA; 903 BP.  
DE Human co-stimulatory molecule encoding cDNA SEQ ID NO:18.  
PN WO2004029197-A2.  
PD 08-APR-2004.

PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1483  
ID ABV94569 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:130.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1484  
ID ABV94495 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:9.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1485  
ID ABV94568 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:129.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1486  
ID ABV94541 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:102.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1487  
ID ABV94565 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:126.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1488  
ID ABV94494 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:8.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1489  
ID ABV94499 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:13.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1490  
ID ABV94502 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:16.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1491  
ID ABV94506 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:20.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.

Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1492  
ID ABV94554 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:115.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1493  
ID ABV94496 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:10.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1494  
ID ABV94577 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:138.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1495  
ID ABV94491 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:5.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1496  
ID ABV94497 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:11.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1497  
ID ABV94539 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:100.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1498  
ID ABV94562 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:123.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1499  
ID ABV94505 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:19.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49  
Query Match: 6.49% Indels: 35  
RESULT 1500  
ID ABV94547 standard; cDNA; 912 BP.  
DE Novel co-stimulatory molecule (NCSM) cDNA SEQ ID NO:108.  
PN WO200200717-A2.  
PD 03-JAN-2002.  
PA (MAXY-) MAXYGEN INC.  
Best Local Similarity: 24.64% Mismatches: 49

Query Match:

6.49%

Indels:

35



GenCore version 5.1.6  
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OM protein - nucleic search, (using frame\_plus p2n model

Run on: September 4, 2005, 06:55:59 ; Search time 3088 Seconds  
(without alignments)  
2613.221 Million cell updates/sec

Title: US-09-989-724-387  
Perfect score: 1102  
Sequence: 1 MLMLFLVTAHAEICQPG.....ENGIPSDPLDMKGILMPS 212

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

Command line parameters:  
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-O=/cgn2\_1/USPTO.spool\_p/US09989724/runat\_02092005\_161402\_19281/app.query.fasta\_1.391  
-DB=EST -QPMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCT=0 -LOOPEXT=0  
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-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hrc.\*  
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6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1089	98.8	669	9 AY399636	Homo sapi
2	1085.5	98.5	792	4 BG400845	AY399636
3	1081	98.1	870	4 BG400845	602464068
4	1078	97.8	663	6 BG1760941	BI760941
5	1067	96.8	629	7 CV028808	CV028808
6	1056	95.8	639	6 BG137859	BI137859
7	1048	95.1	855	4 BG427247	BG427247
8	1039	94.3	866	4 BG429618	BG429618
9	1036	94.0	780	4 BG429174	BG429174

10	1033	93.7	791	4	BG400319
11	1026	93.1	804	4	BG429705
12	1024	92.9	859	4	BG427839
13	1021	92.6	782	4	BG433974
14	1012	91.8	808	4	BG399473
15	1010	91.7	736	4	BG399402
16	1001.5	90.9	850	4	BG430955
17	996	90.4	607	6	CB125058
18	996	90.4	888	4	BG400513
19	988	89.7	677	4	BG427745
20	986	89.5	1081	4	BM811234
21	980	88.9	978	4	BI762437
22	967	87.7	678	4	BG429011
23	945.5	85.8	602	4	BG432624
24	932.5	84.6	801	4	BG428217
25	931	84.5	669	9	AY399638
26	931	84.5	720	4	BI102475
27	931	84.5	755	6	CB955052
28	931	84.5	855	6	CA469220
29	931	84.5	1210	3	AK002337
30	929.5	84.3	884	4	BG399975
31	929	84.3	735	1	AV653898
32	928	84.2	626	7	CK625203
33	928	84.2	656	4	BI143454
34	928	84.2	830	6	CA468084
35	926	84.0	743	7	CN369196
36	926	84.0	793	4	BI103785
37	925	83.9	841	6	CA481009
38	924	83.8	845	6	CA491504
39	924	83.8	853	6	CA494852
40	923	83.8	797	4	BI101134
41	923	83.8	800	6	CA480818
42	922	83.7	897	6	CA467586
43	919.5	83.4	724	6	CB599934
44	919	83.4	874	7	CF550832
45	918	83.3	858	6	CA467976
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47	906	82.2	844	6	CA492750
48	905	82.1	874	6	CA491517
49	905	82.1	981	2	BF784771
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51	904	82.0	1051	4	BG399950
52	903	81.9	750	6	CB599563
53	897	81.4	915	2	BF789250
54	894	81.1	822	6	CA491889
55	893	81.0	782	4	BG969864
56	890	80.8	848	6	CA493268
57	885	80.3	874	6	CA493040
58	883	80.1	669	9	AY399637
59	879	79.8	765	1	AV652853
60	877	79.6	730	6	CD241570
61	869	78.9	742	4	BG969794
62	867	78.7	592	7	CK625448
63	862	78.2	901	2	BF786687
64	857.5	77.8	738	6	CB953900
65	856	77.7	868	6	CA481303
66	854	77.5	529	6	CB134037
67	854	77.5	529	6	CB139939
68	849	77.0	832	4	BG402158
69	844.5	76.6	812	7	CK474508
70	837	76.0	807	4	BI099731
71	832	75.5	515	6	CB139958
72	831	75.4	544	4	BG399046
73	827	75.0	808	2	BF780136
74	826	75.0	824	6	CA492547
75	824	74.8	659	6	BY741654
76	817	74.1	581	2	AW106515
77	812	73.7	846	2	BF780978
78	808	73.3	822	4	BG402232
79	800	72.6	496	4	BG430790
80	792.5	71.9	586	4	BI345729
81	791.5	71.8	704	6	CB955090
82	788.5	71.6	864	4	BG401869

83	788	71.5	554	1	AI788483	uk57907.y	156	555	50.4	479	5	BP769681	BP769681
84	785.5	71.3	728	4	BG426067	602432749	157	550	49.9	416	2	BP846622	BP846622
85	785.5	71.3	832	6	CA468414	AGENCOURT	158	549	49.8	392	2	AW260024	um82c07.y
86	783	71.1	534	4	BM022547	ig61910.y	159	548	49.7	437	2	BP844950	BP844950
87	783	71.1	571	1	AI135913	y127f01.y	160	543	49.3	492	1	AA065156	xm50a10.f
88	782.5	71.0	744	4	BG566957	602589463	161	542.5	49.2	509	9	CG611484	OST296516
89	777	70.5	479	6	CB133561	K-EST0184	162	540	48.9	426	2	BP847279	BP847279
90	777	70.5	547	1	AI789468	uk99612.y	163	539	48.9	429	5	BY006674	BY006674
91	772	70.1	546	1	AI789448	uk99402.y	164	539	48.9	506	9	CG668483	OST46441
92	772	70.1	628	4	BG428990	602501903	165	536	48.6	427	2	BP848288	BP848288
93	769	69.8	620	7	CK624653	m123f12.y	166	531	48.2	412	5	BY006356	BY006356
94	766	69.5	508	2	BF550608	UT-R-C1-k	167	527.5	47.9	361	4	BG181204	RST129 At
95	766	69.5	539	2	AW012244	ul18907.y	168	521	47.3	421	2	BP848169	BP848169
96	759	68.9	511	7	CK624505	m122401.y	169	520	47.2	375	2	BP843933	BP843933
97	758	68.8	831	6	CA469320	AGENCOURT	170	517	46.9	372	2	BP843467	BP843467
98	754.5	68.5	830	4	BG401091	602485157	171	512	46.5	458	2	BP846267	BP846267
99	753	68.3	574	2	AW045074	um17d10.y	172	509	46.2	428	2	AW259271	um89h04.y
100	750	68.1	505	1	AI746613	ul101401.y	173	507	46.0	407	2	BP845600	BP845600
101	747.5	67.8	794	6	CB955392	AGENCOURT	174	506	45.9	370	2	BP843459	BP843459
102	745	67.6	525	1	AI882207	ul131g03.y	175	500	45.4	369	2	BP843868	BP843868
103	735	66.7	513	1	AA445683	vf62h07.f	176	500	45.4	857	7	CN059437	Salamande
104	728	66.1	792	4	BG209271	RST28786	177	495	44.9	455	2	BP845438	BP845438
105	728	66.1	801	4	BG218203	RST37930	178	492.5	44.7	621	4	BI394480	pgp1n.pk0
106	728	66.1	928	7	CF582583	AGENCOURT	179	492	44.6	927	5	BU904108	AGENCOURT
107	726	65.9	881	6	CA468090	AGENCOURT	180	488	44.3	728	7	CF521338	AGENCOURT
108	724	65.7	485	2	AW106894	um34h05.y	181	488	44.3	730	7	CF522204	AGENCOURT
109	723.5	65.7	519	1	AI747322	ul105406.y	182	488	44.3	743	7	CF519814	AGENCOURT
110	723	65.6	446	6	CB133508	AGENCOURT	183	488	44.3	776	7	CF547505	AGENCOURT
111	721	65.4	547	4	BI965141	id34406.y	184	488	44.3	854	6	CB559638	AGENCOURT
112	721	65.4	569	4	BI966990	id27407.y	185	488	44.3	874	6	CB559915	AGENCOURT
113	717	65.1	499	1	AI681737	AJ681737	186	488	44.3	876	5	BU904475	AGENCOURT
114	707	64.2	541	1	AA131483	z008e05.f	187	487	44.2	749	7	CF521728	AGENCOURT
115	705	64.0	533	1	AI663460	uk33b03.y	188	486	44.1	733	7	CF522498	AGENCOURT
116	705	64.0	536	1	AI663506	uk33f11.y	189	485	44.0	845	5	BU904947	AGENCOURT
117	704	63.9	779	4	BG217185	RST36886	190	484	43.9	345	5	BY005657	BY005657
118	693	62.9	788	4	BG211841	RST31414	191	484	43.9	826	4	BG194741	RST13907
119	688	62.4	499	1	AI882240	ul156b05.y	192	481	43.6	366	2	BP847608	BP847608
120	687	62.3	452	1	AA289223	vc93f01.f	193	479	43.5	375	2	BP843929	BP843929
121	686	62.3	925	2	BF784692	602111325	194	478	43.4	341	2	BP846895	BP846895
122	684	62.1	781	4	BI937996	RST12932	195	473	42.9	418	2	BP848084	BP848084
123	684	62.1	866	4	BI88580	RST7605 A	196	470	42.6	430	5	BY006046	BY006046
124	679	61.6	489	2	AW259149	um89b04.y	197	463	42.0	355	1	AA076448	zm91d10.f
125	676	61.3	463	1	AA275670	vc33c12.f	198	460	41.7	459	2	AW244613	BR END09H
126	674	61.2	566	2	AW475605	un68h06.y	199	458	41.6	372	2	BP843455	BP843455
127	673	61.1	582	5	BP370260	BP370260	200	458	41.6	378	5	BY086677	BY086677
128	671	60.9	754	4	BI81765	RST618 At	201	457.5	41.5	1113	6	CA493126	CA493126
129	669	60.7	828	4	BG195252	RST14433	202	456.5	41.4	919	5	BY904746	AGENCOURT
130	664.5	60.3	474	1	AI931440	ul168d11.y	203	451	40.9	304	1	AA068066	m177h10.f
131	656.5	59.6	863	2	BF211834	601813181	204	450	40.8	340	2	BP843625	BP843625
132	655.5	59.5	549	7	CN369195	170060000	205	448.5	40.7	767	5	BY868900	BY868900
133	650	59.0	405	6	CB137251	K-EST0189	206	448	40.7	338	2	BP847006	BP847006
134	644.5	58.5	640	4	BM439885	pgp1n.pk0	207	447.5	40.6	765	5	BX887952	BX887952
135	637	57.8	482	1	AA109637	mm01f02.f	208	444.5	40.3	617	6	CA342735	CA342735
136	619	56.2	405	1	AA273463	vc37b10.f	209	443	40.2	750	5	BY879965	BY879965
137	615	55.8	734	4	BG183334	RST2228 A	210	441.5	40.1	430	5	BY006662	BY006662
138	601	54.5	437	2	BP844940	BP844940	211	440.5	40.0	769	5	BY913677	BY913677
139	597	54.2	532	9	CG532959	OST117705	212	438	39.7	366	2	BP843831	BP843831
140	596	54.1	404	2	BP847292	BP847292	213	437	39.7	290	6	CB137087	CB137087
141	596	54.1	504	1	AJ682987	AJ682987	214	432	39.2	345	2	BP843573	BP843573
142	595	54.0	644	7	CK627074	m131404.y	215	432	39.2	358	5	BY005603	BY005603
143	593	53.8	457	5	BY006328	BY006328	216	430	39.0	303	1	AI119252	ue24c07.y
144	590	53.5	410	1	AA066328	mm14d08.f	217	430	39.0	791	5	BP843479	BP843479
145	589	53.4	688	4	BG776793	602663969	218	430	39.0	375	2	BP843943	BP843943
146	586.5	53.2	698	6	CD217554	pgp1n.pk0	219	416	37.7	317	2	BP848179	BP848179
147	585.5	53.1	716	4	BG400370	602464583	220	414	37.6	494	2	BF654521	BF654521
148	578	52.5	413	2	BP847970	BP847970	221	410.5	37.3	909	6	CA975643	AGENCOURT
149	574.5	52.1	804	4	BG431368	602499982	222	410	37.2	685	6	CA965680	CcLX05a15
150	569	51.6	408	2	BP848163	BP848163	223	409.5	37.2	804	6	CD758550	AGENCOURT
151	569	51.6	838	6	CA947998	AGENCOURT	224	409.5	37.2	818	6	CD759140	AGENCOURT
152	568	51.5	416	2	BP848103	BP848103	225	408	37.0	326	2	AW259274	AW259274
153	568	51.5	514	1	AI765078	wh56h04.x	226	408	37.0	407	5	BY006237	BY006237
154	561	50.9	386	1	AA109535	mm01g04.f	227	405.5	36.8	787	7	CN512318	CN512318
155	557	50.5	547	6	CB222923	1JEB17E10	228	403.5	36.6	836	7	CK238801	CK238801



229	403	36.6	965	6	CA473387	CA473387 AGENCOURT	302	273	24.8	285	2	BB843715
230	400.5	36.3	767	7	CK239480	CK239480 AGENCOURT	303	271.5	24.6	837	6	CA473716
231	400.5	36.3	773	7	CK239430	CK239430 AGENCOURT	C 304	269.5	24.5	903	7	CF582582
232	399.5	36.2	816	7	CK236057	CK236057 AGENCOURT	305	266	24.1	182	1	AA104963
233	398.5	36.2	810	7	CK239284	CK239284 AGENCOURT	306	265	24.0	738	5	AX884918
234	397.5	36.1	784	7	CF348736	CF348736 AGENCOURT	307	261.5	23.7	584	5	BP371391
235	396.5	36.0	860	7	CK016244	CK016244 AGENCOURT	308	261	23.7	773	6	CB559001
236	395	35.8	312	7	CN790738	CN790738 4125362 B	309	258	23.4	391	5	BY050206
237	395	35.8	335	2	BF031348	BF031348 BB847020	C 310	255.5	23.2	574	1	AI116021
238	395	35.8	693	2	BF031348	BF031348 601559115	311	252.5	22.9	695	7	CK950473
239	395	35.8	852	7	CK237456	CK237456 AGENCOURT	312	251	22.8	447	5	BY153686
240	393.5	35.7	836	7	CK236662	CK236662 AGENCOURT	313	248	22.5	680	5	BY1319687
241	393	35.7	527	6	CB954911	CB954911 AGENCOURT	314	247.5	22.5	747	6	CA491783
242	392	35.6	322	4	BG193281	BG193281 RST12409	315	245.5	22.3	322	2	BB146668
243	390.5	35.4	862	6	CA471692	CA471692 AGENCOURT	316	245	22.2	668	4	BG400436
244	390.5	35.4	888	6	CA787423	CA787423 AGENCOURT	C 317	243.5	22.1	669	6	CA043283
245	387.5	35.2	854	6	CA474850	CA474850 AGENCOURT	318	243	22.1	773	6	CB308042
246	386.5	35.1	829	6	CA496216	CA496216 AGENCOURT	319	239	21.7	832	6	CB197355
247	384.5	34.9	1084	2	BF212565	BF212565 601813769	320	234.5	21.3	350	1	AA065710
248	382.5	34.7	891	6	CA472074	CA472074 AGENCOURT	321	232	21.1	567	5	AX086253
249	379	34.4	762	5	BX304380	BX304380 AGENCOURT	322	232	21.1	778	4	BI831019
250	377	34.2	373	2	BB843794	BB843794 AGENCOURT	323	224	20.1	452	4	BG428060
251	376	34.1	620	5	BU472823	BU472823 603761782	324	222.5	20.2	290	2	BB009853
252	376	34.1	1035	1	AL551235	AL551235 AL551235	325	221	20.1	763	5	BX926439
253	376	34.1	1690	3	CR599955	CR599955 full-leng	326	221	20.1	944	6	CB180137
254	376	34.1	3337	3	BC032938	BC032938 Homo sapi	327	219.5	19.9	283	2	BB054531
255	376	34.1	3339	3	BC048144	BC048144 Homo sapi	328	218.5	19.8	637	7	CN984278
256	372.5	33.8	765	5	BX878953	BX878953 BX878953	329	218	19.8	292	9	CG668510
257	372.5	33.8	777	5	BX867294	BX867294 AGENCOURT	330	216.5	19.6	206	2	BB005788
258	372.5	33.8	787	5	BX911789	BX911789 AGENCOURT	331	216.5	19.6	337	2	BB497528
259	368	33.4	329	4	BG189097	BG189097 RST8135 A	332	213	19.3	702	4	BG971735
260	366	33.2	237	1	AA239693	AA239693 mv23H03.1	333	211.5	19.2	381	5	BY153900
261	366	33.2	689	5	BX878867	BX878867 AGENCOURT	C 334	210	19.1	618	6	CB502807
262	360	32.7	1013	7	CO581670	CO581670 ILLUMIGEN	335	209.5	19.0	308	2	BB361016
263	359.5	32.6	590	4	BI884757	BI884757 f06809.y	336	204.5	18.6	303	1	AV235006
264	359.5	32.6	733	5	BX862922	BX862922 BX862922	C 337	204	18.5	615	6	CA041633
265	358	32.5	659	6	CA364229	CA364229 639103 NC	C 338	199	18.1	905	9	CNS02809
266	357	32.4	1603	3	AK008530	AK008530 Mus muscu	339	197	17.9	241	2	BB010750
267	353.5	32.1	732	5	BX867401	BX867401 AGENCOURT	340	197	17.9	273	2	BB010252
268	351.5	31.9	772	5	BX877877	BX877877 BX877877	341	195	17.7	274	2	BB529929
269	351.5	31.9	794	5	BX880013	BX880013 AGENCOURT	342	194.5	17.6	789	7	CN975696
270	350.5	31.8	863	7	CF663100	CF663100 CGLX07a30	343	194.5	17.6	867	7	CN975873
271	345	31.3	355	4	BG184374	BG184374 RST3298 A	344	193	17.5	306	2	BB497018
272	343	31.1	480	6	CA965795	CA965795 CGLX05a19	C 345	190	17.2	499	1	AI931939
273	342	31.0	652	5	BG769682	BG769682 BP769682	C 346	187	17.0	426	1	AI035384
274	336	30.5	835	4	BG564304	BG564304 602590019	347	184.5	16.7	230	6	CA969172
275	332	30.1	552	5	BX086254	BX086254 AGENCOURT	C 348	181	16.4	590	5	BP772872
276	332	30.1	694	7	CK957623	CK957623 409741 B	C 349	180	16.3	677	5	BW232214
277	325.5	29.5	679	5	BX319688	BX319688 BX319688	C 350	179	16.2	392	2	BF334479
278	325	29.5	249	1	AI317693	AI317693 uJ16602.y	351	179	16.2	656	5	BP008792
279	325	29.5	492	2	AW260204	AW260204 um74f04.x	C 352	179	16.2	688	5	BP008792
280	322	29.2	703	5	BU376588	BU376588 603809540	353	179	16.2	693	5	BP014380
281	321	29.1	1154	4	BM460886	BM460886 AGENCOURT	354	177	16.1	686	5	BM332316
282	320	29.0	217	1	AA197784	AA197784 mv03g11.1	355	175	15.9	322	7	CK676494
283	319	28.9	360	4	BG182824	BG182824 RST1685 A	C 356	174	15.8	233	2	BB051098
284	313	28.4	674	7	CK948392	CK948392 4073275 B	357	174	15.8	265	2	BB561901
285	312	28.3	267	2	BB599302	BB599302 BB599302	358	172	15.6	246	2	BB006347
286	308	27.9	374	5	BY042134	BY042134 AGENCOURT	359	170.5	15.5	277	2	BB006347
287	304	27.6	615	2	AW107491	AW107491 um17d10.x	C 360	170.5	15.5	588	5	BM368014
288	304	27.6	1156	6	CD508270	CD508270 CD89-H06	361	170.5	15.5	601	5	BM368888
289	299	27.1	310	5	BY005681	BY005681 BY005681	C 362	169.5	15.4	421	4	BJ748996
290	298.5	27.1	483	2	BF938662	BF938662 fm7908.y	363	168.5	15.3	705	5	BM360038
291	295.5	26.8	688	6	BY708410	BY708410 BY708410	C 364	164	14.9	487	1	AI746288
292	291	26.4	418	2	BB687602	BB687602 BB687602	C 365	164	14.9	648	5	BU124645
293	291	26.4	762	2	BB432035	BB432035 AGENCOURT	366	154.5	14.0	600	6	CB504196
294	289	26.2	718	5	BU262937	BU262937 603508618	C 367	148	13.4	654	1	AI314694
295	285	25.6	307	2	BB843809	BB843809 AGENCOURT	C 368	148	13.4	676	5	BP770276
296	280.5	25.5	335	7	CK961894	CK961894 4076310 B	369	147.5	13.4	527	1	AI476983
297	280.5	25.5	423	6	CD284299	CD284299 G39172.71	370	143	13.0	450	1	AG655099
298	278.5	25.3	699	6	CD810900	CD810900 RPrint_1-C	C 371	142	12.9	285	4	AG655099
299	278.5	25.3	710	5	BX912444	BX912444 AGENCOURT	C 372	141	12.8	498	4	BM022245
300	278	25.2	260	2	BB598752	BB598752 AGENCOURT	C 373	140.5	12.7	435	2	BB683122
301	277	25.1	209	2	AW916399	AW916399 EST377690	C 374	138	12.5	382	7	CR465430

375	138	12.5	451	2	BE722366	190570 MA	448	88	8.0	651	7	CF903857	CF903857 A0414G05-
376	137	12.4	730	5	BU453964	603767942	449	88	8.0	674	7	C0430392	UI-M-HX0-
377	133	12.1	501	4	BU455902	ILLIC3.ab	450	88	8.0	693	4	BG974017	602843702
378	132	12.0	715	6	CD494891	CDAL13-D01	451	88	8.0	752	4	B1696272	B1696272 603345647
379	132	12.0	779	7	CK778629	965794 MA	C 452	88	8.0	814	9	CG694869	ZMMBB029
380	130	11.8	532	1	AA273481	VC37610.r	453	88	8.0	2851	3	AK045226	Mus muscu
381	125	11.3	421	1	AA273564	VC38E10.r	454	87.5	7.9	525	7	CR755333	CR755333
382	124	11.3	289	4	BG200773	BST20223	455	87.5	7.9	908	9	CG357210	OG08076TV
C 383	124	11.3	798	7	CK777040	964032 MA	456	87.5	7.9	1383	9	CG744628	P037-2-B0
384	123	11.2	184	4	BG196762	RST15989	457	87	7.9	498	5	BQ121914	EST607490
385	122	11.1	708	7	CK676883	ZF101-P00	458	87	7.9	631	4	BG589963	EST497805
386	118	10.7	545	2	BE684228	184549 MA	C 459	87	7.9	633	4	BG593455	EST492133
387	118	10.7	840	7	CN507473	AGENCOURT	460	87	7.9	692	6	BY764826	BY764826
388	117	10.6	307	4	BG185958	BST4913.A	461	87	7.9	777	8	BZ464212	BONT045TR
C 389	115.5	10.5	701	5	BM474894	BM474894	462	87	7.9	2098	3	AK011959	Mus muscu
C 390	113.5	10.3	924	9	CNS04EN9	AL287262 Tetraodon	463	87	7.9	3793	3	AK086711	Mus muscu
C 391	112.5	10.2	636	6	CD015482	CD015482 hac22c05.	464	86.5	7.8	572	6	CD898667	G174.109L
C 392	112	10.2	631	1	AI105157	EST214446	C 465	86.5	7.8	621	6	CA332999	hab33c02.
393	111	10.1	940	6	CA496292	AGENCOURT	466	86.5	7.8	697	4	B1143391	602907755
C 394	110.5	10.0	985	2	BF781108	602106752	467	86.5	7.8	827	9	CR084650	Reverse 8
C 395	101.5	9.2	643	6	CA333025	hab33f01.	468	86.5	7.8	4255	3	AK083457	Mus muscu
C 396	100	9.1	536	8	BH344241	BH344241 CH230-131	C 469	86	7.8	409	5	BQ195349	UI-R-CNI-
398	100	9.1	736	8	BZ102223	CH230-238	470	86	7.8	472	1	AJ693058	AJ693058
C 403	94	8.5	408	3	AK031326	Mus muscu	476	86	7.8	517	6	CA563958	K0320B03-
C 405	93.5	8.5	824	8	BH164424	ENTRC59TR	478	86	7.8	521	5	BU710974	SJAAAGD07
C 406	93.5	8.5	874	8	AZ677794	ENTLLD34TR	479	85.5	7.8	3089	9	AY406397	Mus muscu
C 407	93.5	8.5	877	8	BH165886	ENTTK501F	480	85.5	7.8	571	4	B1559726	603522608
C 408	93.5	8.5	3148	9	AY410630	Mus muscu	481	85.5	7.8	691	6	CD035651	mgm020XH
C 409	92	8.3	778	7	CR451583	CR451583	482	85.5	7.8	691	6	CD035651	mgm020XH
C 411	91.5	8.3	1181	6	CD338123	StrPu537.	C 483	85.5	7.8	968	7	W13084	ma89g11.r1
C 412	91.5	8.3	755	7	CO573580	AGENCOURT	C 484	85.5	7.8	976	2	BE420631	HWM000.H0
C 413	91.5	8.3	3806	3	AK028821	Mus muscu	C 485	85	7.7	1040	4	BM558209	AGENCOURT
C 414	91	8.3	596	1	AJ660081	AJ660081	C 486	85	7.7	807	9	CL668256	PR10157b
C 415	91	8.3	700	1	AI878470	fc59B09.x	487	84.5	7.7	693	5	BM313960	BM313960
C 416	91	8.3	780	7	CF996795	AGENCOURT	488	84.5	7.7	710	5	BM298071	BM298071
C 417	91	8.3	823	8	BH703461	BOMH95TF	C 490	84.5	7.7	794	9	CG999435	ZMMBB052
C 418	90.5	8.2	747	9	CG357201	OG0B076TH	C 491	84.5	7.7	921	9	CC987850	ZUA6304TV
C 419	90.5	8.2	785	7	CO551575	ACLy1143	C 492	84.5	7.7	1050	8	CC268405	CC268405
C 420	90.5	8.2	962	7	CO551598	ACLy1178	C 493	84	7.6	1078	1	AL574873	AL574873
C 421	90	8.2	492	1	AI639291	rx041588	494	84	7.6	569	4	BJ332412	BJ332412
C 422	90	8.2	758	5	BX626269	BX626269	C 495	84	7.6	588	9	LBAP063D07	LBAP063D07
C 423	90	8.2	767	4	BG784080	SEAUMC004	C 496	84	7.6	758	5	BU458301	603775705
C 424	90	8.2	982	9	CL118192	LSB1-70D1	C 497	83.5	7.6	934	9	CL299732	ZMMBB008
C 425	90	8.2	2400	9	AY406160	Mus muscu	C 498	83.5	7.6	433	7	CO183504	CO183504
C 426	90	8.2	3161	3	AK044046	Mus muscu	C 499	83.5	7.6	508	3	CNS0A2QL	Arabidops
C 427	90	8.2	3592	3	AK083092	Mus muscu	C 500	83.5	7.6	637	6	CB497107	omykrbna5
C 428	89.5	8.1	445	2	BF437411	7p71f07.x	C 501	83.5	7.6	655	7	CO682479	DG11-154C
C 429	89.5	8.1	472	2	AW771675	hl69f12.x	C 502	83.5	7.6	734	5	BM485364	BM485364
C 430	89.5	8.1	547	1	AA630195	ab99f06.s	C 503	83.5	7.6	803	8	BZ060740	lkg39b04.
C 431	89.5	8.1	578	1	AI023787	AI023787 ox08c06.x	C 504	83.5	7.6	857	9	BX998291	Forward 8
C 432	89.5	8.1	601	1	AA779994	zJ24C09.s	C 505	83.5	7.6	1662	3	CNS0A1RZ	CBX81291 Arabidops
C 433	89.5	8.1	620	5	AX092288	BX092288	C 506	83	7.5	618	6	CB445123	696372 MA
C 434	89.5	8.1	674	1	AI193623	qe71d07.x	C 507	83	7.5	649	2	BE067780	MR4-BT035
C 435	89.5	8.1	1002	5	BQ947843	AGENCOURT	C 508	83	7.5	671	7	CR530161	CR530161
C 436	89	8.1	610	9	CC897858	ZMMBB022	C 509	83	7.5	675	5	BX620252	BX620252
C 437	89	8.1	593	1	AV861790	AV861790	C 510	83	7.5	684	4	BM715255	UI-E-CL1-
C 438	89	8.1	841	6	CD300961	AGENCOURT	C 511	83	7.5	688	4	BM593976	170006874
C 439	89	8.1	1023	6	CB570348	AGENCOURT	C 512	83	7.5	691	9	CC832380	ZMMBB018
C 440	89	8.1	2400	9	AY406158	Homo sapi	C 513	83	7.5	715	5	BX620046	BX620046
C 441	88.5	8.0	664	7	CN776878	taf27d05.	C 514	83	7.5	844	8	BZ742542	OGFBP24TC
C 442	88.5	8.0	787	8	BZ498769	BONNP61TF	C 515	83	7.5	878	4	BI459507	603200512
C 443	88.5	8.0	919	8	BH166832	ENTQY42TR	C 516	83	7.5	944	9	CL465657	SAILL_1243
C 444	88.5	8.0	934	2	BE732416	601569647	C 517	83	7.5	978	9	CL034619	CH216-38G
C 445	88	8.0	464	2	BB744916	BB744916	C 518	83	7.5	1170	9	CG752387	P047-1-E0
C 446	88	8.0	523	1	AA869702	vg44c11.r	C 519	83	7.5	1297	4	BG621714	602618755
C 447	88	8.0	646	7	CF727636	UI-M-HB0-	C 520	82.5	7.5	323	2	BB026649	BB026649

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C 538 82 7.4 488 2 BF498424 AT12817.5  
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C 543 82 7.4 617 2 BF501541 AT16907.5  
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C 546 82 7.4 646 5 BW075252 BW075252  
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561 82 7.4 884 8 AZ683844 ENTLO12TR  
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564 81.5 7.4 476 6 BY594127 BY594127  
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576 81.5 7.4 873 5 BU159711 AGENCOURT  
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578 81.5 7.4 903 5 BU171071 AGENCOURT  
579 81.5 7.4 951 5 BU749000 CH3#024.B  
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581 81.5 7.4 1484 3 CNSOACAI EX814279 Arabidops  
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C 583 81.5 7.4 2278 3 AK014254 Mus muscu  
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585 81 7.4 528 4 BJ157889 BJ157889  
586 81 7.4 607 6 CB421089 CB421089  
587 81 7.4 639 1 AI064587 GH05049.5  
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C 589 81 7.4 766 5 CUS03QNK AL256169 Tetraodon  
C 590 81 7.4 782 5 BU689227 UI-CF-ECL1  
591 81 7.4 806 9 CR014350 Reverse S  
C 592 81 7.4 835 9 CG929636 CG929636  
C 593 81 7.4 949 9 CL206890 ZMMBB056

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595 81 7.4 1001 9 CL091751 CL091751  
596 81 7.4 1392 4 CB960943 CB960943  
597 81 7.4 1682 5 BQ057290 BQ057290  
598 80.5 7.3 464 6 BY557776 BY557776  
599 80.5 7.3 468 7 CN072945 ECOCBA002  
600 80.5 7.3 520 1 AI181583 AI181583  
C 601 80.5 7.3 523 8 AZ350238 AZ350238  
602 80.5 7.3 528 6 CB514695 CB514695  
603 80.5 7.3 541 2 BE753323 BE753323  
604 80.5 7.3 543 1 AL600861 DKF2P313J  
605 80.5 7.3 609 6 CB438531 687176 MA  
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617 80.5 7.3 1297 9 CG752515 P047-2-B0  
618 80.5 7.3 2614 3 AK028271 Mus muscu  
C 619 80 7.3 487 9 CG827541 ZMMBB0031  
C 620 80 7.3 567 1 AV853028 AV853028  
621 80 7.3 572 9 CR132879 Forward 8  
622 80 7.3 587 1 AV836338 AV836338  
623 80 7.3 596 7 CK661479 LP21023.5  
624 80 7.3 597 1 AI532160 SD03544.5  
C 625 80 7.3 606 1 AV858773 AV858773  
C 626 80 7.3 611 4 BM660240 952033C10  
627 80 7.3 616 1 AI062404 GH01590.5  
628 80 7.3 617 6 CB451960 706778 MA  
C 629 80 7.3 635 8 AQ797646 HS-2161.B  
C 630 80 7.3 643 8 AQ797646 HS-2161.B  
C 631 80 7.3 658 9 BX130469 Danio rer  
C 632 80 7.3 660 6 CB453430 708410 MA  
633 80 7.3 662 9 CR094345 Forward 8  
634 80 7.3 677 1 AV862639 AV862639  
C 635 80 7.3 678 1 AV853029 AV853029  
C 636 80 7.3 684 8 AZ210191 SP\_0153.A  
637 80 7.3 687 8 BH647609 BOMKN82TF  
638 80 7.3 693 5 BQ511976 EST619391  
639 80 7.3 697 2 BF479666 L48-3369T  
640 80 7.3 705 4 BM407592 EST581931  
641 80 7.3 708 5 BQ426975 C9Hem\_017  
C 642 80 7.3 710 8 AZ842157 2M0140F03  
643 80 7.3 718 8 BH938305 odf67B03.  
644 80 7.3 726 4 BM108388 EST555924  
645 80 7.3 731 4 BM406875 EST581202  
646 80 7.3 735 7 CO569559 AGENCOURT  
647 80 7.3 782 7 CK020767 AGENCOURT  
C 648 80 7.3 826 8 BH695657 BOMW56TF  
649 80 7.3 848 7 CF700404 CCAHJ94TR  
650 80 7.3 883 5 BH132364 ENTBO70TR  
C 651 80 7.3 934 8 CL033185 CH216-47I  
652 80 7.3 1056 9 AL092929 QV-BT202-  
653 79.5 7.2 368 1 AI909279 QV-BT202-  
654 79.5 7.2 444 7 CF907336 CF907326 A050C03-  
655 79.5 7.2 447 6 BY591645 BY591645  
656 79.5 7.2 466 9 CG404704 ZMMBB024  
657 79.5 7.2 471 6 BY593153 BY593153  
658 79.5 7.2 525 6 CB887398 Lice\_1.B0  
659 79.5 7.2 551 5 BU778559 SJEETC10  
660 79.5 7.2 561 8 AQ029936 HS\_3160.A  
C 661 79.5 7.2 567 8 AQ029936 HS\_3160.A  
662 79.5 7.2 572 5 BU800255 SJE2C0F09  
663 79.5 7.2 578 5 BU800759 SJE2CUG10  
664 79.5 7.2 602 6 CA893998 B0182F10-  
665 79.5 7.2 614 5 BU800682 SJE2CTR12  
C 666 79.5 7.2 638 9 CC829599 ZMMBB0017

667	79.5	7.2	639	7	CF108876	CF108876 Shultzomi	740	78.5	7.1	565	6	CB438465	CB438465
668	79.5	7.2	641	6	CD469504	leukoS2.4	c 741	78.5	7.1	573	1	AV552096	AV552096
669	79.5	7.2	643	4	BM578737	170006871	c 742	78.5	7.1	575	7	CV247525	CV247525
c 670	79.5	7.2	668	6	CD038414	UTPP1006	c 743	78.5	7.1	578	8	BZ303811	BZ303811
c 671	79.5	7.2	676	4	BJ227887	BJ227887	c 744	78.5	7.1	594	6	CD158972	CD158972
c 672	79.5	7.2	680	7	CF360497	821834 MA	c 745	78.5	7.1	596	2	BE158457	BE158457
673	79.5	7.2	684	8	CO093580	CSU-K34.1	c 746	78.5	7.1	605	4	BG506300	BG506300
674	79.5	7.2	744	5	BU338560	603515926	c 747	78.5	7.1	616	5	BP381326	BP381326
675	79.5	7.2	773	5	BU771494	SUEDAP07	c 748	78.5	7.1	625	6	CB578135	CB578135
c 676	79.5	7.2	839	7	CK451821	907387 MA	c 749	78.5	7.1	631	1	AL896355	AL896355
677	79.5	7.2	853	7	CR565405	CR565405	c 750	78.5	7.1	631	2	AW305900	AW305900
c 678	79.5	7.2	965	5	CNS07DD3	T3 end of	c 751	78.5	7.1	696	7	CN400426	CN400426
679	79	7.2	348	5	BY108227	BY108227	c 752	78.5	7.1	702	7	CF208959	CF208959
c 680	79	7.2	376	9	CL555196	OB_BA000	c 753	78.5	7.1	724	6	CA369614	CA369614
c 681	79	7.2	431	6	CD968637	QAC16208	c 754	78.5	7.1	738	7	CF712234	CF712234
c 682	79	7.2	441	6	CD968554	QAC15A07	c 755	78.5	7.1	768	6	CB893267	CB893267
c 683	79	7.2	495	6	CD393184	Gm ck1265	c 756	78.5	7.1	774	2	AW622069	AW622069
c 684	79	7.2	497	6	CD969080	QAC21b10	c 757	78.5	7.1	776	7	CF707329	CF707329
c 685	79	7.2	515	1	AI172977	ue90A08.x	c 758	78.5	7.1	789	7	CF675841	CF675841
c 686	79	7.2	517	7	CO329642	EX293317	c 759	78.5	7.1	791	1	AV897532	AV897532
687	79	7.2	519	8	AZ929347	479.dif25	c 760	78.5	7.1	806	4	BG490593	BG490593
c 688	79	7.2	524	6	CD871413	CD871413	c 761	78.5	7.1	818	6	CB976145	CB976145
c 689	79	7.2	529	6	CD969209	QAC23b01	c 762	78.5	7.1	827	7	CF377275	CF377275
c 690	79	7.2	536	6	CD969257	QAC23g01	c 763	78.5	7.1	827	7	CV263905	CV263905
c 691	79	7.2	559	6	CD969496	QAC3f11.s	c 764	78.5	7.1	830	8	BZ084054	BZ084054
c 692	79	7.2	572	5	BX268177	BX268177	c 765	78.5	7.1	834	7	CK770082	CK770082
c 693	79	7.2	575	7	CK621920	m130d08.y	c 766	78.5	7.1	862	7	CR438250	CR438250
c 694	79	7.2	597	1	AI790451	u101Q01.x	c 767	78.5	7.1	872	7	CF677456	CF677456
c 695	79	7.2	605	1	AI238548	GH14613.5	c 768	78.5	7.1	903	8	AZ675479	AZ675479
c 696	79	7.2	617	6	CD407166	Gm ck3218	c 769	78.5	7.1	904	7	CV207001	CV207001
c 697	79	7.2	623	6	CA569367	K042D07	c 770	78.5	7.1	947	5	BX704191	BX704191
c 698	79	7.2	625	7	CO169340	NDL1_6_H1	c 771	78.5	7.1	965	1	AL961609	AL961609
c 699	79	7.2	633	4	BJ495527	BJ495527	c 772	78.5	7.1	971	8	AZ668799	AZ668799
c 700	79	7.2	639	7	CO350551	DR_AOV_FL	c 773	78.5	7.1	1071	9	AG114790	AG114790
c 701	79	7.2	673	4	BJ343303	BJ343303	c 774	78.5	7.1	1136	6	CD501309	CD501309
c 702	79	7.2	675	5	BU447924	603766163	c 775	78.5	7.1	1290	3	CNS0ABQD	CNS0ABQD
c 703	79	7.2	701	5	BQ840737	WHE4202.H	c 776	78.5	7.1	4186	3	AK049652	AK049652
c 704	79	7.2	715	9	CG405962	ZMWBb026	c 777	78	7.1	437	1	AL908383	AL908383
c 705	79	7.2	718	5	BW258558	BW258558	c 778	78	7.1	442	7	CO315018	CO315018
c 706	79	7.2	720	8	AZ749847	RECI-24-8	c 779	78	7.1	506	7	CV230090	CV230090
c 707	79	7.2	721	7	CK660449	LF19051.5	c 780	78	7.1	516	9	CL243664	CL243664
c 708	79	7.2	737	4	BI632260	SD25984.5	c 781	78	7.1	519	7	CF610361	CF610361
c 709	79	7.2	744	8	BZ392916	BI632916	c 782	78	7.1	529	4	BJ302994	BJ302994
710	79	7.2	761	9	AG314417	Mus muscu	c 783	78	7.1	536	4	BJ481326	BJ481326
711	79	7.2	809	5	BQ165171	EST611040	c 784	78	7.1	577	7	CV510016	CV510016
712	79	7.2	842	7	CV125404	OSTF30039	c 785	78	7.1	584	8	BZ314285	BZ314285
713	79	7.2	976	4	BG614909	602644109	c 786	78	7.1	607	8	BZ314285	BZ314285
714	79	7.2	1013	6	BY706641	BY706641	c 787	78	7.1	629	5	BQ772790	BQ772790
715	79	7.2	1207	8	CC187192	CH261-6E1	c 788	78	7.1	666	7	CV511121	CV511121
716	79	7.2	1349	3	AK006650	Mus muscu	c 789	78	7.1	675	5	BW364962	BW364962
717	79	7.2	1395	8	BZ574094	msh2_3508	c 790	78	7.1	688	7	CK717541	CK717541
718	79	7.2	2145	3	AK050203	Mus muscu	c 791	78	7.1	690	7	CK970512	CK970512
c 719	79	7.2	2827	3	CNS0A4X9	Arabidops	c 792	78	7.1	693	1	AV370429	AV370429
c 720	78.5	7.1	279	9	CG691990	ZMWBb028	c 793	78	7.1	708	6	CA357172	CA357172
721	78.5	7.1	442	2	AW335806	22020.MAR	c 794	78	7.1	717	8	BZ314286	BZ314286
722	78.5	7.1	446	6	BY563519	BY563519	c 795	78	7.1	720	6	CD353955	CD353955
723	78.5	7.1	458	6	BY527078	BY527078	c 796	78	7.1	752	9	CC745065	CC745065
724	78.5	7.1	458	6	BY572778	BY572778	c 797	78	7.1	756	7	CK696083	CK696083
725	78.5	7.1	458	6	BY596920	BY596920	c 798	78	7.1	761	5	BW296847	BW296847
726	78.5	7.1	459	6	BY590207	BY590207	c 799	78	7.1	779	7	CV302242	CV302242
727	78.5	7.1	462	6	BY570317	BY570317	c 800	78	7.1	785	9	CG621243	CG621243
728	78.5	7.1	462	6	BY595833	BY595833	c 801	78	7.1	818	7	CV078352	CV078352
729	78.5	7.1	462	6	BY598803	BY598803	c 802	78	7.1	821	7	CF694722	CF694722
730	78.5	7.1	463	6	BY596632	BY596632	c 803	78	7.1	821	9	CW518219	CW518219
731	78.5	7.1	465	6	BY590270	BY590270	c 804	78	7.1	840	6	CA985720	CA985720
732	78.5	7.1	467	6	BY558129	BY558129	c 805	78	7.1	879	8	CC423865	CC423865
733	78.5	7.1	469	6	BY559085	BY559085	c 806	78	7.1	881	6	CA791584	CA791584
734	78.5	7.1	469	6	BY559336	BY559336	c 807	78	7.1	893	5	BQ226125	BQ226125
735	78.5	7.1	477	9	CE631421	tLgr-988-	c 808	78	7.1	1201	3	CR693185	CR693185
736	78.5	7.1	480	5	BP609622	BP609622	c 809	77.5	7.0	338	9	CV783110	CV783110
c 737	78.5	7.1	499	9	CG412186	ZMWBb027	c 810	77.5	7.0	432	1	AV738613	AV738613
738	78.5	7.1	521	6	CA888687	B0147H01-	c 811	77.5	7.0	507	9	CL243688	CL243688
739	78.5	7.1	552	2	AW659186	96144.MAR	c 812	77.5	7.0	516	5	BQ830802	BQ830802

C 813	77.5	7.0	520	9	CC785402	886	77.5	7.0	3863	3	BC035034	BC035034 Homo sapi
814	77.5	7.0	558	6	CB929743	887	77.5	7.0	3934	3	AK051023	AK051023 Mus muscu
C 815	77.5	7.0	563	2	AW245541	888	77	7.0	406	5	BY447004	BY447004
C 816	77.5	7.0	566	8	BH397731	889	77	7.0	421	4	BM501422	BM501422 PAC00000
817	77.5	7.0	568	5	BW211784	890	77	7.0	482	9	CL985780	CL985780 ZMMBB000
818	77.5	7.0	569	6	CD419428	891	77	7.0	487	7	CO997875	CO997875 caa01-3ms
819	77.5	7.0	571	6	CB933598	892	77	7.0	511	7	CV001081	CV001081 caa02-4ms
820	77.5	7.0	579	5	BF213909	893	77	7.0	517	2	AW657052	AW657052 109666 MA
C 821	77.5	7.0	581	6	CB932202	894	77	7.0	532	7	CR989667	CR989667 BQHC-2.53
C 822	77.5	7.0	583	2	AW756584	895	77	7.0	538	1	AL921144	AL921144 AL921144
C 823	77.5	7.0	587	6	CB932366	896	77	7.0	561	9	CC761015	CC761015 ZMMBB0020
824	77.5	7.0	591	4	BG732867	897	77	7.0	626	4	BM426993	BM426993 p5f2n.pk0
825	77.5	7.0	593	6	CB830526	898	77	7.0	632	6	CB338937	CB338937 p136f11-y
826	77.5	7.0	593	6	CB931480	899	77	7.0	637	6	CB366880	CB366880 170005316
827	77.5	7.0	598	6	CB931387	900	77	7.0	639	6	CAB45630	CAB45630 hab72809.7
C 828	77.5	7.0	599	4	BM309647	901	77	7.0	649	5	BL173270	BL173270 BW173270
C 829	77.5	7.0	606	8	AZ258479	902	77	7.0	665	9	CL904948	CL904948 OA ABA000
C 830	77.5	7.0	608	1	AV601564	903	77	7.0	667	7	CO058529	CO058529 Lr_PAHCF
C 831	77.5	7.0	608	8	CC149775	904	77	7.0	669	9	CE838653	CE838653 t1gr-q86-
C 832	77.5	7.0	608	9	CC738988	905	77	7.0	674	5	BW336314	BW336314 BW336314
C 833	77.5	7.0	622	9	CC899297	906	77	7.0	682	5	BQ015937	BQ015937 UI-H-DT1-
C 834	77.5	7.0	635	9	CC937887	907	77	7.0	705	7	CK944888	CK944888 406899 B
835	77.5	7.0	638	2	BE264820	908	77	7.0	716	7	CF113574	CF113574 Shultxomi
C 836	77.5	7.0	644	7	CK002077	909	77	7.0	716	7	CC867744	CC867744 NDL.55F21
837	77.5	7.0	654	1	AU296539	910	77	7.0	718	5	BM082986	BM082986
838	77.5	7.0	673	5	BW346119	911	77	7.0	733	7	CR764237	CR764237 DRP2468P
C 839	77.5	7.0	676	7	CF208503	912	77	7.0	734	9	CL412013	CL412013 RPC14.43
C 840	77.5	7.0	680	6	CD482648	913	77	7.0	737	5	BW077263	BW077263 BX077263
C 841	77.5	7.0	685	4	BF977967	914	77	7.0	762	5	BX333847	BX333847 CS333847
842	77.5	7.0	685	2	BZ002116	915	77	7.0	767	9	AG509315	AG509315 Mus muscu
843	77.5	7.0	689	8	BE263758	916	77	7.0	769	7	CV225191	CV225191 CS hyp.21
C 844	77.5	7.0	689	8	BH010506	917	77	7.0	784	5	BP435442	BP435442 BF435442
C 845	77.5	7.0	690	5	BM076140	918	77	7.0	790	5	BM084869	BM084869
C 846	77.5	7.0	692	6	CB438991	919	77	7.0	829	7	CK180479	CK180479 EST769799
847	77.5	7.0	695	7	CO549975	920	77	7.0	831	6	CB646857	CB646857 OSJNEB091
C 848	77.5	7.0	699	4	BJ706243	921	77	7.0	833	9	CR150079	CR150079 Reverse.8
C 849	77.5	7.0	704	4	BJ708672	922	77	7.0	837	7	CK182212	CK182212 EST771531
C 850	77.5	7.0	706	9	CC969745	923	77	7.0	840	5	BZ260388	BZ260388 603504413
C 851	77.5	7.0	710	5	BM182781	924	77	7.0	856	8	BZ263159	BZ263159 CH230-521
C 852	77.5	7.0	711	8	BZ517713	925	77	7.0	873	5	BP144370	BP144370 BP144370
C 853	77.5	7.0	716	9	BX132818	926	77	7.0	882	7	CK182211	CK182211 EST771531
854	77.5	7.0	723	4	BI764067	927	77	7.0	902	9	CL007658	CL007658 ZMMBB0054
C 855	77.5	7.0	733	4	BG828455	928	77	7.0	920	9	CNS0597L	AL327666 Tetraodon
C 856	77.5	7.0	742	2	BE740855	929	77	7.0	938	4	BG247976	BG247976 602359906
857	77.5	7.0	760	6	CD081874	930	77	7.0	940	7	CK180480	CK180480 EST769800
C 858	77.5	7.0	764	5	BP141829	931	77	7.0	947	5	BQ635597	BQ635597 AGENCOURT
859	77.5	7.0	767	6	CB309568	932	77	7.0	989	9	CNS06M3N	AL404985 T7 end of
860	77.5	7.0	771	7	CF726880	933	77	7.0	1154	8	CC280065	CC280065 CH261-24F
C 861	77.5	7.0	785	7	CK128510	934	77	7.0	1202	3	CR720608	CR720608 Tetraodon
C 862	77.5	7.0	820	7	CN076960	935	77	7.0	1261	9	CL648972	CL648972 CH213-207
C 863	77.5	7.0	823	4	BG429719	936	77	7.0	1261	9	CL648972	CL648972 CH213-207
864	77.5	7.0	823	9	CC610912	937	76.5	6.9	367	2	BE765094	BE765094 CM1-NT008
865	77.5	7.0	833	8	BH486991	938	76.5	6.9	371	8	AZ932147	AZ932147 474.dhz95
866	77.5	7.0	874	8	AZ542114	939	76.5	6.9	409	1	AV026493	AV026493 AV026493
867	77.5	7.0	882	8	CC328947	940	76.5	6.9	469	5	BWS23539	BWS23539 ZMMBB0019
868	77.5	7.0	897	5	EX729304	941	76.5	6.9	489	9	CB835781	CB835781 ZMMBB0019
869	77.5	7.0	902	6	CA979662	942	76.5	6.9	497	5	BW512180	BW512180
C 870	77.5	7.0	907	9	AG123863	943	76.5	6.9	500	5	BP185883	BP185883 BP185883
C 871	77.5	7.0	921	9	CNS005K2	944	76.5	6.9	513	9	CL242205	CL242205 ZMMBB0038
C 872	77.5	7.0	966	9	CNS0570K	945	76.5	6.9	515	9	CC785997	CC785997 ZMMBB0015
C 873	77.5	7.0	998	9	AL546677	946	76.5	6.9	521	9	CG469914	CG469914 ZMMBB0026
874	77.5	7.0	1045	1	AL546677	947	76.5	6.9	534	7	CR538057	CR538057 DRP2468P
875	77.5	7.0	1081	8	CC203857	948	76.5	6.9	544	7	CR581737	CR581737 CR581737
876	77.5	7.0	1082	5	BQ955528	949	76.5	6.9	547	5	BQ626733	BQ626733 p226C12.Y
877	77.5	7.0	1087	5	BX460202	950	76.5	6.9	566	2	AW369405	AW369405 QV1-BN000
878	77.5	7.0	1228	3	CR721286	951	76.5	6.9	569	5	BQ827786	BQ827786 L6in2177
C 879	77.5	7.0	1513	4	BG621971	952	76.5	6.9	573	1	AA763366	AA763366 vms3e02.r
880	77.5	7.0	1548	3	CR716539	953	76.5	6.9	574	7	CK528820	CK528820 rawfa0.00
C 881	77.5	7.0	1621	3	BF693946	954	76.5	6.9	584	7	CK747450	CK747450 ltu01-1ms
C 882	77.5	7.0	1729	3	CR597623	955	76.5	6.9	597	1	AA203269	AA203269 zxs5f12.r
883	77.5	7.0	1797	3	CB617323	956	76.5	6.9	632	7	CK519966	CK519966 rwea0.00
884	77.5	7.0	3854	3	BC044597	957	76.5	6.9	645	2	AV956803	AV956803
885	77.5	7.0	3857	5	BQ828498	958	76.5	6.9	661	6	CB418932	CB418932 591763 MA

c 959	76.5	6.9	663	2	BB118984	BB118984	1032	76	6.9	715	4	BJ727193	BJ727193
960	76.5	6.9	664	8	AZ570205	27LPvP11	1033	76	6.9	716	5	AX719954	AX719954
961	76.5	6.9	665	6	CD775531	UT-M-AQ0-	1034	76	6.9	724	5	BP698307	BP698307
c 962	76.5	6.9	677	8	BH878037	h879g10.b	1035	76	6.9	724	8	AG293575	AG293575
963	76.5	6.9	693	5	EX866383	EX866383	1036	76	6.9	725	5	AG293575	MUS muscu
964	76.5	6.9	694	5	BU270220	603817325	1037	76	6.9	734	4	BJ131903	BJ131903
965	76.5	6.9	711	9	CI22C5	CI22C5	c1038	76	6.9	745	8	BZ622791	BZ622791
c 966	76.5	6.9	713	9	CO524261	CIona int	1039	76	6.9	758	7	CV117300	CV117300
c 967	76.5	6.9	717	2	AW967044	EST379118	1040	76	6.9	764	4	BJ151697	BJ151697
968	76.5	6.9	717	5	EX102344	EX102344	1041	76	6.9	764	7	CK285945	EST748667
969	76.5	6.9	721	5	BU884374	RO09G08 P	1042	76	6.9	780	7	CK289055	EST751777
c 970	76.5	6.9	722	9	CI194155	Forward S	1043	76	6.9	787	9	CL771845	OR BBA008
c 971	76.5	6.9	727	4	BG967765	602833292	c1044	76	6.9	796	4	BG775373	602649832
972	76.5	6.9	727	8	BH935656	oq53e08	1045	76	6.9	798	2	BF260996	HVSMF002
c 973	76.5	6.9	738	7	CO808682	AGENCOURT	1046	76	6.9	800	7	CN754867	ID0AAA14A
974	76.5	6.9	759	7	CO595947	AGENCOURT	c1047	76	6.9	807	7	CO234997	WS0263.B2
c 975	76.5	6.9	766	2	BF046891	EST988 Ma	1048	76	6.9	826	7	CO551680	AcLy1293
976	76.5	6.9	768	7	CK594823	AGENCOURT	c1049	76	6.9	826	5	AX709900	AX709900
977	76.5	6.9	769	7	CV103168	AGENCOURT	1050	76	6.9	827	9	CL655564	PR10124a
978	76.5	6.9	794	5	BU929272	AGENCOURT	1051	76	6.9	837	7	CO980285	GM89007B1
c 979	76.5	6.9	794	7	CF873219	tric004xi	1052	76	6.9	845	9	CL393573	CL393573
980	76.5	6.9	804	4	BI462165	603205167	1053	76	6.9	847	8	BZ622790	1980F07.b
981	76.5	6.9	804	4	BI852652	603379307	1054	76	6.9	857	5	AX415121	AX415121
982	76.5	6.9	814	1	AJ568476	AJ568476	1055	76	6.9	878	7	CN175080	CN175080
c 983	76.5	6.9	906	9	CG459199	PUIKG31TD	1056	76	6.9	879	6	CD302554	AGENCOURT
c 984	76.5	6.9	907	5	BU111384	603126911	1057	76	6.9	885	8	AZ549942	AZ549942
c 985	76.5	6.9	945	9	CG281500	QG0DP76TV	c1058	76	6.9	885	8	AZ670390	AZ670390
c 986	76.5	6.9	954	5	BQ719706	AGENCOURT	1059	76	6.9	888	7	CK015888	AGENCOURT
c 987	76.5	6.9	968	7	CK423610	AUF IpSpn	1060	76	6.9	889	7	CO553084	ACMY380 S
c 988	76.5	6.9	1042	5	BQ880673	AGENCOURT	1061	76	6.9	892	5	BU909008	AGENCOURT
989	76.5	6.9	1794	3	CSMOA507	AXabidops	1062	76	6.9	898	7	CF272349	AGENCOURT
c 990	76.5	6.9	3422	3	HSM800477	AL050181 Homo sapi	1063	76	6.9	901	3	CNS0A5BA	CNS0A5BA
991	76	6.9	274	1	AV051417	AV051417	c1064	76	6.9	902	8	AZ690869	ENTK058TR
c 992	76	6.9	289	1	AV052229	AV052229	c1065	76	6.9	904	4	BM046821	603626990
c 993	76	6.9	308	1	AA253689	mx85b01.r	c1066	76	6.9	927	9	CG061421	CG061421
994	76	6.9	412	2	AW886726	RC1-OT008	1067	76	6.9	951	8	BZ138778	CH230-288
995	76	6.9	420	6	CB145337	K-EST0200	c1068	76	6.9	956	5	BU108814	603112491
c 996	76	6.9	428	6	CD562340	B046D08-	1069	76	6.9	970	5	BU766188	BU766188
997	76	6.9	431	5	BY447147	BY447147	1070	76	6.9	971	7	CF225302	CF225302
998	76	6.9	453	1	AA421070	zu08G09.r	1071	76	6.9	981	4	BG774910	602649832
c 999	76	6.9	459	7	CO301190	EX180403.	c1072	76	6.9	994	9	CL044938	CL044938
c1000	76	6.9	487	8	BZ709370	QGDJA45TM	c1073	76	6.9	999	4	BG492592	602536556
c1001	76	6.9	501	9	CG792450	ZMMBBb029	c1074	76	6.9	1065	9	CNS043PW	CNS043PW
c1002	76	6.9	506	8	AQ236234	HS 2045.B	1075	76	6.9	1109	2	BF527859	BF527859
c1003	76	6.9	510	9	CC750618	ZMMBBb013	c1076	76	6.9	1113	2	BF131862	BF131862
c1004	76	6.9	519	1	AV558418	AV558418	c1077	76	6.9	1324	9	AG073938	AG073938
c1005	76	6.9	533	2	AW213414	un55G06.y	1078	76	6.9	1390	3	AY222926	AY222926
c1006	76	6.9	538	2	AW980503	EST391656	c1079	76	6.9	1614	3	AG073938	AG073938
c1007	76	6.9	540	2	BE374799	601226615	1080	76	6.9	1830	2	BF129578	BF129578
c1008	76	6.9	542	2	AW385539	PM1-LT001	c1081	76	6.9	282	1	AL783013	AL783013
c1009	76	6.9	550	1	AV536049	AV536049	1082	75.5	6.9	351	5	BP619023	BP619023
c1010	76	6.9	554	1	AV538992	AV538992	1083	75.5	6.9	370	7	CK823853	CK823853
c1011	76	6.9	561	1	AL908379	AL908379	1084	75.5	6.9	397	7	CO519972	CO519972
c1012	76	6.9	566	5	BU579415	1m84B04.y	1085	75.5	6.9	421	1	AA183446	mt23f01.r
1013	76	6.9	570	4	BM789626	K-EST0069	c1086	75.5	6.9	424	1	AA183446	mt23f01.r
c1014	76	6.9	595	1	AI997311	701553249	1087	75.5	6.9	437	4	BM686872	UI-E-CR1-
c1015	76	6.9	594	6	CD730222	4038624.1	1088	75.5	6.9	469	1	AA411006	AY36C04.s
c1016	76	6.9	595	2	BE678477	AV59G11.x	c1089	75.5	6.9	470	6	BY568816	BY568816
c1017	76	6.9	609	1	AV518023	AV518023	1090	75.5	6.9	479	1	AA411006	AY36C04.s
c1018	76	6.9	618	5	BM935391	UT-M-CGOp	1091	75.5	6.9	479	4	BM745435	BM745435
c1019	76	6.9	635	8	AQ471652	CJTBI-EI-	c1092	75.5	6.9	478	9	CL388280	RPCI44.28
c1020	76	6.9	662	7	CK003438	AGENCOURT	1093	75.5	6.9	480	4	BM852127	BM852127
1021	76	6.9	663	7	CO525206	AcLy638.S	1094	75.5	6.9	502	4	BM746832	K-EST0021
1022	76	6.9	666	4	BU143427	BU143427	1095	75.5	6.9	510	1	AL803134	AL803134
1023	76	6.9	680	7	CK284532	EST747254	1096	75.5	6.9	512	8	AQ189477	HS 3209.A
1024	76	6.9	683	7	CK971483	4087045.B	1097	75.5	6.9	527	4	BM831319	K-EST0105
1025	76	6.9	686	4	BJ031694	BJ031694	1098	75.5	6.9	529	4	BM833236	K-EST0107
1026	76	6.9	690	6	BY763945	BY763945	c1099	75.5	6.9	533	5	BM701322	BM701322
1027	76	6.9	691	4	BJ777858	BJ777858	c1100	75.5	6.9	535	1	AI796528	AI796528
c1028	76	6.9	693	1	AV783776	AV783776	1101	75.5	6.9	539	1	AA429321	zw07G12.r
1029	76	6.9	694	5	EX850208	EX850208	1102	75.5	6.9	541	2	BE031556	BE031556
1030	76	6.9	695	4	BJ154330	BJ154330	1103	75.5	6.9	542	1	AL961949	AL961949
c1031	76	6.9	708	5	BQ999759	QGG22P17.	c1104	75.5	6.9	542	7	CV022882	EST00052

C1105	75.5	6.9	545	5	BX757779	BX757779	1178	75.5	6.9	752	7	CN532926	UI-M-HOO
C1106	75.5	6.9	558	8	BH109327	RPCI-24-2	1179	75.5	6.9	758	4	BG977005	BG977005
C1107	75.5	6.9	559	4	BW793304	K-EST0074	1180	75.5	6.9	759	9	CR831594	CR831594
C1108	75.5	6.9	559	5	BY491176	BY491176	1181	75.5	6.9	760	9	CN080647	AL415395 T3 end of
C1109	75.5	6.9	560	8	BZ363168	id81e11.g	1182	75.5	6.9	764	4	BJ813754	BJ813754
C1110	75.5	6.9	561	4	BG383021	100901.MA	1183	75.5	6.9	765	7	CO423356	CO423356
C1111	75.5	6.9	563	2	AW387919	MR4-ST011	1184	75.5	6.9	766	7	CF211126	GGE2HT100
C1112	75.5	6.9	575	4	BW75490	BW75490	1185	75.5	6.9	766	9	CC942418	CC942418
C1113	75.5	6.9	575	5	BW452356	BW452356	1186	75.5	6.9	773	7	CV1111960	CV1111960
C1114	75.5	6.9	586	6	CD427338	SA1_18.A0	1187	75.5	6.9	775	5	BU454570	BU454570
C1115	75.5	6.9	590	1	AA429320	zw07d11.r	1188	75.5	6.9	798	4	BG740690	BG740690
C1116	75.5	6.9	592	4	BJ614376	BJ614376	1189	75.5	6.9	800	1	AI664579	AI664579
C1117	75.5	6.9	592	8	AZ253029	RPCI-23-6	1190	75.5	6.9	804	7	CR375482	CR375482
C1118	75.5	6.9	593	4	BW741056	K-EST0013	1191	75.5	6.9	815	5	BX764805	BX764805
C1119	75.5	6.9	601	5	BW428389	BW428389	1192	75.5	6.9	828	6	CA489620	CA489620
C1120	75.5	6.9	605	1	AL500157	AL500157	1193	75.5	6.9	835	5	BW794634	BW794634
C1121	75.5	6.9	607	7	CV022881	EST00051	1194	75.5	6.9	837	8	BZ436815	BZ436815
C1122	75.5	6.9	609	8	BH010723	ep68d08.b	1195	75.5	6.9	839	5	BX776036	BX776036
C1123	75.5	6.9	614	1	AL629130	AL629130	1196	75.5	6.9	842	8	BZ444528	BZ444528
C1124	75.5	6.9	614	1	AL180505	AL180505	1197	75.5	6.9	851	8	BZ547010	BZ547010
C1125	75.5	6.9	615	4	BG812408	dad34a11.	1198	75.5	6.9	858	5	BX777427	BX777427
C1126	75.5	6.9	618	8	BH007785	ee76c02.x	1199	75.5	6.9	859	8	BZ277013	BZ277013
C1127	75.5	6.9	618	8	BH010713	ep68c05.b	1200	75.5	6.9	869	7	CN167709	CN167709
C1128	75.5	6.9	629	4	BW791452	K-EST0071	1201	75.5	6.9	872	8	BZ487656	BZ487656
C1129	75.5	6.9	638	8	BH010966	ep72c11.b	1202	75.5	6.9	874	5	BQ918845	BQ918845
C1130	75.5	6.9	639	1	AL850544	AL850544	1203	75.5	6.9	878	8	AZ542312	AZ542312
C1131	75.5	6.9	642	1	AL895541	AL895541	1204	75.5	6.9	880	5	BQ881320	BQ881320
C1132	75.5	6.9	644	4	B1828583	603078483	1205	75.5	6.9	886	5	BX777443	BX777443
C1133	75.5	6.9	647	4	BJ795355	BJ795355	1206	75.5	6.9	889	5	BX755112	BX755112
C1134	75.5	6.9	651	4	BJ786862	BJ786862	1207	75.5	6.9	892	5	BQ282870	BQ282870
C1135	75.5	6.9	653	7	CF766346	CES007141	1208	75.5	6.9	892	8	AZ542268	AZ542268
C1136	75.5	6.9	653	9	CC869674	NDL.113K2	1209	75.5	6.9	896	5	CG834072	CG834072
C1137	75.5	6.9	656	1	AL889538	AL889538	1210	75.5	6.9	900	6	CA478255	CA478255
C1138	75.5	6.9	656	1	AL891818	AL891818	1211	75.5	6.9	904	5	CN50510K	CN50510K
C1139	75.5	6.9	656	9	CC750735	ZMWBb013	1212	75.5	6.9	909	9	CN50510K	CN50510K
C1140	75.5	6.9	658	4	BJ796532	BJ796532	1213	75.5	6.9	910	9	CC651268	CC651268
C1141	75.5	6.9	660	1	AL889939	AL889939	1214	75.5	6.9	914	6	CA489602	CA489602
C1142	75.5	6.9	661	1	AL883320	AL883320	1215	75.5	6.9	914	6	CG861069	CG861069
C1143	75.5	6.9	664	1	AL897339	AL897339	1216	75.5	6.9	915	9	CR224403	CR224403
C1144	75.5	6.9	664	4	BW794696	BW794696	1217	75.5	6.9	927	4	BG698098	BG698098
C1145	75.5	6.9	664	9	AG134324	Pan.trog1	1218	75.5	6.9	938	9	CN501E7S	AL140201 Anopheles
C1146	75.5	6.9	666	4	BJ816460	BJ816460	1219	75.5	6.9	944	5	BQ282821	AGENCYCOURT
C1147	75.5	6.9	668	1	AL889316	AL889316	1220	75.5	6.9	954	7	CF548070	AGENCYCOURT
C1148	75.5	6.9	668	8	AZ575371	339PVD02	1221	75.5	6.9	967	2	BF529561	BF529561
C1149	75.5	6.9	670	4	BJ814296	BJ814296	1222	75.5	6.9	1025	9	CNS05COK	AL313445 Tetraodon
C1150	75.5	6.9	670	4	BW817771	K-EST0084	1223	75.5	6.9	1034	9	CNS05COK	AL313445 Tetraodon
C1151	75.5	6.9	687	4	BJ796382	BJ796382	1224	75.5	6.9	1041	9	AY403695	AY403695
C1152	75.5	6.9	687	8	BZ078130	l1g02e05.	1225	75.5	6.9	1089	9	CL948599	CL948599
C1153	75.5	6.9	689	4	BW780767	BW780767	1226	75.5	6.9	1176	2	BF347168	BF347168
C1154	75.5	6.9	689	8	BZ035244	BZ035244	1227	75.5	6.9	1241	3	CR596859	CR596859
C1155	75.5	6.9	692	8	BZ040241	oeh2g912.	1228	75.5	6.9	1264	5	BM908422	BM908422
C1156	75.5	6.9	692	9	CG436867	CG436867	1229	75.5	6.9	1342	5	B0230413	B0230413
C1157	75.5	6.9	694	8	BZ052368	jnr56h06.	1230	75.5	6.9	1461	3	CNS0AC7A	BM908422
C1158	75.5	6.9	696	8	BZ044329	l1k17b10.	1231	75.5	6.9	1717	2	BE965698	BE965698
C1159	75.5	6.9	697	9	CG436861	CG436861	1232	75.5	6.8	297	1	AV118609	AV118609
C1160	75.5	6.9	697	8	BH920423	od112c09.	1233	75.5	6.8	386	1	AU251252	AU251252
C1161	75.5	6.9	715	7	CF454089	AGENCYCOURT	1234	75.5	6.8	416	8	BZ701258	BZ701258
C1162	75.5	6.9	715	8	BH980386	odf01g10.	1235	75.5	6.8	424	7	R08797	R08797
C1163	75.5	6.9	716	8	BZ075725	l1k53c02.	1236	75.5	6.8	429	7	CF792577	CF792577
C1164	75.5	6.9	717	5	BX773510	BX773510	1237	75.5	6.8	438	4	BW062714	BW062714
C1165	75.5	6.9	720	2	BE972411	601652232	1238	75.5	6.8	441	1	AA717806	AA717806
C1166	75.5	6.9	722	5	BX696613	BX696613	1239	75.5	6.8	442	5	BX362108	BX362108
C1167	75.5	6.9	724	8	BZ370218	id81e11.b	1240	75.5	6.8	443	2	BB746485	BB746485
C1168	75.5	6.9	725	5	BX749758	BX749758	1241	75.5	6.8	467	1	AL743397	AL743397
C1169	75.5	6.9	725	5	BX759211	BX759211	1242	75.5	6.8	469	2	BE772148	BE772148
C1170	75.5	6.9	726	8	BZ645564	OGAOJ05TM	1243	75.5	6.8	475	2	AW804171	AW804171
C1171	75.5	6.9	736	1	BH007784	ee76c02.x	1244	75.5	6.8	492	2	W6944626	W6944626
C1172	75.5	6.9	736	1	AL543556	AL543556	1245	75.5	6.8	498	7	W66598	W66598
C1173	75.5	6.9	736	8	BZ085015	l1j32h04.	1246	75.5	6.8	502	7	TA84523	TA84523
C1174	75.5	6.9	741	9	AG562226	Mus_muscu	1247	75.5	6.8	523	1	AA881588	AA881588
C1175	75.5	6.9	743	8	BZ041912	l1r008b12.	1248	75.5	6.8	525	2	BF012429	BF012429
C1176	75.5	6.9	745	1	AV399434	AV399434	1249	75.5	6.8	527	5	BQ002907	BQ002907
C1177	75.5	6.9	747	9	CG330296	OGAO15TH	1250	75.5	6.8	549	4	BM798135	BM798135

1251	75	6.8	552	4	BJ765658	BJ765658	BJ765658	CL324	74.5	6.8	317	5	BU881303	BU881303 UM61TA09
1252	75	6.8	566	4	BJ493274	BJ493274	BJ493274	CL325	74.5	6.8	346	6	CD159564	CD159564 ML1-0062P
1253	75	6.8	574	9	CG877946	CG877946	ZMMBBb049	CL326	74.5	6.8	348	1	AI944150	AI944150 614036C12
1254	75	6.8	576	5	BQ331665	BQ331665	FM3-ET026	1327	74.5	6.8	384	2	BF720881	BF720881 mad38H11.
1255	75	6.8	581	5	BQ832449	BQ832449	LI6in2254	1328	74.5	6.8	384	6	CB703345	CB703345 AMGNNUC:M
1256	75	6.8	593	1	AU299417	AU299417	LI6in2254	1329	74.5	6.8	391	6	CD159531	CD159531 ML1-0062P
1257	75	6.8	594	7	BZ703963	BZ703963	E048IH12-	1330	74.5	6.8	394	7	CN649056	CN649056 EG_PSPGRB
1258	75	6.8	602	8	CN331060	CN331060	hw06a05-b	1331	74.5	6.8	405	9	CL458421	CL458421 ZMMBBb048
1259	75	6.8	608	6	CD817158	CD817158	BN20_0400	1332	74.5	6.8	425	1	AU032906	AU032906 AU032906
1260	75	6.8	616	2	BF456680	BF456680	AI10571.5	1333	74.5	6.8	427	7	CO256542	CO256542 WS0083.B2
1261	75	6.8	643	4	BI837925	BI837925	603083750	1334	74.5	6.8	438	2	BF732227	BF732227 BF732227
1262	75	6.8	652	5	BU046320	BU046320	PP_LRa002	1335	74.5	6.8	447	7	CF324070	CF324070 HDN--05-I
1263	75	6.8	655	7	CO503970	CO503970	GGZCZCB103	1336	74.5	6.8	452	7	CK611978	CK611978 LPsb_I09
1264	75	6.8	658	2	BF506350	BF506350	AT08793.5	1337	74.5	6.8	454	9	CC738389	CC738389 ZMMBBb010
1265	75	6.8	660	5	BU039952	BU039952	PP_LRa000	1338	74.5	6.8	471	8	AQ226650	AQ226650 HS_2010_A
1266	75	6.8	667	8	CC304888	CC304888	CHZ61-1B9	1339	74.5	6.8	479	8	BH438425	BH438425 BOGT411TF
1267	75	6.8	668	2	BB632840	BB632840	BB632840	1340	74.5	6.8	481	5	BX280393	BX280393 BX280393
1268	75	6.8	673	4	BM174501	BM174501	Tm_ad_30B	1341	74.5	6.8	491	9	CC787077	CC787077 ZMMBBb015
1269	75	6.8	674	5	BW211376	BW211376	AG121203	1342	74.5	6.8	505	9	CG914309	CG914309 ZMMBBb037
1270	75	6.8	676	9	AG121203	AG121203	Pan Trogl	1343	74.5	6.8	505	9	CL204603	CL204603 ZMMBBb056
1271	75	6.8	678	4	BM602659	BM602659	170006870	1344	74.5	6.8	511	9	CC902419	CC902419 ZMMBBb024
1272	75	6.8	678	5	BM040082	BM040082	BM040082	1345	74.5	6.8	547	9	CL203934	CL203934 ZMMBBb001
1273	75	6.8	678	7	CV516549	CV516549	0048P0015	1346	74.5	6.8	549	9	CL203934	CL203934 ZMMBBb055
1274	75	6.8	686	6	CB350286	CB350286	CAB2SG000	1347	74.5	6.8	569	8	AZ978117	AZ978117 2M0254F15
1275	75	6.8	690	4	BI484291	BI484291	RB67370.5	1348	74.5	6.8	572	7	CF262141	CF262141 AUA_IpOLF
1276	75	6.8	690	4	BI579655	BI579655	RE73722.5	1349	74.5	6.8	582	6	CB390830	CB390830 OSTF141F7
1277	75	6.8	696	1	AI515444	AI515444	LD47281.5	1350	74.5	6.8	586	6	CD076416	CD076416 MA3-0001U
1278	75	6.8	697	1	AJ823800	AJ823800	AJ823800	1351	74.5	6.8	590	6	CD075584	CD075584 MA3-0001U
1279	75	6.8	702	1	AA391382	AA391382	LD10265.5	1352	74.5	6.8	601	2	BE020747	BE020747 BM24352
1280	75	6.8	702	1	AA391382	AA391382	170006000	1353	74.5	6.8	601	2	BE020747	BE020747 BM24352
1281	75	6.8	705	5	BM945961	BM945961	UT-M-EMO-	1354	74.5	6.8	603	6	CB581979	CB581979 AMGNNUC:N
1282	75	6.8	707	6	CB030281	CB030281	TGESTzyd8	1355	74.5	6.8	606	4	BI290539	BI290539 UT-R-DKO-
1283	75	6.8	709	4	BJ461213	BJ461213	BJ461213	1356	74.5	6.8	615	6	CA428479	CA428479 UT-H-PE1-
1284	75	6.8	709	8	BZ052211	BZ052211	Jnr69b10.	1357	74.5	6.8	619	7	CV057787	CV057787 rt54C05.Y
1285	75	6.8	712	4	BI577925	BI577925	RE71695.5	1358	74.5	6.8	626	7	CV049440	CV049440 EST_14757
1286	75	6.8	716	5	BM438532	BM438532	BM438532	1359	74.5	6.8	629	7	CN657797	CN657797 rt54C05.Y
1287	75	6.8	720	4	BJ484892	BJ484892	BJ484892	1360	74.5	6.8	631	4	BJ626364	BJ626364 BJ626364
1288	75	6.8	724	7	CO088472	CO088472	GR_Ba07H	1361	74.5	6.8	632	7	CK760924	CK760924 ltu01-6ms
1289	75	6.8	729	4	BG917999	BG917999	602818939	1362	74.5	6.8	632	7	CN657792	CN657792 rt54C05.Y
1290	75	6.8	730	7	CO118740	CO118740	GR_EB021	1363	74.5	6.8	633	5	BW345888	BW345888 BM345888
1291	75	6.8	753	6	CB320645	CB320645	AGENCOURT	1364	74.5	6.8	641	9	CL349976	CL349976 RPI144_31
1292	75	6.8	768	7	CV228607	CV228607	WS01910.B	1365	74.5	6.8	653	6	CB378676	CB378676 rq19F05.Y
1293	75	6.8	786	4	BI695672	BI695672	603345013	1366	74.5	6.8	653	6	CL158929	CL158929 ML1-0060T
1294	75	6.8	794	6	CD102586	CD102586	AGENCOURT	1367	74.5	6.8	658	1	AU237043	AU237043 AU237043
1295	75	6.8	796	1	AA940935	AA940935	LD23279.5	1368	74.5	6.8	666	8	AZ038998	AZ038998 RPI1-23-2
1296	75	6.8	803	9	CC926127	CC926127	LD866208a	1369	74.5	6.8	671	5	BZ073193	BZ073193 603531454
1297	75	6.8	811	5	BU299412	BU299412	603609755	1370	74.5	6.8	671	7	CV126943	CV126943 AGENCOURT
1298	75	6.8	818	5	BX890252	BX890252	EX890252	1371	74.5	6.8	677	4	BM602321	BM602321 170006870
1299	75	6.8	852	7	CV478050	CV478050	58018.1 D	1372	74.5	6.8	680	1	AL965443	AL965443 AL965443
1300	75	6.8	854	6	CC644372	CC644372	QGWBR32TV	1373	74.5	6.8	685	9	CE552523	CE552523 tigr-gss-
1301	75	6.8	884	9	CD379869	CD379869	PTMM05038	1374	74.5	6.8	691	5	BU415707	BU415707 603669232
1302	75	6.8	881	1	AL666684	AL666684	AL666684	1375	74.5	6.8	692	7	CN321687	CN321687 AGENCOURT
1303	75	6.8	888	7	CF585286	CF585286	AGENCOURT	1376	74.5	6.8	693	6	CA216394	CA216394 SCRLFL402
1304	75	6.8	908	8	AZ539324	AZ539324	ENTGI64TF	1377	74.5	6.8	695	6	CB251492	CB251492 818_Aedes
1305	75	6.8	924	2	CL076356	CL076356	CH216-139	1378	74.5	6.8	699	8	BZ018588	BZ018588 oeh03c11.
1306	75	6.8	935	2	BF180553	BF180553	601804365	1379	74.5	6.8	700	8	BH970842	BH970842 oed84g06.
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1309	75	6.8	965	5	BU914206	BU914206	AGENCOURT	1382	74.5	6.8	703	5	BW363301	BW363301 BM363301
1310	75	6.8	984	9	AY413906	AY413906	Mus muscu	1383	74.5	6.8	711	9	AG578448	AG578448 Mus muscu
1311	75	6.8	1010	9	CL236033	CL236033	ZMMBBb057	1384	74.5	6.8	713	8	BZ078225	BZ078225 l1e34e12.
1312	75	6.8	1056	3	CG687662	CG687662	Tetraodon	1385	74.5	6.8	718	4	BJ713176	BJ713176 AGENCOURT
1313	75	6.8	1114	4	BG675273	BG675273	602621565	1386	74.5	6.8	720	7	CV106780	CV106780 AGENCOURT
1314	75	6.8	1266	9	AG382204	AG382204	Mus muscu	1387	74.5	6.8	722	4	BJ625910	BJ625910 BJ625910
1315	75	6.8	1579	3	AK016826	AK016826	Mus muscu	1388	74.5	6.8	722	8	BZ057991	BZ057991 l1b60H07.
1316	75	6.8	1723	2	BF676063	BF676063	602084038	1389	74.5	6.8	723	8	BZ470167	BZ470167 BOAP39TR
1317	75	6.8	1934	2	BF038930	BF038930	601461743	1390	74.5	6.8	726	4	BI967228	BI967228 GW830001A
1318	75	6.8	2010	3	AK003477	AK003477	Mus muscu	1391	74.5	6.8	727	3	CNS099KX	CNS099KX Single re
1319	75	6.8	2913	3	AK033477	AK033477	Mus muscu	1392	74.5	6.8	729	9	CR2063385	CR2063385 l1kx26c09.
1320	75	6.8	2957	9	AY406850	AY406850	Mus muscu	1393	74.5	6.8	730	9	CR210584	CR210584 Forward s
1321	75	6.8	3129	9	AY406395	AY406395	Homo sapi	1394	74.5	6.8	732	3	AY432415	AY432415 Aedes aeg
1322	75	6.8	3976	9	AY418589	AY418589	Mus muscu	1395	74.5	6.8	732	8	BZ442362	BZ442362 BOA142TF
1323	74.5	6.8	280	7	CO261624	CO261624	4133923 B	1396	74.5	6.8	738	7	CV109290	CV109290 AGENCOURT





ORIGIN

Alignment Scores: 3.67e-125 Length: 669  
Pred. No.: 1089.00 Matches: 212  
Score: 1089.00  
Percent Similarity: 99.53% Conservative: 0  
Best Local Similarity: 99.53% Mismatches: 0  
Query Match: 98.82% Indels: 1  
DB: 9 Gaps: 0

US-09-989-724-387 (1-212) x AY399636 (1-669)

QY 1 MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20  
DB 1 ATGTTGGTGGCTGCTCTTTTTCGTTGAGTGCCTCATCTGCTGAATCTGTCAACCAAGT 60  
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40  
DB 61 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 120  
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60  
DB 121 GCCTGGGATACCAATGAAGTAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAA 180  
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80  
DB 181 GTTCCCAACAGAGAAGCAAGAAATTTCCCATGTCTTCTTTCATTTGCAATGTAACCCAGAG 240  
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100  
DB 241 GTATCATCTGGTTTGGTGTACAGACCTTCAAAAATACACACCTTCTCTGCTGTTGAG 300  
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120  
DB 301 GTGCAATAGCCATAAGAATGAACAAGAACCGGATCAACAATGCCCTTCTTTCTAAATGAC 360  
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140  
DB 361 CAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACCCAGGACCCATCTGTG 420  
QY 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160  
DB 421 CCATCTGGATATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 480  
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180  
DB 481 CTGATTTTATCAGGGATCTGGCAACGCTAGAAGAAAGAACAAACCAATCTGAAAGTGGAT 540  
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200  
DB 541 GACGCTGAAGATAAGTGTGAACAATGATCACAATTTGAAATGGCATCCCTCTGATCCC 600  
QY 201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212  
DB 601 CTGGACATGAAGGAGGCATATTATGATGCCTTCA 637

RESULT 2  
BG400845 792 bp mRNA linear EST 12-MAR-2001  
LOCUS 602464068F1 NIH\_MGC\_75 Homo sapiens cDNA clone IMAGE:4592296 5',  
DEFINITION mRNA sequence.  
ACCESSION BG400845  
VERSION BG400845.1 GI:13294293  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 792)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov  
Tissue Procurement: CLONTECH Laboratories, Inc.  
CDNA Library Prepared by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCMI330 row: g column: 17  
High quality sequence stop: 784.  
Location/Qualifiers  
1. .792  
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/mol\_type="mRNA"  
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/clone="IMAGE:4592296"  
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FEATURES

source

ORIGIN

Alignment Scores:  
Pred. No.: 1.26e-124 Length: 792  
Score: 1085.50 Matches: 211  
Percent Similarity: 99.06% Conservative: 0  
Best Local Similarity: 99.06% Mismatches: 1  
Query Match: 98.50% Indels: 1  
DB: 4 Gaps: 1  
US-09-989-724-387 (1-212) x BG400845 (1-792)

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DB 32 ATGTTGGTGGCTGCTCTTTTTCGTTGAGTGCCTCATCTGCTGAATCTGTCAACCAAGT 91  
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40  
DB 92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 151  
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60  
DB 152 GCCTGGGATACCAATGAAGAAATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAA 211  
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80  
DB 212 GTTCCCAACAGAGAAGCAAGAAATTTCCCATGCTTCTTGTCAATGTAACCCAGAG 271  
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100  
DB 272 GTATCATCTGGTTTGGTGTACAGACCTTCAAAAATACACACCTTCTCTGCTGTTGAG 331  
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120  
DB 332 GTGCAATCAGCCATGAAGTAAGAACAGAACCGGATCAACAATGGCTTCTTTCTTAATGAC 391  
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140  
DB 392 CAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACCCAGGACCCATCTGTG 451  
QY 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160  
DB 452 CCATCTGGATATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTA 511  
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180

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Db      512 CTGATTTTATCAGGGATCTGCACCTAGACAGAAAGAACCAACCACTCTGAAGTGGAT 571
      181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
      572 GACGCTGAAGATAAGTGTGAAGAAACATGATCAATGAAATGGATGCCCTCTGATCCC 631
      201 LeuAspMetLysGly--GlyIleLeuMetMetProSer 212
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RESULT 3
LOCUS   BI760941                870 bp    mRNA    linear    EST 25-SEP-2001
DEFINITION 603043142P1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5183554 5',
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ACCESSION BI760941
VERSION   BI760941.1 GI:15752519
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 870)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
         Email: cgapbs-remail.nih.gov
         Tissue Procurement: Life Technologies, Inc.
         cDNA Library Preparation: Life Technologies, Inc.
         DNA Sequencing by: Incyte Genomics, Inc.
         Clone distribution: MGC clone distribution information can be
         found through the I.M.A.G.E. Consortium/LLNL at:
         http://image.llnl.gov
         Plate: LUAM11458 row: c column: 11
         High quality sequence stop: 844.
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             /clone_lib="NIH_MGC_116"
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             PCMV-SPO16; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
             source anonymous pool of 3 colons, age 26 yo male, 49 yo
             female, 71 yo male colon; 46 yo male kidney, and pool of 2
             stomachs, 62 yo male and 70 yo female. Library is
             oligo-dT primed and directionally cloned (EcoRV site is
             destroyed upon cloning). Average insert size 1.4 kb,
             insert size range 1-3 kb. Library is normalized and
             enriched for full-length clones and was constructed by C.
             Gruber (Invitrogen). Research Genetics tracking code
             023. Note: this is a NIH_MGC Library."

FEATURES             source
source               1..870
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5183554"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_116"
                     /note="Organ: pooled colon, kidney, stomach; Vector:
                     PCMV-SPO16; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 3 colons, age 26 yo male, 49 yo
                     female, 71 yo male colon; 46 yo male kidney, and pool of 2
                     stomachs, 62 yo male and 70 yo female. Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon cloning). Average insert size 1.4 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was constructed by C.
                     Gruber (Invitrogen). Research Genetics tracking code
                     023. Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.:      5.24e-124      Length:      870
Score:          1081.00      Matches:    210
Percent Similarity: 99.53%      Conservative: 1
Best Local Similarity: 99.06%      Mismatches: 0
Query Match:    98.09%      Indels:     1
DB:             4             Gaps:      0

US-09-989-724-387 (1-212) x BI760941 (1-870)

Qy      2 LeuTrpLeuLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGlyAla 21
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      11 GTGTGGTGCTCTTTTCTGGTGAAGTCCATTCATGCACTCTGCAACCAAGGTGCA 70

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Qy      22 GluAsnAlaPheLysValArgLeuSerIleArgThrAlaIleuGlyAspLysAlaTyxAla 41
      Db      71 GAAATTCGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCC 130
      Qy      42 TrpAspThrAsnGluGluTyLeuPheLysAlaMetValAlaPheSerMetArgLysVal 61
      Db      131 TGGGATACCAATGAAAGATACCTCTTCAAGCGATGGTAGCTTCTCCATGAGAAAGTT 190
      Qy      62 ProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArgVal 81
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      Qy      102 GlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAspGln 121
      Db      311 CNAACGCCATAGAAATGAACAGAACGGATCAACAATGCTTCTTCTTAATGACCA 370
      Qy      122 ThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerValPro 141
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      Qy      142 IleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeuLeu 161
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      Qy      182 AlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspProLeu 201
      Db      551 GCTGAAGATAAGTGTGAACACATGATCACATTTGAAATGGCATCCCTCTGTATCCCTG 610
      Qy      202 AspMetLysGly-GlyIleLeuMetMetProSer 212
      Db      611 GACATGAAGGGAGGGCATATTAATGATGCGCTTCA 644

RESULT 4
CB139945
LOCUS   CB139945                663 bp    mRNA    linear    EST 29-JAN-2003
DEFINITION K-EST0193043 L4SNU3681 Homo sapiens cDNA clone L4SNU3681-5-H10
            5', mRNA sequence.
ACCESSION CB139945
VERSION   CB139945.1 GI:28113403
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 663)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
         Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
         Kim,Y.S.
TITLE     21C Frontier Korean EST Project 2001
JOURNAL   Unpublished (2002)
COMMENT   Contact: Kim YS
         Genome Research Center
         Korea Research Institute of Bioscience & Biotechnology
         52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
         Tel: +82-42-860-4470
         Fax: +82-42-860-4409
         Email: yongsung@mail.kribb.re.kr
         Plate: 5 row: H column: 10
         High quality sequence stop: 663.
         Location/Qualifiers
           1..663
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 Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including  
 EcoRI site by treatment of T4 RNA ligase and the first  
 strand cDNA was synthesized from oligo dT-selected mRNA by  
 priming with dT-tailed vector. The dT-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10F' by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library. After analyzing and  
 sequencing about 2,000 - 3,000 colonies in original cDNA  
 library, the abundant cDNAs were selected and amplified by  
 PCR reaction using vector region primer including T7  
 promoter as 5' primer and N(dT)14 as 3' primer. The PCR  
 products were used as template for synthesis of  
 biotinylated single stranded RNA by in vitro transcription  
 reaction. The synthesized RNA probes were hybridized with  
 antisense single stranded cDNAs prepared from original  
 library and incubated with avidin-gel. After removing  
 DNA-RNA hybrids by centrifuge, the substracted cDNA  
 libraries were constructed by transformatoin of the  
 remaining DNA into competent cells E. coli Top10F' with  
 electroporation method."

## ORIGIN

Alignment Scores:  
 Pred. No.: 8,58e-124 Length: 663  
 Score: 1078.00 Matches: 210  
 Percent Similarity: 99.53% Conservative: 0  
 Best Local Similarity: 99.53% Mismatches: 0  
 Query Match: 97.82% Indels: 1  
 DB: 6 Gaps: 0

US-09-989-724-387 (1-212) x CB139945 (1-663)

QY 1 MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20  
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 QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40  
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 DB 91 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT 150  
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 QY 41 AlaTrpAsnThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60  
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 DB 151 GCTGGGATACCAATGAAGAATACCTCTTCAAGCGCATGGTAGCTTCTCCATGAGAAA 210  
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 QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80  
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 DB 211 GTTCCACAGACAGACACAGAAATTTCCCATGCTCTACTTGTGCAATGTACCCAGAGG 270  
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 QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100  
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 QY 101 ValGlnSerAlaIleArgMetAnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120  
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 DB 331 GTGCAATCAGCCATAGATGAACAGAACCCGGATCAACAATGCCCTCTTCTTAAATGAC 390  
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 QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140  
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 LOCUS  
 DEFINITION  
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 CV028808  
 ACCESSION  
 VERSION  
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 EST.  
 KEYWORDS  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE  
 1 (bases 1 to 629)  
 AUTHORS  
 Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,  
 Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,  
 Clingingsmith,F.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,  
 Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,U., Le Peuch,C.,  
 Vandenhaute,J., Cusick,M.E., Albaladejo,J.S., Hill,D.E. and Vidal,M.  
 Human ORFeome Version 1.1: a Platform for Reverse Proteomics  
 Genome Res. (2004) In press  
 TITLE  
 JOURNAL  
 COMMENT  
 Contact: Vidal M  
 Marc Vidal Laboratory  
 Dana Farber Cancer Institute  
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
 Tel: 617 632 5180  
 Fax: 617 632 5739  
 Email: Marc.Vidal@dfci.harvard.edu  
 ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF  
 results from a PCR reaction using an MGC full-length cDNA as  
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 PCR Primers  
 FORWARD: ATGTTGTGGCTGCTCTTTTCT  
 BACKWARD: CAGAGAGGGTGAGCCTTCAT  
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 /note="Vector: mixed; The ORFs were PCR amplified from the  
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 Donor vector. Reference: MGC (Mammalian Gene Collection)  
 Program Team, Generation and Initial Analysis of more than  
 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS,  
 2002, 99(26), 16899-16903"

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,89e-122 Length: 629  
 Score: 1067.00 Matches: 205  
 Percent Similarity: 99.51% Conservativity: 0  
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 DB: 7 Gaps: 0

US-09-989-724-387 (1-212) x CV028808 (1-629)

QY 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20  
 DB 1 ATGTTGGTGGCTGCTCTTTTCTGGTACTGCCATTATGCTGAACCTCTGTCACACAGGT 60

QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40  
 DB 61 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGACAGCTCTGGGAGATAAGCATAT 120

QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60  
 DB 121 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAA 180

QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80  
 DB 181 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGCTCTTTCGAATGTAACCCAGAGG 240

QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100  
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QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAlaPheLeuAsnAsp 120  
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QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140  
 DB 361 CAATCTCGGAATTTTAAATAATCCCTTCCACATTCGACCCACCATGAGCCCATCTGTG 420

QY 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu 160  
 DB 421 CCCATCTGGATATATATTTGGTGTGATATTTGGCATCATCATGTTGCATGTGACTA 480

QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180  
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QY 201 LeuAspMetLysGlyGly 206  
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 5', mRNA sequence.  
 ACCESSION CBI37859  
 VERSION CBI37859.1  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 639)  
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,  
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and  
 Kim,Y.S.  
 TITLE 21C Frontier Korean EST Project 2001  
 JOURNAL Unpublished (2002)

COMMENT Contact: Kim YS  
 Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Eoem-dong Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409  
 Email: yongsung@mail.kribb.re.kr  
 Plate: 11 row: F column: 08  
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 Site 2: NotI; The poly (A) + RNA was dephosphorylated with  
 bacterial alkaline phosphatase (BAP) and then decapped  
 with tobacco acid pyrophosphatase (TAP). The decapped  
 intact mRNA was ligated with DNA-RNA linker including  
 EcoRI site by treatment of T4 RNA ligase and the first  
 strand cDNA was synthesized from oligo dT-selected mRNA by  
 priming with dT-tailed vector. The dT-tailed vector was  
 adjusted to have about 60nt. The cDNA vector was  
 circularized with E. coli DNA ligase after digestion of  
 EcoRI which site is also included in vector. An RNA strand  
 converted to a DNA strand by Okayama-Berg method. The  
 obtained cDNA vectors were used for transformation of  
 competent cells E. coli Top10' by electroporation method.  
 The cDNA libraries constructed by this method are  
 full-length enriched cDNA library. After analyzing and  
 sequencing about 2,000 - 3,000 colonies in original cDNA  
 library, the abundant cDNAs were selected and amplified by  
 PCR reaction using vector region primer including T7  
 promoter as 5' primer and N(dT)14 as 3' primer. The PCR  
 products were used as template for synthesis of  
 biotinylated single stranded RNA by in vitro transcription  
 reaction. The synthesized RNA probes were hybridized with  
 antisense single stranded cDNAs prepared from original  
 library and incubated with avidin-gel. After removing  
 DNA-RNA hybrids by centrifuge, the substracted cDNA  
 libraries were constructed by transfection of the  
 remaining DNA into competent cells E. coli Top10' with  
 electroporation method."

ORIGIN  
 Alignment Scores: 4,58e-121 Length: 639  
 Pred. No.: 1056.00 Matches: 203  
 Score: 1006.00 Conservativity: 0  
 Percent Similarity: 100.00% Mismatches: 0  
 Best Local Similarity: 100.00% Indels: 0  
 Query Match: 95.83% Gaps: 0  
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US-09-989-724-387 (1-212) x CBI37859 (1-639)

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QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40  
 DB 91 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGACAGCTCTGGGAGATAAGCATAT 150

QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60  
 DB 151 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAA 210



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REFERENCE
1 (bases 1 to 866)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Email: cgaaps-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHCMI367 row: 9 column: 02
High quality sequence stop: 707.
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/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggccattatggcc); Site 2: SfiI (ggccattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.: 9.23e-119 Length: 866
Score: 1039.00 Matches: 206
Percent Similarity: 97.65% Conservatives: 2
Best Local Similarity: 96.71% Mismatches: 3
Query Match: 94.28% Indels: 3
DB: 4 Gaps: 0
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Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
34 GTGTGGCTGCTCTTTTCTGGTGACTGCCATTCCTGACTGCTGACTGCTGACTGCTG 93
Qy 22 GluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyrAla 41
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
94 GMAAATGCTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATATGCC 153
Qy 42 TrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLysVal 61
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
154 TGGGATACCAATGAAGAATACCTCTTCAAGCGCATGGTAGCTTCTCCATGAGAAAAGTT 213
Qy 62 ProAsnArgGluAlaThrGluLeuSerHisValLeuLeuCysAsnValThrGlnArgVal 81
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214 CCCAACAGAGAGACACAGAAATTTCCCATGCTCTACTTTGCAATGTAAACCCAGAGGTA 273
Qy 82 SerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGluVal 101
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
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Qy 102 GlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPheLeuAsnAspGln 121
Db ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
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Qy 122 ThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerValPro 141
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394 ACTCTGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGGAGCCCATCTGTGCC 453

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Qy 142 ILeTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeuLeu 161
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Qy 162 IleLeuSerGlyIleTrpGlnArgArgLysGluAsnLysGluProSerGluValAsp 181
Db 514 ATTTTATCAGGATCTGGCAACCTAGAGAAAGACAAAGAACCACTCTGAAGTGGATGAC 573
Qy 182 AlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspProLeu 201
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Qy 202 AspMetLysGly--GlyIleLeuMetMetProSer 212
Db 633 GACATGACGGGCGAGGCATATTATTATGTCCTTCA 667
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VERSION BG429174.1 GI:13335680
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 780)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaaps-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHCMI359 row: 0 column: 07
High quality sequence stop: 718.
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/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
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3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCCGAGCGGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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Query Match: 94.01% Indels: 1
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Db 62 ATCAGAACACGCTCTGGGAGATAAGCATATAGCCTGGGATACCAATGAAGAATACCTCTTC 121
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Db 122 AAAGCGATGTAGCTTCTCCATGAGAAAAGTTCCCAACAGAGAACCAAGAAAATTTCC 181
QY 71 HisValLeuLeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspPro 90
Db 182 CATGTCTACTTTGCAATGTAACCCAGAGGGTATCATCTCTGGTTTGTGGTTACAGACCCT 241
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Db 242 TCAAAAATCACACCCCTTCCTGCTGTGTAGGTGCAATCAGCCATAAGAATGAACAAGAAC 301
QY 111 ArgIleAsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSer 130
Db 302 CGGATCAACAATGCTTCTTCTTAATGACCAACTCTGGAATTTTAAAAATCCCTTCC 361
QY 131 ThrLeuAlaProProMetAspProSerValProIleTrpIleIleIlePheGlyValIle 150
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QY 151 PheCysIleIleIleValAlaIleAlaLeuLeuIleuSerGlyIleTrpGlnArgArg 170
Db 422 TTTTGCATCATCATAGTTGCAATTGCAATTGCACTACTGATTTATCAGGGATCTGGCAACGTAGA 481
QY 171 ArgLysAsnLysGluProSerGluValAspAspAlaGluAspLysCysGluAsnMetIle 190
Db 482 AGAAGAACAAAGAACCACTGAAGTGGATGACCTGAAGATGAAGTGAAGACATGATC 541
QY 191 ThrIleGluAsnGlyIleProSerAspProLeuAspMetLysGly-GlyIleLeuMetMe 210
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QY 210 tProSer 212
Db 602 GCCTTCA 608

RESULT 10
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LOCUS mRNA sequence.
DEFINITION BG400319 BG400319.1 GI:13293767
ACCESSION EST.
VERSION BG400319.1
KEYWORDS
SOURCE NIH-MGC http://mgs.nci.nih.gov/
ORGANISM National Institutes of Health, Mammalian Gene Collection (MGC)
REFERENCE Unpublished (1999)
AUTHORS Contact: Robert Strausberg, Ph.D.
TITLE Email: cgabs-r@mail.nih.gov
JOURNAL Tissue Procurement: CLONTECH Laboratories, Inc.
COMMENT CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: L1CM1331 row: C column: 08
High quality sequence stop: 711.
Location/Qualifiers
1..791
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4592575"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_75"
/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1:
SfiI (ggcgcctcgcc); Site 2: SfiI (ggcattatggcc); 5' and
3' adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGCGGCGGCCGACATG-dt(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.65
kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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ORIGIN

Alignment Scores:					
Pred. No.:	4.59e-118	Length:	791		
Score:	1033.00	Matches:	205		
Percent Similarity:	99.03%	Conservative:	0		
Best Local Similarity:	99.03%	Mismatches:	1		
Query Match:	93.74%	Indels:	2		
DB:	4	Gaps:	0		
US-09-989-724-387 (1-212) x BG400319 (1-791)					
QY 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20					
Db 31 ATGTTTGTGGCTGCTCTCTTTTCTGTGGTACTGCGCATTCATGCTGTCAACCCAGGT 90					
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGluAspLysAlaTyr 40					
Db 91 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGATTAAGCATAT 150					
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60					
Db 151 GCCTGGATACCAATGAAGAATACCTCTTCAAAGCGATGTAGCTTTCTCCATGAGAAA 210					
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80					
Db 211 GTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTACTTTTGAATGTAAACCCAGAG 270					
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100					
Db 271 GTATCATTTCTGGTTGTGGTTACAGACCTTCAAATAATCACACCTTCTCTGCTGTGAG 330					
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120					
Db 331 GTGCAATCAGCCATAAGAATGAACAGACCGGATCAACAATGCCTTTCTTCTAAATGAC 390					
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140					
Db 391 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGACACCCATGACCCATCTGTG 450					
QY 141 ProIleTrpIleIleIle-PheGlyValIlePheCysIleIleIleValAlaIleAlaLe 160					
Db 451 CCCATCTGGATATTATATTTCGGTGTGATATTTTGCATCATCATAGTTGCAATTCGACT 510					
QY 160 uLeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAs 180					
Db 511 ACTGAT-TTATCAGGGATCTGCAACAGTAGAAGAAAGAACAAAGAACCATCTGAAAGTGA 569					
QY 180 pAspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPr 200					
Db 570 TGACGCTGAAGATAAGTGTGAAAACATGATCATCAATTTGAAAATGGCATCCCTCTGATCC 629					
QY 200 oLeuAspMetLysGlyGly 206					
Db 630 CCTGGACATGAAGGGAGGG 648					
RESULT 11					



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BG429705      BG429705      804 bp      mRNA      linear      EST 14-MAR-2001
LOCUS         602493709F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4607499 5',
DEFINITION    mRNA sequence.
ACCESSION     BG429705
VERSION       BG429705.1 GI:13336211
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1. (bases 1 to 804)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
               Tissue Procurement: CLONTECH Laboratories, Inc.
               cDNA Library Preparation: CLONTECH Laboratories, Inc.
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LNCM1348 row: a column: 04
               High quality sequence stop: 731.
FEATURES      Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="mRNA"
                /db_xref="taxon:9606"
                /clones="IMAGE:4607499"
                /lab_host="DH10B (T1 phage-resistant)"
                /clone_lib="NIH_MGC_75"
                /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc); 5' and
                3' adaptors were used in cloning as follows: 5' adaptor
                sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                5'-ATTCTAGAGCGCGGCGGCATG-dt(30)BN-3' (where B = A,
                C, or G and N = A, C, G, or T). Average insert size 1.65
                kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
                by PCR. This library was enriched for full-length clones
                and was constructed by Clontech Laboratories (Palo Alto,
                CA). Note: this is a NIH_MGC Library."
ORIGIN
Alignment Scores:
Pred. No.:      3.52e-117      Length:      804
Score:          1026.00      Matches:    206
Percent Similarity: 96.73%      Conservative: 1
Best Local Similarity: 96.26%      Mismatches: 5
Query Match:    93.10%      Indels:    3
DB:             4      Gaps:      0

US-09-989-724-387 (1-212) x BG429705 (1-804)
Qy      1 MetLeuTrpLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db      32 ATGTGTGGTGGCTGCTTTTTCGGTACTGCCATTATGCTGAACTGTGCAACCAAGGT 91
Qy      21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db      92 GCAGAAATGCTTTTAAAGTCAGACTTAGTATCAGACAGCTCTGGGAGATAAGCATAT 151
Qy      41 AlaTrpAspThrAsnGluGluTyrlleuPheLysAlaMetValAlaPheSerMetArgLys 60
Db      152 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGTCTTCTCCATGAGAAA 211
Qy      61 ValProhenArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db      212 GTTCCCAACAGAGAAGCAACAGAATTTCCTATGCTCTTCCATGTAAACCAAGG 271
Qy      81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100

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272 GTATCATTTCTGGTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTCGTGTGTGAG 331
Qy      101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db      332 GTGCATACAGCCATAAGATGAACAGAACCGGATCAACAATGCTTCTTCTTAAATGAC 391
Qy      121 GlnThrIleuGluPheLeuLysIleProSerThrLeuAlaProMetAspProSerVal 140
Db      392 CAAACTCTGGAATTTTAAAAATCCCTTCCACACTTGCACACCCCATGAGCCCATCTGTG 451
Qy      141 ProIleTrpIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu 160
Db      452 CCATCTGGATATTATATTGTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCAC 511
Qy      161 LeuIleLeuSerGlyIleTrpGlnArgArg-ArGlyAsnLysGluProSerGluValAs 180
Db      512 CTGATTTTATCAGGATCTGGCAACGTAGAGCAAGAACAGAACCAATCTGAAGTGA 571
Qy      180 pAspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPr 200
Db      572 TGACGCTGAAGATAAGTGTGAAAAACATGATCACAATTGACAAATGGCATCCCTCTGATCC 631
Qy      200 oLeuAspMetLysGly-GlyIleLeuMetMetProSer 212
Db      632 CTG-GACATGAGGGAGGGCATATTAAATGATGCTTCA 668

RESULT 12
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LOCUS         602501524F1 NIH_MGC_75 Homo sapiens cDNA clone IMAGE:4615156 5',
DEFINITION    mRNA sequence.
ACCESSION     BG427839
VERSION       BG427839.1 GI:13334345
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens
REFERENCE     1. (bases 1 to 859)
AUTHORS       NIH-MGC http://mgc.nci.nih.gov/.
TITLE         National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL       Unpublished (1999)
COMMENT       Contact: Robert Strausberg, Ph.D.
               Email: cgaabs-x@mail.nih.gov
               Tissue Procurement: CLONTECH Laboratories, Inc.
               cDNA Library Preparation: CLONTECH Laboratories, Inc.
               DNA Sequencing by: Incyte Genomics, Inc.
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LNCM1367 row: p column: 05
               High quality sequence stop: 661.
FEATURES      Location/Qualifiers
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                /lab_host="DH10B (T1 phage-resistant)"
                /clone_lib="NIH_MGC_75"
                /note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site_1:
                SfiI (ggccattatggcc); Site_2: SfiI (ggccattatggcc); 5' and
                3' adaptors were used in cloning as follows: 5' adaptor
                sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                5'-ATTCTAGAGCGGCGGCATG-dt(30)BN-3' (where B = A,
                C, or G and N = A, C, G, or T). Average insert size 1.65
                kb (range 0.5-4.0 kb). 15/15 colonies contained inserts
                by PCR. This library was enriched for full-length clones
                and was constructed by Clontech Laboratories (Palo Alto,
                CA). Note: this is a NIH_MGC Library."
ORIGIN

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Alignment Scores:				
Pred. No.:	6.84e-117	Length:	859	
Score:	1024.00	Matches:	205	
Percent Similarity:	98.10%	Conservative:	1	
Best Local Similarity:	97.62%	Mismatches:	1	
Query Match:	92.92%	Indels:	3	
DB:	4	Gaps:	0	
US-09-989-724-387 (1-212) x BG427839 (1-859)				
QY	5	LeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGlyAlaGluAsnAla	24	
Db	1	GTCTTTTCTGGTGACTGCAATTCATGCTGAATCTGTCAACACCGGTGCAGAAAATGCT	60	
QY	25	PheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaIleValThrAspThr	44	
Db	61	TTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAAGCATATGCTGGGATACC	120	
QY	45	AsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLysValProAsnArg	64	
Db	121	ATATGAGATACCTCTTCAAGCGATGTAGCTTCTCCATGAGAAAAGTTCCCAACAGA	180	
QY	65	GluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArgValSerPheThr	84	
Db	181	GAAGCAACAGAAATTTCCCATGTCCTACTTTGCAATGTAACCCAGAGGCTATCATTTCTGG	240	
QY	85	PheValValThrAspProSerLysAsnHisThrLeuProAlaValGluValGlnSerAla	104	
Db	241	TTTGTGGTTTACAGACCTTCAAAAAATCACACCTTCCTGCTGTGAGGTGCAATCAGCC	300	
QY	105	IleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAspGlnThrLeuGlu	124	
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QY	125	PheLeuLysIleProSerThrLeuAlaProProMetAspProSerValProIleIleThrIle	144	
Db	361	TTTTTAAATAATCCTTCCACACTTGACACCCATGACCCATCTGTGCCATCTCGATT	420	
QY	145	IleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeuLeuIleLeuSer	164	
Db	421	ATTATATTTGGTGTGATATTTTGCAATCATCATATGTTGCAATGCACTACTGATTTTATCA	480	
QY	165	GlyIleTyrGlnArgArgLysAsnLysGluProSerGluValAspAlaGluAsp	184	
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QY	185	LysCysGluAsnMetIleThrIleGluAsn-GlyIleProSerAspProLeu-AspMetL	204	
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QY	204	ysGly-GlyIleLeuMetMetPro	211	
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RESULT 13				
BG433974				
LOCUS				
DEFINITION				
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mRNA sequence.				
ACCESSION				
BG433974				
VERSION				
BG433974.1 GI:13340480				
KEYWORDS				
EST.				
SOURCE				
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ORGANISM				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE				
1 (bases 1 to 782)				
AUTHORS				
NIH-MGC <a href="http://mgi.nci.nih.gov/">http://mgi.nci.nih.gov/</a>				
TITLE				
National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL				
Unpublished (1999)				
COMMENT				
Contact: Robert Strausberg, Ph.D.				
Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a>				

FEATURES

source

1..782

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:4611018"

/lab\_host="DH10B (T1 phage-resistant)"

/clone\_lib="NIH\_MGC\_75"

/note="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggccattggcc); Site 2: SfiI (ggccattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCGCATTTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.: 1.43e-116 Length: 782

Score: 1021.00 Matches: 206

Percent Similarity: 97.22% Conservative: 4

Best Local Similarity: 95.37% Mismatches: 2

Query Match: 92.65% Indels: 4

DB: 4 Gaps: 0

US-09-989-724-387 (1-212) x BG433974 (1-782)

QY 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20

Db 32 ATGTTGTGGCTGCTCTTTTCTGTGTGACTGCCATTCATGCTGTAACACAGT 91

QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40

Db 92 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGAGATAAGCATAT 151

QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60

Db 152 GCCTGGAATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAA 211

QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80

Db 212 GTTCCCAACAGAGAAGCAACAGAAATTTCCCATGCTCTACTTTGCAATGTAACCCAGAG 271

QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100

Db 272 GTATCATTTCTGTTTGTGTGTACAGACCTTCAAAAAATCACACCTTCTGCTGTGAG 331

QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120

Db 332 GTGCAATCAGCCATAAGAATGAACAAGAACCCGATCAACAATGCCTTCTTCTAAATGAC 391

QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140

Db 392 CAAACTCTGGAATTTTTTAAAAATCCCTTCCACACTTGCACTGACCCATGACCCATCTGTG 451

QY 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160

Db 452 CCCATCTGGATTATATATTTGGTGTGATATTTTGCATCATCATATGTTGCATTGCAC 511

QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp 180

Tissue Procurement: CLONTECH Laboratories, Inc.  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Plate: LLCM1357 row: c column: 19  
High quality sequence stop: 701.



/notes="Organ: kidney; Vector: pDNR-LIB (Clontech); Site 1: SfiI (ggcgctcgcc); Site 2: SfiI (ggccattatggcc); 5' and 3' adaptors used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGCGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.65 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library."

ORIGIN

Alignment Scores:

Pred. No.:	3.12e-115	Length:	736
Score:	1010.00	Matches:	204
Percent Similarity:	98.09%	Conservative:	1
Best Local Similarity:	97.61%	Mismatches:	2
Query Match:	91.65%	Indels:	3
DB:	4	Gaps:	0

US-09-989-724-387 (1-212) x BG399402 (1-736)

QY	5	LeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGlyAlaGluAsnAla	24
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QY	25	PheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaIyrAlaIrpAspThr	44
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QY	45	AsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLysValProAsnArg	64
Db	124	AATGAAGAATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAAAGTTCCCAACAGA	183
QY	65	GluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArgValSerPheTrp	84
Db	184	GAAGCAACAGAAATTTCCCATGTCTTACATTGCAATGTAACCCAGAGGGTATCATTCTGG	243
QY	85	PheValValThrAspProSerLysAsnHisThrLeuProAlaValGluValGlnSerAla	104
Db	244	TTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGCTGTTGAGGTGCAATCAGCC	303
QY	105	IleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAspGlnThrLeuGlu	124
Db	304	ATRAGAATGAACAGAACCGGATCAACATGCCCTTTCTTCTAAATGACCAACTCTGGAA	363
QY	125	PheLeuLysIleProSerThrLeuAlaProProMetAspProSerValProIleTrpIle	144
Db	364	TTTTTAAAAATCCCTTCCACACTTGACCACCCCATGACCCCATCTGTGCCCATCTGGATT	423
QY	145	IleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeuLeuIleLeuSer	164
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QY	165	GlyIleTrpGlnArgArg-LysAsnLysGluProSerGluValAspAlaGluAs	184
Db	484	GGGATCTGGCAGCGTAGAAGAAAGAACCAACCATCTGAAGTGGATGACGCTGAAGA	543
QY	184	pLysCysGluAsnMetIleThrIle-GluAsnGlyIleProSerAspProLeuAspMetL	204
Db	544	TAAGTGTGAAACATGATCACAAATTGAAAAATGGCATCCCTCTGATCCCTG-GACATGA	602
QY	204	ysGlyGlyIleLeuMetMetPro	211
Db	603	GGGAGGGCATATTAAATCATGCCT	625

Search completed: September 4, 2005, 10:01:50  
Job time : 3153 secs



86	75.5	6.9	601	4	US-09-949-016-162823	Sequence 162823,	159	73	6.6	588	4	US-09-543-681A-3813	Sequence 3813, Ap
87	75.5	6.9	859	4	US-10-029-517-103	Sequence 103, App	c 160	73	6.6	601	4	US-09-949-016-96451	Sequence 96451, A
88	75.5	6.9	1721	4	US-10-029-517-3	Sequence 3, Appli	c 161	73	6.6	601	4	US-09-949-016-96717	Sequence 96717, A
89	75.5	6.9	1804	4	US-10-029-517-17	Sequence 17, Appli	c 162	73	6.6	601	4	US-09-949-016-96983	Sequence 96983, A
90	75.5	6.9	2835	4	US-09-107-532A-1210	Sequence 1210, Ap	c 163	73	6.6	601	4	US-09-949-016-97249	Sequence 97249, A
91	75.5	6.9	2976	4	US-09-949-016-5710	Sequence 5710, Ap	c 164	73	6.6	601	4	US-09-949-016-97515	Sequence 97515, A
92	75.5	6.9	6192	2	US-08-479-537A-1	Sequence 1, Appli	c 165	73	6.6	601	4	US-09-949-016-97781	Sequence 97781, A
93	75.5	6.9	6192	3	US-09-083-116-1	Sequence 1, Appli	c 166	73	6.6	601	4	US-09-949-016-98047	Sequence 98047, A
94	75.5	6.9	6192	3	US-09-334-916A-1	Sequence 1, Appli	c 167	73	6.6	601	4	US-09-949-016-98313	Sequence 98313, A
95	75.5	6.9	7646	4	US-08-956-171B-121	Sequence 121, App	c 168	73	6.6	601	4	US-09-949-016-98579	Sequence 98579, A
96	75.5	6.9	7646	4	US-08-781-986A-121	Sequence 121, App	c 169	73	6.6	601	4	US-09-949-016-98845	Sequence 98845, A
97	75.5	6.9	9461	3	US-09-221-017B-513	Sequence 513, App	c 170	73	6.6	601	4	US-09-949-016-99111	Sequence 99111, A
98	75.5	6.9	29977	4	US-09-949-016-17452	Sequence 17452, A	c 171	73	6.6	601	4	US-09-949-016-99377	Sequence 99377, A
99	75.5	6.9	31166	4	US-09-949-016-13464	Sequence 13464, A	c 172	73	6.6	601	4	US-09-949-016-99643	Sequence 99643, A
100	75.5	6.9	41612	4	US-09-949-016-12769	Sequence 12769, A	c 173	73	6.6	601	4	US-09-949-016-99909	Sequence 99909, A
101	75.5	6.9	41639	4	US-09-949-016-12773	Sequence 12773, A	c 174	73	6.6	601	4	US-09-949-016-100175	Sequence 100175, A
102	75.5	6.9	49301	4	US-09-949-016-16296	Sequence 16296, A	c 175	73	6.6	601	4	US-09-949-016-100441	Sequence 100441, A
103	75.5	6.9	86980	4	US-09-949-016-15344	Sequence 15344, A	c 176	73	6.6	601	4	US-09-949-016-100707	Sequence 100707, A
104	75.5	6.9	194933	4	US-09-949-016-14172	Sequence 14172, A	c 177	73	6.6	601	4	US-09-949-016-101011	Sequence 101011, A
105	75	6.8	414	4	US-09-513-999C-8461	Sequence 8461, Ap	c 178	73	6.6	601	4	US-09-949-016-101277	Sequence 101277, A
106	75	6.8	601	4	US-09-949-016-59911	Sequence 59911, A	c 179	73	6.6	601	4	US-09-949-016-101543	Sequence 101543, A
107	75	6.8	3546	1	US-08-086-634-1	Sequence 1, Appli	c 180	73	6.6	601	4	US-09-949-016-101809	Sequence 101809, A
108	75	6.8	5349	4	US-09-949-016-4876	Sequence 4876, Ap	c 181	73	6.6	601	4	US-09-949-016-105820	Sequence 105820, A
109	75	6.8	5361	4	US-09-949-016-318	Sequence 318, App	c 182	73	6.6	601	4	US-09-949-016-146088	Sequence 146088, A
110	75	6.8	5373	4	US-09-023-655-1318	Sequence 1318, Ap	c 183	73	6.6	601	4	US-09-949-016-146356	Sequence 146356, A
111	75	6.8	5373	3	US-09-000-004B-3	Sequence 3, Appli	c 184	73	6.6	1002	4	US-09-919-039-257	Sequence 257, App
112	75	6.8	8827	3	US-09-245-041-1	Sequence 1, Appli	c 185	73	6.6	1354	4	US-09-477-135A-121	Sequence 121, App
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117	75	6.8	52655	4	US-09-949-016-13495	Sequence 13495, A	c 190	73	6.6	1930	4	US-09-270-767-9205	Sequence 9205, Ap
118	75	6.8	205044	4	US-09-949-016-15851	Sequence 15851, A	c 191	73	6.6	1930	4	US-09-270-767-24487	Sequence 24487, A
119	75	6.8	205044	4	US-09-949-016-15852	Sequence 15852, A	c 192	73	6.6	2103	4	US-08-933-711B-1	Sequence 1, Appli
120	75	6.8	205044	4	US-09-949-016-15853	Sequence 15853, A	c 193	73	6.6	6798	4	US-09-949-016-12102	Sequence 12102, A
121	75	6.8	223471	4	US-09-949-016-12387	Sequence 12387, A	c 194	73	6.6	6798	4	US-09-949-016-13819	Sequence 13819, A
122	75	6.8	223471	4	US-09-949-016-12724	Sequence 12724, A	c 195	73	6.6	92155	4	US-09-949-016-17484	Sequence 17484, A
123	75	6.8	223471	4	US-09-949-016-12725	Sequence 12725, A	c 196	73	6.6	98708	4	US-09-949-016-16392	Sequence 16392, A
124	74.5	6.8	601	4	US-09-949-016-59268	Sequence 59268, A	c 197	73	6.6	260247	4	US-09-949-016-13358	Sequence 13358, A
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126	74.5	6.8	36519	3	US-08-923-137-2	Sequence 2, Appli	c 199	73	6.6	818128	4	US-09-949-016-14547	Sequence 14547, A
127	74.5	6.8	119032	4	US-09-949-016-12160	Sequence 12160, A	c 200	73	6.6	818128	4	US-09-949-016-14548	Sequence 14548, A
128	74.5	6.8	119032	4	US-09-949-016-17268	Sequence 17268, A	c 201	73	6.6	818128	4	US-09-949-016-14549	Sequence 14549, A
129	74.5	6.8	192506	4	US-09-949-016-15830	Sequence 15830, A	c 202	73	6.6	818128	4	US-09-949-016-14550	Sequence 14550, A
130	74	6.7	467	4	US-09-821-976-1390	Sequence 1390, Ap	c 203	73	6.6	818128	4	US-09-949-016-14551	Sequence 14551, A
131	74	6.7	797	4	US-09-399-081A-9	Sequence 9, Appli	c 204	73	6.6	818128	4	US-09-949-016-14552	Sequence 14552, A
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133	74	6.7	60141	4	US-09-949-016-15874	Sequence 15874, A	c 206	73	6.6	818128	4	US-09-949-016-14554	Sequence 14554, A
134	74	6.7	343352	4	US-09-949-016-13498	Sequence 13498, A	c 207	73	6.6	818128	4	US-09-949-016-14555	Sequence 14555, A
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136	73.5	6.7	753	3	US-09-134-001C-1562	Sequence 1562, Ap	c 209	73	6.6	818128	4	US-09-949-016-14557	Sequence 14557, A
137	73.5	6.7	882	4	US-09-248-796A-11728	Sequence 11728, A	c 210	73	6.6	818128	4	US-09-949-016-14558	Sequence 14558, A
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140	73.5	6.7	1368	4	US-09-248-796A-3432	Sequence 3432, Ap	c 213	73	6.6	818128	4	US-09-949-016-14561	Sequence 14561, A
141	73.5	6.7	1605	4	US-09-710-279-919	Sequence 919, App	c 214	73	6.6	818128	4	US-09-949-016-14562	Sequence 14562, A
142	73.5	6.7	1689	4	US-09-489-039A-1403	Sequence 1403, Ap	c 215	73	6.6	818128	4	US-09-949-016-14564	Sequence 14564, A
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147	73.5	6.7	2625	4	US-09-654-328-1	Sequence 1, Appli	c 220	73	6.6	1230230	4	US-09-438-185A-1	Sequence 1, Appli
148	73.5	6.7	2730	4	US-09-949-016-4103	Sequence 4103, Ap	c 221	73	6.6	4403765	3	US-09-103-840A-2	Sequence 2, Appli
149	73.5	6.7	2998	4	US-09-710-279-3894	Sequence 3894, Ap	c 222	73	6.6	4411529	3	US-09-103-840A-2	Sequence 1, Appli
150	73.5	6.7	3118	4	US-09-710-279-3798	Sequence 3798, Ap	c 223	72.5	6.6	585	4	US-09-023-655-1382	Sequence 1382, Ap
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154	73.5	6.7	21978	4	US-09-949-016-16646	Sequence 16646, A	c 227	72.5	6.6	601	4	US-09-949-016-120841	Sequence 120841, A
155	73.5	6.7	41062	4	US-09-949-016-12761	Sequence 12761, A	c 228	72.5	6.6	759	4	US-10-029-517-10	Sequence 10, Appli
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232	72.5	6.6	7489	4	US-09-674-677-5	Sequence 5, Appli	Sequence 5, Appli	71	6.4	148567	4	US-10-667-442-3	Sequence 3, Appli	
233	72.5	6.6	46603	4	US-09-949-016-15636	Sequence 15636, A	Sequence 15636, A	71	6.4	198942	4	US-09-949-016-13209	Sequence 13209, A	
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c 236	72.5	6.6	218940	4	US-09-949-016-17539	Sequence 17539, A	Sequence 17539, A	c 309	70.5	6.4	1659	1	US-08-440-179-1	Sequence 1, Appli
c 237	72.5	6.6	222691	4	US-09-949-016-11762	Sequence 11762, A	Sequence 11762, A	c 310	70.5	6.4	1659	1	US-09-039-657-1	Sequence 1, Appli
c 238	72.5	6.6	222697	4	US-09-949-016-15842	Sequence 15842, A	Sequence 15842, A	c 311	70.5	6.4	1659	5	PCT-US91-02339-2	Sequence 2, Appli
239	72	6.5	577	4	US-10-029-517-14	Sequence 14, Appl	Sequence 14, Appl	70.5	6.4	1910	3	US-09-149-476-297	Sequence 297, App	
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242	72	6.5	591	2	US-09-083-661-2	Sequence 2, Appli	Sequence 2, Appli	70.5	6.4	2430	4	US-09-620-312D-176	Sequence 176, App	
c 243	72	6.5	601	4	US-09-949-016-64187	Sequence 64187, A	Sequence 64187, A	316	6.4	2768	4	US-09-949-016-5686	Sequence 5686, Ap	
c 244	72	6.5	1162	2	US-08-332-562A-135	Sequence 135, App	Sequence 135, App	317	6.4	2923	3	US-09-619-353-9	Sequence 9, Appli	
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246	72	6.5	1445	4	US-09-461-325-13	Sequence 13, Appl	Sequence 13, Appl	70.5	6.4	3158	4	US-09-710-279-4054	Sequence 4054, Ap	
247	72	6.5	1445	4	US-10-012-542-13	Sequence 13, Appl	Sequence 13, Appl	70.5	6.4	4079	4	US-09-016-434-1208	Sequence 1208, Ap	
248	72	6.5	1445	4	US-10-115-123-13	Sequence 13, Appl	Sequence 13, Appl	70.5	6.4	4132	4	US-09-300-958A-10	Sequence 10, Appl	
249	72	6.5	1533	4	US-09-540-236-228	Sequence 228, App	Sequence 228, App	70.5	6.4	4204	4	US-09-023-655-1292	Sequence 1292, Ap	
c 250	72	6.5	1599	2	US-08-417-495-5	Sequence 3, Appli	Sequence 3, Appli	70.5	6.4	7475	2	US-08-971-036-1	Sequence 1, Appli	
c 251	72	6.5	1599	2	US-08-284-391B-3	Sequence 3, Appli	Sequence 3, Appli	70.5	6.4	7475	3	US-09-096-570-1	Sequence 1, Appli	
c 252	72	6.5	1599	3	US-09-218-950-3	Sequence 3, Appli	Sequence 3, Appli	70.5	6.4	7475	3	US-09-265-617B-1	Sequence 1, Appli	
c 253	72	6.5	1599	4	US-08-394-388A-3	Sequence 3, Appli	Sequence 3, Appli	70.5	6.4	33155	4	US-09-949-016-16207	Sequence 16207, A	
c 254	72	6.5	1599	5	PCT-US92-01785-3	Sequence 3, Appli	Sequence 3, Appli	70.5	6.4	34001	4	US-09-596-002-18	Sequence 18, Appl	
c 255	72	6.5	1599	5	PCT-US95-00454-3	Sequence 3, Appli	Sequence 3, Appli	70.5	6.4	37580	4	US-09-949-016-16658	Sequence 16658, A	
c 256	72	6.5	1977	4	US-09-614-891-5	Sequence 5, Appli	Sequence 5, Appli	70.5	6.4	100550	4	US-09-949-016-11835	Sequence 11835, A	
c 257	72	6.5	15016	4	US-09-601-198-60	Sequence 60, Appl	Sequence 60, Appl	70.5	6.4	100551	4	US-09-949-016-16207	Sequence 16207, A	
c 258	72	6.5	183202	4	US-09-949-016-13614	Sequence 13614, A	Sequence 13614, A	70.5	6.4	251769	4	US-09-949-016-13185	Sequence 13185, A	
c 259	71.5	6.5	1419	4	US-09-543-681A-2388	Sequence 2388, Ap	Sequence 2388, Ap	70.5	6.4	251769	4	US-09-949-016-13186	Sequence 13186, A	
c 260	71.5	6.5	1788	1	US-09-041-075A-9	Sequence 9, Appli	Sequence 9, Appli	70.5	6.4	260247	4	US-09-949-016-13358	Sequence 13358, A	
c 261	71.5	6.5	6470	4	US-09-620-312D-255	Sequence 255, App	Sequence 255, App	70.5	6.4	266748	4	US-09-949-016-13187	Sequence 13187, A	
c 262	71.5	6.5	7680	4	US-09-953-318-3	Sequence 3, Appli	Sequence 3, Appli	70.5	6.4	266748	4	US-09-949-016-13188	Sequence 13188, A	
c 263	71.5	6.5	51927	4	US-09-949-016-17347	Sequence 17347, A	Sequence 17347, A	70	6.4	703	4	US-09-023-655-1097	Sequence 1097, Ap	
c 264	71.5	6.5	51927	4	US-09-949-016-17348	Sequence 17348, A	Sequence 17348, A	70	6.4	1016	4	US-09-270-767-976	Sequence 976, App	
c 265	71.5	6.5	73853	4	US-09-949-016-12029	Sequence 12029, A	Sequence 12029, A	70	6.4	1016	4	US-09-370-767-16258	Sequence 16258, A	
c 266	71.5	6.5	106380	4	US-09-949-016-17553	Sequence 17553, A	Sequence 17553, A	70	6.4	1056	4	US-09-248-796A-9572	Sequence 9572, Ap	
c 267	71.5	6.5	174259	4	US-09-949-016-11968	Sequence 11968, A	Sequence 11968, A	70	6.4	1223	4	US-09-949-016-2283	Sequence 2283, Ap	
c 268	71.5	6.5	174262	4	US-09-949-016-14259	Sequence 14259, A	Sequence 14259, A	70	6.4	1278	4	US-09-489-039A-2274	Sequence 2274, Ap	
c 269	71	6.4	601	4	US-09-949-016-50469	Sequence 50469, A	Sequence 50469, A	70	6.4	1317	4	US-09-248-796A-9956	Sequence 9956, Ap	
c 270	71	6.4	1042	4	US-09-799-451-745	Sequence 745, App	Sequence 745, App	70	6.4	3172	6	5196511-1	Patent No. 5196511	
c 271	71	6.4	1117	4	US-09-949-016-3274	Sequence 3274, Ap	Sequence 3274, Ap	70	6.4	3172	6	5196511-1	Patent No. 5196511	
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c 274	71	6.4	1683	4	US-09-943-075A-8	Sequence 8, Appli	Sequence 8, Appli	70	6.4	3303	3	US-09-409-648-6	Sequence 6, Appli	
c 275	71	6.4	1794	3	US-09-213-719-1	Sequence 1, Appli	Sequence 1, Appli	70	6.4	13508	4	US-08-956-171B-120	Sequence 120, App	
c 276	71	6.4	1794	4	US-09-949-016-97	Sequence 97, Appl	Sequence 97, Appl	70	6.4	13508	4	US-08-781-986A-120	Sequence 120, App	
c 277	71	6.4	2669	1	US-09-985-799-91	Sequence 91, Appl	Sequence 91, Appl	70	6.4	42931	4	US-08-311-731A-129	Sequence 129, App	
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c 279	71	6.4	2669	1	US-09-977-371-91	Sequence 91, Appl	Sequence 91, Appl	69.5	6.3	304	4	US-09-621-976-10937	Sequence 10937, A	
c 280	71	6.4	2669	1	US-09-977-371-101	Sequence 101, App	Sequence 101, App	69.5	6.3	359	4	US-09-389-681-294	Sequence 294, App	
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c 294	71	6.4	6000	5	PCT-US94-10166-6	Sequence 6, Appli	Sequence 6, Appli	69.5	6.3	371	4	US-09-476-496A-145	Sequence 145, App	
c 295	71	6.4	6363	4	US-09-023-655-879	Sequence 879, App	Sequence 879, App	69.5	6.3	371	4	US-09-630-940B-145	Sequence 145, App	
c 296	71	6.4	6370	3	US-09-245-041-12	Sequence 12, Appl	Sequence 12, Appl	69.5	6.3	371	4	US-09-285-479-145	Sequence 145, App	
c 297	71	6.4	6370	4	US-09-358-055B-12	Sequence 12, Appl	Sequence 12, Appl	69.5	6.3	601	4	US-09-949-016-120365	Sequence 120365, A	
c 298	71	6.4	8589	3	US-09-893-238-12	Sequence 12, Appl	Sequence 12, Appl	372	69.5	6.3	601	4	US-09-949-016-166302	Sequence 166302, A
c 299	71	6.4	8589	3	US-09-245-041-14	Sequence 14, Appl	Sequence 14, Appl	372	69.5	6.3	601	4	US-09-949-016-177703	Sequence 177703, A
c 300	71	6.4	8589	4	US-09-358-055B-14	Sequence 14, Appl	Sequence 14, Appl	69.5	6.3	842	4	US-09-270-76		





c 524	68	6.2	942	4	US-09-322-409-45	Sequence 45, Appl	597	67	6.1	1064	2	US-08-529-878B-40	Sequence 40, Appl
c 525	68	6.2	942	4	US-09-451-527-43	Sequence 43, Appl	598	67	6.1	1152	4	US-09-583-110-616	Sequence 616, App
c 526	68	6.2	942	4	US-09-451-527-45	Sequence 45, Appl	599	67	6.1	1302	4	US-09-328-352-2377	Sequence 2377, A
c 527	68	6.2	1623	4	US-09-248-796A-4215	Sequence 4215, App	600	67	6.1	1479	4	US-09-252-991A-3960	Sequence 3960, A
c 528	68	6.2	2198	4	US-09-620-312D-852	Sequence 852, App	601	67	6.1	1482	4	US-09-710-279-1831	Sequence 1831, Ap
c 529	68	6.2	3450	4	US-09-902-540-9001	Sequence 9001, Ap	602	67	6.1	1514	4	US-09-023-655-1316	Sequence 1316, Ap
c 530	68	6.2	4994	4	US-09-814-915A-52	Sequence 9001, Ap	603	67	6.1	1782	3	US-09-134-001C-1154	Sequence 1154, Ap
c 531	68	6.2	6563	3	US-09-453-702B-192	Sequence 52, Appl	604	67	6.1	1815	4	US-10-329-668-3	Sequence 3, Appl
c 532	68	6.2	7305	4	US-09-902-540-961	Sequence 192, App	c 605	67	6.1	2060	4	US-09-270-767-12193	Sequence 351, App
c 533	68	6.2	8091	4	US-09-230-652-1	Sequence 961, App	606	67	6.1	2431	3	US-09-221-017B-351	Sequence 351, App
c 534	68	6.2	8257	3	US-09-484-970B-65	Sequence 65, Appl	607	67	6.1	2523	4	US-09-715-962-1	Sequence 1, Appli
c 535	68	6.2	16365	4	US-09-949-016-16970	Sequence 16970, A	608	67	6.1	2763	4	US-09-949-016-3798	Sequence 2, Appli
c 536	68	6.2	19167	4	US-09-949-016-17174	Sequence 17174, A	609	67	6.1	3037	2	US-08-849-480A-2	Sequence 2, Appli
c 537	68	6.2	29037	4	US-09-949-016-14476	Sequence 14476, A	c 610	67	6.1	3301	4	US-09-710-279-4209	Sequence 4209, Ap
c 538	68	6.2	29043	4	US-09-949-016-14131	Sequence 14131, A	611	67	6.1	3394	4	US-09-710-279-3705	Sequence 3705, Ap
c 539	68	6.2	29769	4	US-09-949-016-16422	Sequence 16422, A	612	67	6.1	4086	4	US-09-614-221A-478	Sequence 478, App
c 540	68	6.2	35707	4	US-09-949-016-17120	Sequence 17120, A	613	67	6.1	5322	4	US-09-949-016-14845	Sequence 14845, A
c 541	68	6.2	38983	4	US-09-949-016-15700	Sequence 15700, A	614	67	6.1	7053	4	US-09-949-016-17436	Sequence 17436, A
c 542	68	6.2	51807	4	US-09-949-016-15333	Sequence 15333, A	c 615	67	6.1	7179	4	US-09-949-016-12365	Sequence 12365, A
c 543	68	6.2	70947	4	US-09-949-016-15165	Sequence 15165, A	c 616	67	6.1	10544	4	US-09-949-001-28	Sequence 28, Appl
c 544	68	6.2	157822	4	US-09-949-016-16723	Sequence 16723, A	c 617	67	6.1	10544	4	US-09-949-001-33	Sequence 33, Appl
c 545	68	6.2	254964	4	US-09-949-016-12583	Sequence 12583, A	618	67	6.1	19269	4	US-09-902-540-1175	Sequence 1175, Ap
c 546	68	6.2	254964	4	US-09-949-016-17392	Sequence 17392, A	619	67	6.1	22871	4	US-09-949-016-15688	Sequence 15688, A
c 547	68	6.2	325791	4	US-09-768-185A-1	Sequence 1, Appli	620	67	6.1	22871	4	US-09-949-016-15689	Sequence 15689, A
c 548	68	6.2	1664976	4	US-08-316-421B-1	Sequence 1, Appli	621	67	6.1	22871	4	US-09-949-016-12504	Sequence 12504, A
c 549	68	6.2	1664976	4	US-09-692-570-1	Sequence 1, Appli	622	67	6.1	27684	4	US-09-949-016-12390	Sequence 12390, A
c 550	67.5	6.1	601	4	US-09-949-016-22627	Sequence 22627, A	623	67	6.1	29614	4	US-09-949-016-12390	Sequence 12390, A
c 551	67.5	6.1	601	4	US-09-949-016-58699	Sequence 58699, A	624	67	6.1	41318	4	US-09-949-016-16225	Sequence 16225, A
c 552	67.5	6.1	601	4	US-09-949-016-82617	Sequence 82617, A	625	67	6.1	41737	4	US-09-949-016-12204	Sequence 12204, A
c 553	67.5	6.1	601	4	US-09-949-016-88746	Sequence 88746, A	626	67	6.1	41741	4	US-09-949-016-16983	Sequence 16983, A
c 554	67.5	6.1	601	4	US-09-949-016-103774	Sequence 103774, A	627	67	6.1	51835	4	US-09-949-016-17101	Sequence 17101, A
c 555	67.5	6.1	834	3	US-08-339-214-15	Sequence 15, Appl	628	67	6.1	52032	4	US-09-949-016-11789	Sequence 11789, A
c 556	67.5	6.1	925	3	US-08-339-214-46	Sequence 46, Appl	c 629	67	6.1	119211	4	US-09-596-002-40	Sequence 40, Appl
c 557	67.5	6.1	1143	4	US-09-540-236-1067	Sequence 1067, Ap	630	67	6.1	128123	4	US-09-949-016-17533	Sequence 17533, A
c 558	67.5	6.1	1623	3	US-08-339-214-25	Sequence 25, Appl	631	67	6.1	151295	4	US-09-949-016-14568	Sequence 14568, A
c 559	67.5	6.1	1696	4	US-08-774-528-151	Sequence 151, App	632	67	6.1	151295	4	US-09-949-016-14569	Sequence 14569, A
c 560	67.5	6.1	2440	4	US-09-949-016-1036	Sequence 1036, Ap	633	67	6.1	151295	4	US-09-949-016-14570	Sequence 14570, A
c 561	67.5	6.1	2440	4	US-09-949-016-1454	Sequence 1454, Ap	634	67	6.1	151295	4	US-09-949-016-14571	Sequence 14571, A
c 562	67.5	6.1	6263	4	US-09-023-655-1473	Sequence 1473, Ap	635	67	6.1	156942	4	US-09-949-016-14572	Sequence 14572, A
c 563	67.5	6.1	7072	4	US-09-220-132-24	Sequence 24, Appl	636	67	6.1	156950	4	US-09-949-016-15946	Sequence 15946, A
c 564	67.5	6.1	9674	4	US-09-949-016-13467	Sequence 13467, A	637	67	6.1	198632	4	US-09-949-016-12781	Sequence 12781, A
c 565	67.5	6.1	9901	4	US-09-949-016-15184	Sequence 15184, A	638	67	6.1	198637	4	US-09-949-016-17393	Sequence 17393, A
c 566	67.5	6.1	12122	4	US-09-949-016-16902	Sequence 16902, A	639	67	6.1	199471	4	US-09-949-016-14083	Sequence 14083, A
c 567	67.5	6.1	16287	4	US-09-949-016-17203	Sequence 17203, A	640	67	6.1	203475	4	US-09-949-016-14516	Sequence 14516, A
c 568	67.5	6.1	27600	4	US-09-949-016-15290	Sequence 15290, A	641	67	6.1	203475	4	US-09-949-016-14517	Sequence 14517, A
c 569	67.5	6.1	32616	4	US-09-949-016-13407	Sequence 13407, A	642	67	6.1	203475	4	US-09-949-016-14518	Sequence 14518, A
c 570	67.5	6.1	42376	4	US-09-949-016-16276	Sequence 16276, A	643	67	6.1	203475	4	US-09-949-016-14519	Sequence 14519, A
c 571	67.5	6.1	44499	4	US-09-949-016-12711	Sequence 12711, A	644	67	6.1	203475	4	US-09-949-016-17226	Sequence 17226, A
c 572	67.5	6.1	65792	4	US-09-596-002-31	Sequence 31, Appl	645	67	6.1	203475	4	US-09-949-016-17227	Sequence 17227, A
c 573	67.5	6.1	121068	4	US-09-949-016-14138	Sequence 14138, A	646	67	6.1	203475	4	US-09-949-016-17228	Sequence 17228, A
c 574	67.5	6.1	172677	4	US-09-949-016-13444	Sequence 13444, A	647	67	6.1	203475	4	US-09-949-016-17229	Sequence 17229, A
c 575	67.5	6.1	198632	4	US-09-949-016-12781	Sequence 12781, A	648	67	6.1	248968	4	US-09-949-016-12614	Sequence 12614, A
c 576	67.5	6.1	198637	4	US-09-949-016-17393	Sequence 17393, A	649	67	6.1	250958	4	US-09-949-016-16061	Sequence 16061, A
c 577	67.5	6.1	229354	4	US-09-705-400-64	Sequence 64, Appl	650	67	6.1	393753	4	US-09-949-016-14573	Sequence 14573, A
c 578	67.5	6.1	264358	4	US-09-949-016-15725	Sequence 15725, A	651	67	6.1	393753	4	US-09-949-016-14574	Sequence 14574, A
c 579	67.5	6.1	269223	4	US-09-596-002-41	Sequence 41, Appl	652	67	6.1	786431	4	US-09-751-389-3	Sequence 3, Appli
c 580	67	6.1	510	4	US-09-248-796A-8443	Sequence 8443, Ap	653	67	6.1	818128	4	US-09-949-016-14546	Sequence 14546, A
c 581	67	6.1	601	4	US-09-949-016-95253	Sequence 95253, A	654	67	6.1	818128	4	US-09-949-016-14547	Sequence 14547, A
c 582	67	6.1	601	4	US-09-949-016-95431	Sequence 95431, A	655	67	6.1	818128	4	US-09-949-016-14548	Sequence 14548, A
c 583	67	6.1	601	4	US-09-949-016-95609	Sequence 95609, A	656	67	6.1	818128	4	US-09-949-016-14549	Sequence 14549, A
c 584	67	6.1	601	4	US-09-949-016-95787	Sequence 95787, A	657	67	6.1	818128	4	US-09-949-016-14550	Sequence 14550, A
c 585	67	6.1	601	4	US-09-949-016-112543	Sequence 112543, A	658	67	6.1	818128	4	US-09-949-016-14551	Sequence 14551, A
c 586	67	6.1	601	4	US-09-949-016-191546	Sequence 191546, A	659	67	6.1	818128	4	US-09-949-016-14552	Sequence 14552, A
c 587	67	6.1	601	4	US-09-949-016-191724	Sequence 191724, A	660	67	6.1	818128	4	US-09-949-016-14553	Sequence 14553, A
c 588	67	6.1	601	4	US-09-949-016-191902	Sequence 191902, A	661	67	6.1	818128	4	US-09-949-016-14554	Sequence 14554, A
c 589	67	6.1	601	4	US-09-949-016-192080	Sequence 192080, A	662	67	6.1	818128	4	US-09-949-016-14555	Sequence 14555, A
c 590	67	6.1	601	4	US-08-812-046A-1	Sequence 1, Appli	663	67	6.1	818128	4	US-09-949-016-14556	Sequence 14556, A
c 591	67	6.1	660	3	US-08-812-046A-1	Sequence 1, Appli	664	67	6.1	818128	4	US-09-949-016-14557	Sequence 14557, A
c 592	67	6.1	708	4	US-09-543-681A-2848	Sequence 2848, Ap	665	67	6.1	818128	4	US-09-949-016-14558	Sequence 14558, A
c 593	67	6.1	795	4	US-09-248-796A-1027	Sequence 1027, Ap	666	67	6.1	818128	4	US-09-949-016-14559	Sequence 14559, A
c 594	67	6.1	815	4	US-09-369-247-15	Sequence 15, Appl	667	67	6.1	818128	4	US-09-949-016-14560	Sequence 14560, A
c 595	67	6.1	1053	4	US-09-107-433-555	Sequence 555, App	668	67	6.1	818128	4	US-09-949-016-14561	Sequence 14561, A
c 596	67	6.1	1060	4	US-09-270-767-13544	Sequence 13544, A	669	67	6.1	818128	4	US-09-949-016-14562	Sequence 14562, A

c 670	67	6.1	818128	4	US-09-949-016-14564	Sequence 14564, A	743	66.5	6.0	38506	4	US-09-657-440-19	Sequence 19, Appl
c 671	67	6.1	818128	4	US-09-949-016-14565	Sequence 14565, A	744	66.5	6.0	44166	4	US-09-949-016-15829	Sequence 15829, A
c 672	67	6.1	818128	4	US-09-949-016-14566	Sequence 14566, A	745	66.5	6.0	44439	4	US-09-949-016-17102	Sequence 17102, A
c 673	67	6.1	818128	4	US-09-949-016-14567	Sequence 14567, A	746	66.5	6.0	47683	4	US-09-949-016-16460	Sequence 16460, A
c 674	66.5	6.0	468	4	US-09-893-737-175	Sequence 175, App	747	66.5	6.0	47968	4	US-09-949-016-15240	Sequence 15240, A
c 675	66.5	6.0	589	4	US-09-870-767-13259	Sequence 13259, A	748	66.5	6.0	54180	4	US-09-949-016-14894	Sequence 14894, A
c 676	66.5	6.0	601	4	US-09-949-016-23864	Sequence 23864, A	749	66.5	6.0	65415	4	US-09-949-016-16699	Sequence 16699, A
c 677	66.5	6.0	601	4	US-09-949-016-52706	Sequence 52706, A	750	66.5	6.0	67156	4	US-09-949-016-12284	Sequence 12284, A
c 678	66.5	6.0	601	4	US-09-949-016-58697	Sequence 58697, A	751	66.5	6.0	67157	4	US-09-949-016-16558	Sequence 16558, A
c 679	66.5	6.0	601	4	US-09-949-016-58698	Sequence 58698, A	752	66.5	6.0	66877	4	US-09-949-016-15491	Sequence 15491, A
c 680	66.5	6.0	601	4	US-09-949-016-91216	Sequence 91216, A	753	66.5	6.0	86877	4	US-09-949-016-15492	Sequence 15492, A
c 681	66.5	6.0	601	4	US-09-949-016-91217	Sequence 91217, A	754	66.5	6.0	107421	4	US-09-949-016-15532	Sequence 15532, A
c 682	66.5	6.0	601	4	US-09-949-016-187653	Sequence 187653, A	755	66.5	6.0	154600	4	US-09-949-016-14757	Sequence 14757, A
c 683	66.5	6.0	601	4	US-09-949-016-197807	Sequence 197807, A	756	66.5	6.0	175236	4	US-09-949-016-14353	Sequence 14353, A
c 684	66.5	6.0	601	4	US-09-949-016-197854	Sequence 197854, A	757	66.5	6.0	187580	4	US-09-949-016-13266	Sequence 13266, A
c 685	66.5	6.0	897	4	US-09-248-796A-3257	Sequence 3257, App	758	66.5	6.0	212139	4	US-09-949-016-16065	Sequence 16065, A
c 686	66.5	6.0	1095	4	US-08-914-372D-6	Sequence 6, Appl	759	66.5	6.0	256287	4	US-09-949-016-14608	Sequence 14608, A
c 687	66.5	6.0	1291	4	US-09-394-142B-1	Sequence 1, Appl	760	66.5	6.0	263693	4	US-09-949-016-12386	Sequence 12386, A
c 688	66.5	6.0	1335	4	US-09-826-509-550	Sequence 550, App	761	66.5	6.0	263694	4	US-09-949-016-16915	Sequence 16915, A
c 689	66.5	6.0	1384	1	US-08-414-625-3	Sequence 3, Appl	762	66.5	6.0	1230230	4	US-09-438-185A-1	Sequence 1, Appl
c 690	66.5	6.0	1411	4	US-09-949-016-3794	Sequence 3794, App	763	66	6.0	246	4	US-09-016-434-751	Sequence 751, App
c 691	66.5	6.0	1413	4	US-09-866-028-60	Sequence 60, Appl	764	66	6.0	366	4	US-09-489-039A-5836	Sequence 5836, App
c 692	66.5	6.0	1413	4	US-09-944-457-60	Sequence 60, Appl	765	66	6.0	585	4	US-09-248-796A-8824	Sequence 8824, App
c 693	66.5	6.0	1512	2	US-08-270-581-1	Sequence 1, Appl	766	66	6.0	601	4	US-09-949-016-50483	Sequence 50483, A
c 694	66.5	6.0	1512	2	US-09-146-893-1	Sequence 1, Appl	767	66	6.0	601	4	US-09-949-016-50484	Sequence 50484, A
c 695	66.5	6.0	1569	4	US-09-949-016-3898	Sequence 3898, App	768	66	6.0	601	4	US-09-949-016-112542	Sequence 112542, A
c 696	66.5	6.0	1598	4	US-09-778-510-19	Sequence 19, Appl	769	66	6.0	601	4	US-09-949-016-202686	Sequence 202686, A
c 697	66.5	6.0	1633	3	US-09-119-788-1	Sequence 1, Appl	770	66	6.0	1023	3	US-09-724-517-3	Sequence 3, Appl
c 698	66.5	6.0	1776	4	US-09-248-796A-291	Sequence 291, App	771	66	6.0	1023	3	US-09-641-807A-3	Sequence 3, Appl
c 699	66.5	6.0	1804	3	US-09-548-372D-1	Sequence 1, Appl	772	66	6.0	1023	3	US-09-723-096-3	Sequence 3, Appl
c 700	66.5	6.0	1804	3	US-09-548-367D-1	Sequence 1, Appl	773	66	6.0	1135	4	US-09-203-958A-3	Sequence 3, Appl
c 701	66.5	6.0	1804	4	US-09-551-853D-1	Sequence 1, Appl	774	66	6.0	1146	4	US-09-540-236-1895	Sequence 1895, App
c 702	66.5	6.0	1804	4	US-09-416-901B-1	Sequence 1, Appl	775	66	6.0	1359	4	US-09-248-796A-819	Sequence 819, App
c 703	66.5	6.0	1804	4	US-09-548-376D-1	Sequence 1, Appl	776	66	6.0	1434	4	US-09-583-110-894	Sequence 894, App
c 704	66.5	6.0	1804	4	US-09-794-927A-1	Sequence 1, Appl	777	66	6.0	1449	4	US-09-107-532A-1214	Sequence 1214, App
c 705	66.5	6.0	1804	4	US-09-548-373D-1	Sequence 1, Appl	778	66	6.0	1616	4	US-09-270-767-2247	Sequence 2247, App
c 706	66.5	6.0	1804	4	US-09-795-847B-1	Sequence 1, Appl	779	66	6.0	1616	4	US-09-270-767-17529	Sequence 17529, A
c 707	66.5	6.0	1804	4	US-09-869-414-1	Sequence 1, Appl	780	66	6.0	1755	4	US-09-248-796A-1126	Sequence 1126, App
c 708	66.5	6.0	1804	4	US-09-548-366F-1	Sequence 1, Appl	781	66	6.0	1874	4	US-09-270-767-17369	Sequence 12369, A
c 709	66.5	6.0	1804	4	US-09-548-368D-1	Sequence 1, Appl	782	66	6.0	1977	4	US-09-614-891-5	Sequence 5, Appl
c 710	66.5	6.0	1804	4	US-09-794-925A-1	Sequence 1, Appl	783	66	6.0	2114	4	US-09-949-016-1960	Sequence 1960, App
c 711	66.5	6.0	1804	4	US-09-806-194A-1	Sequence 1, Appl	784	66	6.0	2198	4	US-09-949-016-5582	Sequence 5582, App
c 712	66.5	6.0	1862	3	US-08-999-723-1	Sequence 1, Appl	785	66	6.0	2203	4	US-09-917-254-29	Sequence 29, Appl
c 713	66.5	6.0	1862	3	US-09-434-427-1	Sequence 1, Appl	786	66	6.0	2203	4	US-09-949-016-596	Sequence 596, App
c 714	66.5	6.0	1863	4	US-09-886-143-1	Sequence 1, Appl	787	66	6.0	2269	3	US-09-394-645-1	Sequence 1, Appl
c 715	66.5	6.0	1868	4	US-09-949-016-5204	Sequence 5204, App	788	66	6.0	2269	3	US-09-243-560B-1	Sequence 1, Appl
c 716	66.5	6.0	1873	4	US-09-215-450-18	Sequence 18, Appl	789	66	6.0	2433	4	US-09-300-958A-24	Sequence 24, Appl
c 717	66.5	6.0	1894	4	US-09-949-016-69	Sequence 69, Appl	790	66	6.0	2498	4	US-09-620-312D-90	Sequence 90, Appl
c 718	66.5	6.0	1897	4	US-09-949-016-5146	Sequence 5146, App	791	66	6.0	2574	4	US-09-270-767-10955	Sequence 10955, A
c 719	66.5	6.0	1935	4	US-09-778-510-21	Sequence 21, Appl	792	66	6.0	2818	1	US-08-366-276-1	Sequence 1, Appl
c 720	66.5	6.0	2158	4	US-09-023-655-1073	Sequence 1073, App	793	66	6.0	2939	2	US-08-560-398-11	Sequence 11, Appl
c 721	66.5	6.0	2429	4	US-09-215-450-1	Sequence 1, Appl	794	66	6.0	3361	4	US-09-710-279-4125	Sequence 4125, App
c 722	66.5	6.0	2513	3	US-09-228-986-13	Sequence 13, Appl	795	66	6.0	3461	3	US-08-468-856B-6	Sequence 6, Appl
c 723	66.5	6.0	2513	4	US-10-101-464A-13	Sequence 13, Appl	796	66	6.0	3461	3	US-08-468-859A-6	Sequence 6, Appl
c 724	66.5	6.0	2962	1	US-09-902-540-6991	Sequence 6991, App	797	66	6.0	3708	1	US-08-185-232A-1	Sequence 1, Appl
c 725	66.5	6.0	3448	1	US-08-236-014A-3	Sequence 3, Appl	798	66	6.0	3708	1	US-08-416-523-1	Sequence 1, Appl
c 726	66.5	6.0	3448	2	US-08-596-405-3	Sequence 3, Appl	799	66	6.0	3708	3	US-08-789-478-1	Sequence 1, Appl
c 727	66.5	6.0	3448	2	US-08-877-620-3	Sequence 3, Appl	800	66	6.0	3837	3	US-09-724-517-1	Sequence 1, Appl
c 728	66.5	6.0	3448	4	US-09-287-368-3	Sequence 3, Appl	801	66	6.0	3837	3	US-09-641-807A-1	Sequence 1, Appl
c 729	66.5	6.0	3448	4	US-09-626-795-3	Sequence 3, Appl	802	66	6.0	3937	3	US-09-723-096-1	Sequence 1, Appl
c 730	66.5	6.0	4873	4	US-09-902-540-610	Sequence 610, App	803	66	6.0	4052	2	US-08-833-226-1	Sequence 1, Appl
c 731	66.5	6.0	5078	4	US-09-620-312D-565	Sequence 565, App	804	66	6.0	7620	4	US-08-956-171E-36	Sequence 36, Appl
c 732	66.5	6.0	6422	4	US-09-976-594-715	Sequence 715, App	805	66	6.0	7620	4	US-08-781-986A-36	Sequence 36, Appl
c 733	66.5	6.0	8297	4	US-09-949-016-14843	Sequence 14843, A	806	66	6.0	9350	4	US-09-949-016-16640	Sequence 16640, A
c 734	66.5	6.0	12739	4	US-09-902-540-1011	Sequence 1011, App	807	66	6.0	9365	3	US-09-608-285A-8	Sequence 8, Appl
c 735	66.5	6.0	13773	4	US-09-949-016-15536	Sequence 15536, A	808	66	6.0	9365	3	US-09-350-836B-8	Sequence 8, Appl
c 736	66.5	6.0	18613	4	US-08-956-171B-112	Sequence 112, App	809	66	6.0	9365	3	US-09-370-265-8	Sequence 8, Appl
c 737	66.5	6.0	18613	4	US-08-781-986A-112	Sequence 112, App	810	66	6.0	9365	4	US-09-557-800C-8	Sequence 8, Appl
c 738	66.5	6.0	31754	4	US-09-949-016-16451	Sequence 16451, A	811	66	6.0	9365	4	US-09-370-625A-8	Sequence 8, Appl
c 739	66.5	6.0	34047	4	US-09-949-016-13503	Sequence 13503, A	812	66	6.0	11758	4	US-09-949-016-11859	Sequence 11859, A
c 740	66.5	6.0	34047	4	US-09-949-016-13415	Sequence 13415, A	813	66	6.0	12232	4	US-09-949-016-12570	Sequence 12570, A
c 741	66.5	6.0	38506	3	US-09-320-878-19	Sequence 19, Appl	814	66	6.0	12240	4	US-09-949-016-16209	Sequence 16209, A
c 742	66.5	6.0	38506	4	US-09-141-908-1	Sequence 1, Appl	815	66	6.0	13206	3	US-08-961-527-33	Sequence 33, Appl

816	66	6.0	16236	4	US-09-949-016-16238	Sequence 16298, A	889	65.5	5.9	1635	4	US-09-489-039A-7125	Sequence 7125, Ap
817	66	6.0	19167	4	US-09-949-016-12432	Sequence 1432, A	890	65.5	5.9	1671	4	US-09-614-221A-554	Sequence 554, Ap
818	66	6.0	22407	4	US-09-596-002-16	Sequence 16, Appl	891	65.5	5.9	1683	4	US-09-866-510-23	Sequence 23, Appl
819	66	6.0	25603	4	US-09-819-607-3	Sequence 3, Appl	892	65.5	5.9	1863	4	US-09-248-796A-1704	Sequence 1704, Ap
820	66	6.0	26103	4	US-09-949-016-15685	Sequence 15685, A	893	65.5	5.9	1931	4	US-09-949-016-4419	Sequence 4419, Ap
821	66	6.0	26105	4	US-09-949-016-11879	Sequence 11879, A	894	65.5	5.9	2308	4	US-09-949-016-65	Sequence 65, Appl
822	66	6.0	28555	4	US-09-949-016-13046	Sequence 13046, A	895	65.5	5.9	2335	4	US-09-023-655-1312	Sequence 1312, Ap
823	66	6.0	33753	4	US-09-949-016-15741	Sequence 15741, A	896	65.5	5.9	2387	4	US-09-949-016-2268	Sequence 2268, Ap
824	66	6.0	33756	4	US-09-949-016-12006	Sequence 12006, A	897	65.5	5.9	2722	3	US-08-804-439A-10	Sequence 10, Appl
825	66	6.0	56678	4	US-09-949-016-17453	Sequence 17453, A	898	65.5	5.9	2722	3	US-08-720-229-10	Sequence 10, Appl
826	66	6.0	69813	4	US-09-949-016-12455	Sequence 12455, A	899	65.5	5.9	2839	5	PCT-US94-07297-38	Sequence 38, Appl
827	66	6.0	69813	4	US-09-949-016-13905	Sequence 13905, A	900	65.5	5.9	2986	4	US-09-023-655-930	Sequence 930, Appl
828	66	6.0	69813	4	US-09-949-016-13906	Sequence 13906, A	901	65.5	5.9	3116	4	US-09-710-279-3721	Sequence 3721, Ap
829	66	6.0	69833	4	US-09-949-016-12861	Sequence 12861, A	902	65.5	5.9	3321	4	US-09-866-510-13	Sequence 13, Appl
830	66	6.0	76848	4	US-09-949-016-14201	Sequence 14201, A	903	65.5	5.9	3321	4	US-09-866-510-15	Sequence 15, Appl
831	66	6.0	85869	4	US-09-949-016-12017	Sequence 12017, A	904	65.5	5.9	3321	4	US-09-866-510-17	Sequence 17, Appl
832	66	6.0	85878	4	US-09-949-016-16321	Sequence 16321, A	905	65.5	5.9	3321	4	US-09-866-510-19	Sequence 19, Appl
833	66	6.0	101981	4	US-09-949-016-13995	Sequence 13995, A	906	65.5	5.9	3321	4	US-09-866-510-21	Sequence 21, Appl
834	66	6.0	101982	4	US-09-949-016-12590	Sequence 12590, A	907	65.5	5.9	3419	4	US-09-332-5228-1	Sequence 1, Appl
835	66	6.0	103377	4	US-09-949-016-14089	Sequence 14089, A	908	65.5	5.9	3478	1	US-08-396-479B-1	Sequence 1, Appl
836	66	6.0	107140	4	US-09-949-016-14834	Sequence 14834, A	909	65.5	5.9	3478	1	US-08-818-823-1	Sequence 1, Appl
837	66	6.0	110585	4	US-09-949-016-13427	Sequence 13427, A	910	65.5	5.9	3516	4	US-09-417-197-130	Sequence 130, App
838	66	6.0	121049	4	US-09-949-016-17513	Sequence 17513, A	911	65.5	5.9	3546	4	US-09-417-197-132	Sequence 132, App
839	66	6.0	126176	4	US-09-949-016-16137	Sequence 16137, A	912	65.5	5.9	4182	1	US-08-296-014A-1	Sequence 1, Appl
840	66	6.0	126176	4	US-09-949-016-16138	Sequence 16138, A	913	65.5	5.9	4182	2	US-08-596-405-1	Sequence 1, Appl
841	66	6.0	300598	4	US-09-949-016-11868	Sequence 11868, A	914	65.5	5.9	4182	2	US-08-877-620-1	Sequence 1, Appl
842	66	6.0	302604	4	US-09-949-016-14588	Sequence 14588, A	915	65.5	5.9	4182	2	US-09-287-368-1	Sequence 1, Appl
843	66	6.0	302604	4	US-09-949-016-14589	Sequence 14589, A	916	65.5	5.9	4182	4	US-09-626-795-1	Sequence 1, Appl
844	66	6.0	308362	4	US-09-949-016-17119	Sequence 17119, A	917	65.5	5.9	4465	1	US-08-180-195-1	Sequence 1, Appl
845	65.5	5.9	425	4	US-09-541-094-10	Sequence 10, Appl	918	65.5	5.9	4465	1	US-08-477-329-1	Sequence 1, Appl
846	65.5	5.9	489	4	US-09-540-236-639	Sequence 639, App	919	65.5	5.9	4465	2	US-08-475-458-1	Sequence 1, Appl
847	65.5	5.9	601	4	US-09-949-016-74178	Sequence 74178, A	920	65.5	5.9	4465	3	US-08-980-400-1	Sequence 1, Appl
848	65.5	5.9	601	4	US-09-949-016-77181	Sequence 77181, A	921	65.5	5.9	4465	3	US-09-583-459A-1	Sequence 1, Appl
849	65.5	5.9	601	4	US-09-949-016-103775	Sequence 103775, A	922	65.5	5.9	4465	3	US-09-583-210-1	Sequence 1, Appl
850	65.5	5.9	601	4	US-09-949-016-145574	Sequence 145574, A	923	65.5	5.9	4465	3	US-09-583-449A-1	Sequence 1, Appl
851	65.5	5.9	635	4	US-10-029-517-107	Sequence 107, App	924	65.5	5.9	4465	3	US-09-435-059-1	Sequence 1, Appl
852	65.5	5.9	645	4	US-09-583-110-1974	Sequence 1974, App	925	65.5	5.9	4937	2	US-08-822-166A-3	Sequence 3, Appl
853	65.5	5.9	804	4	US-09-322-409-22	Sequence 22, Appl	926	65.5	5.9	5427	1	US-08-168-917-1	Sequence 1, Appl
854	65.5	5.9	804	4	US-09-322-409-24	Sequence 24, Appl	927	65.5	5.9	5427	1	US-08-460-510-1	Sequence 1, Appl
855	65.5	5.9	804	4	US-09-451-527-22	Sequence 22, Appl	928	65.5	5.9	5427	2	US-08-460-490-1	Sequence 1, Appl
856	65.5	5.9	804	4	US-09-451-527-22	Sequence 24, Appl	929	65.5	5.9	5427	3	US-08-462-728-3	Sequence 3, Appl
857	65.5	5.9	882	4	US-09-322-409-9	Sequence 9, Appl	930	65.5	5.9	5427	3	US-08-461-917-3	Sequence 3, Appl
858	65.5	5.9	882	4	US-09-322-409-10	Sequence 10, Appl	931	65.5	5.9	5427	4	US-08-464-436-3	Sequence 3, Appl
859	65.5	5.9	882	4	US-09-451-527-9	Sequence 9, Appl	932	65.5	5.9	5427	4	US-08-464-436-3	Sequence 3, Appl
860	65.5	5.9	882	4	US-09-451-527-10	Sequence 10, Appl	933	65.5	5.9	5427	5	PCT-US92-00730-1	Sequence 1, Appl
861	65.5	5.9	983	4	US-09-512-363-1	Sequence 1, Appl	934	65.5	5.9	5427	5	PCT-US92-00862-1	Sequence 1, Appl
862	65.5	5.9	983	4	US-09-176-200-1	Sequence 1, Appl	935	65.5	5.9	5570	4	US-09-023-655-1193	Sequence 1193, Ap
863	65.5	5.9	983	4	US-09-915-593-1	Sequence 1, Appl	936	65.5	5.9	5727	4	US-09-628-188A-1	Sequence 1, Appl
864	65.5	5.9	1013	4	US-09-322-409-6	Sequence 6, Appl	937	65.5	5.9	5999	4	US-09-949-016-13536	Sequence 13536, A
865	65.5	5.9	1013	4	US-09-322-409-8	Sequence 8, Appl	938	65.5	5.9	7742	1	US-08-221-750A-1	Sequence 1, Appl
866	65.5	5.9	1013	4	US-09-451-527-6	Sequence 6, Appl	939	65.5	5.9	18891	4	US-09-949-016-16523	Sequence 16523, A
867	65.5	5.9	1013	4	US-09-451-527-8	Sequence 8, Appl	940	65.5	5.9	30656	4	US-09-949-016-14613	Sequence 14613, A
868	65.5	5.9	1058	3	US-08-818-112-45	Sequence 45, Appl	941	65.5	5.9	44789	4	US-09-949-016-13909	Sequence 13909, A
869	65.5	5.9	1058	3	US-08-818-111-45	Sequence 45, Appl	942	65.5	5.9	51773	4	US-09-949-016-16002	Sequence 16002, A
870	65.5	5.9	1058	3	US-09-056-556-45	Sequence 45, Appl	943	65.5	5.9	52314	4	US-09-949-016-16222	Sequence 16222, A
871	65.5	5.9	1058	3	US-09-072-596-45	Sequence 45, Appl	944	65.5	5.9	68490	4	US-09-949-016-15849	Sequence 15849, A
872	65.5	5.9	1058	4	US-09-072-967-45	Sequence 45, Appl	945	65.5	5.9	95255	4	US-09-949-016-17067	Sequence 17067, A
873	65.5	5.9	1068	4	US-09-270-767-12721	Sequence 12721, A	946	65.5	5.9	99797	4	US-09-949-016-15255	Sequence 15255, A
874	65.5	5.9	1095	1	US-08-680-726A-55	Sequence 55, Appl	947	65.5	5.9	229354	4	US-09-705-400-64	Sequence 64, Appl
875	65.5	5.9	1095	3	US-09-092-409-55	Sequence 55, Appl	948	65.5	5.9	235452	4	US-09-949-016-13675	Sequence 13675, A
876	65.5	5.9	1095	3	US-08-914-372C-5	Sequence 5, Appl	949	65.5	5.9	580073	4	US-08-545-528D-1	Sequence 1, Appl
877	65.5	5.9	1095	4	US-08-914-372C-36	Sequence 36, Appl	950	65	5.9	417	4	US-09-134-000C-3173	Sequence 3173, Ap
878	65.5	5.9	1104	4	US-09-489-039A-5309	Sequence 5309, Ap	951	65	5.9	438	4	US-09-582-337-11	Sequence 11, Appl
879	65.5	5.9	1121	4	US-09-949-016-5103	Sequence 5103, Ap	952	65	5.9	566	4	US-09-270-767-17816	Sequence 17816, Ap
880	65.5	5.9	1151	3	US-09-430-503-1	Sequence 1, Appl	953	65	5.9	566	4	US-09-792-568-2	Sequence 2, Appl
881	65.5	5.9	1151	3	US-09-430-503-3	Sequence 3, Appl	954	65	5.9	570	4	US-09-792-568-4	Sequence 4, Appl
882	65.5	5.9	1151	3	US-09-430-503-5	Sequence 5, Appl	955	65	5.9	570	4	US-09-252-991A-1754	Sequence 1754, Ap
883	65.5	5.9	1151	3	US-09-430-503-7	Sequence 7, Appl	956	65	5.9	594	4	US-09-949-016-42159	Sequence 42159, A
884	65.5	5.9	1152	1	US-08-221-750A-10	Sequence 10, Appl	957	65	5.9	601	4	US-09-949-016-112544	Sequence 112544, A
885	65.5	5.9	1239	4	US-09-248-796A-6655	Sequence 6655, Ap	958	65	5.9	601	4	US-09-949-016-116427	Sequence 116427, A
886	65.5	5.9	1266	4	US-09-270-767-6939	Sequence 6939, Ap	959	65	5.9	601	4	US-09-949-016-120590	Sequence 120590, A
887	65.5	5.9	1266	4	US-09-270-767-22221	Sequence 22221, A	960	65	5.9	601	4	US-09-949-016-120590	Sequence 120590, A
888	65.5	5.9	1474	5	PCT-US94-00545-19	Sequence 19, Appl	961	65	5.9	601	4	US-09-949-016-202688	Sequence 202688, A

C 962	65	5.9	622	4	US-09-270-767-8377	Sequence 8377, Ap	c1035	65	5.9	124884	4	US-09-913-514-1	Sequence 1, Appli
C 963	65	5.9	622	4	US-09-270-767-23659	Sequence 23659, A	c1036	65	5.9	125157	4	US-09-913-514-2	Sequence 2, Appli
C 964	65	5.9	666	4	US-09-248-796A-985	Sequence 985, App	c1037	65	5.9	133719	4	US-09-949-016-15092	Sequence 15092, A
C 965	65	5.9	668	4	US-09-270-767-1567	Sequence 1567, App	c1038	65	5.9	233345	4	US-09-949-016-12656	Sequence 12656, A
C 966	65	5.9	668	4	US-09-270-767-16849	Sequence 16849, A	c1039	65	5.9	253364	4	US-09-949-016-13639	Sequence 13639, A
C 967	65	5.9	714	4	US-09-543-681A-389	Sequence 389, App	c1040	65	5.9	360470	4	US-09-949-016-13173	Sequence 13173, A
C 968	65	5.9	969	4	US-10-101-464A-297	Sequence 297, App	c1041	65	5.9	417	4	US-09-134-000C-3275	Sequence 3275, Ap
C 969	65	5.9	1145	4	US-08-956-171B-777	Sequence 777, App	c1042	64.5	5.9	453	4	US-09-248-796A-3291	Sequence 9291, Ap
C 970	65	5.9	1145	4	US-08-781-986A-777	Sequence 777, App	c1043	64.5	5.9	513	4	US-09-134-000C-906	Sequence 906, App
C 971	65	5.9	1236	4	US-09-248-796A-191	Sequence 191, App	c1044	64.5	5.9	525	4	US-09-252-991A-1824	Sequence 1824, Ap
C 972	65	5.9	1236	4	US-09-710-279-2079	Sequence 2079, Ap	c1045	64.5	5.9	601	4	US-09-949-016-89002	Sequence 89002, A
C 973	65	5.9	1305	2	US-08-332-562A-80	Sequence 80, Appl	c1046	64.5	5.9	601	4	US-09-949-016-157840	Sequence 157840
C 974	65	5.9	1328	3	US-09-370-838-24	Sequence 24, Appl	c1047	64.5	5.9	940	4	US-09-023-655-537	Sequence 537, App
C 975	65	5.9	1328	4	US-09-954-133-24	Sequence 24, Appl	c1048	64.5	5.9	1029	4	US-09-252-991A-1752	Sequence 1752, Ap
C 976	65	5.9	1347	4	US-09-252-991A-1974	Sequence 1974, Ap	c1049	64.5	5.9	1074	4	US-09-512-363-5	Sequence 5, Appli
C 977	65	5.9	1600	4	US-09-270-767-12283	Sequence 12283, A	c1050	64.5	5.9	1074	4	US-09-176-200-5	Sequence 5, Appli
C 978	65	5.9	1647	3	US-08-123-934A-7	Sequence 7, Appli	c1051	64.5	5.9	1074	4	US-09-915-593-5	Sequence 5, Appli
C 979	65	5.9	1647	4	US-09-874-628-7	Sequence 7, Appli	c1052	64.5	5.9	1074	4	US-09-169-205D-1	Sequence 1, Appli
C 980	65	5.9	1647	5	PCT-US94-10080-7	Sequence 7, Appli	c1053	64.5	5.9	1215	4	US-09-252-991A-1975	Sequence 1975, Ap
C 981	65	5.9	1731	4	US-09-326-480A-2	Sequence 2, Appli	c1054	64.5	5.9	1217	4	US-09-016-434-1164	Sequence 1164, Ap
C 982	65	5.9	1764	2	US-08-318-723-2	Sequence 2, Appli	c1055	64.5	5.9	1230	4	US-09-252-991A-2136	Sequence 2136, Ap
C 983	65	5.9	1764	2	US-09-337-507-2	Sequence 210, App	c1056	64.5	5.9	1245	4	US-09-902-540-2561	Sequence 2561, Ap
C 984	65	5.9	2022	4	US-09-620-312D-210	Sequence 210, App	c1057	64.5	5.9	1269	4	US-09-602-787A-431	Sequence 431, App
C 985	65	5.9	2160	3	US-09-382-256-15	Sequence 15, Appl	c1058	64.5	5.9	1461	4	US-09-543-681A-2028	Sequence 2028, Ap
C 986	65	5.9	2160	3	US-09-395-115-15	Sequence 15, Appl	c1059	64.5	5.9	1473	2	US-08-602-725-31	Sequence 31, Appl
C 987	65	5.9	2160	3	US-08-436-265-15	Sequence 15, Appl	c1060	64.5	5.9	1473	4	US-09-949-016-245	Sequence 245, App
C 988	65	5.9	2160	3	US-08-679-187-15	Sequence 15, Appl	c1061	64.5	5.9	1475	4	US-09-949-016-1654	Sequence 1654, Ap
C 989	65	5.9	2160	4	US-09-267-963D-15	Sequence 15, Appl	c1062	64.5	5.9	1482	4	US-09-543-681A-2582	Sequence 2582, Ap
C 990	65	5.9	2256	4	US-09-949-016-2427	Sequence 2427, Ap	c1063	64.5	5.9	1630	3	US-08-468-856B-2	Sequence 2, Appli
C 991	65	5.9	2256	4	US-09-949-016-2428	Sequence 2428, Ap	c1064	64.5	5.9	1630	3	US-08-468-859A-2	Sequence 2, Appli
C 992	65	5.9	2724	1	US-08-349-006-1	Sequence 1, Appli	c1065	64.5	5.9	1630	3	US-09-248-796A-9084	Sequence 9084, Ap
C 993	65	5.9	2724	3	US-09-171-699-1	Sequence 1, Appli	c1066	64.5	5.9	1671	4	US-08-362-525-11	Sequence 11, Appl
C 994	65	5.9	2724	5	PCT-US94-04180-1	Sequence 1, Appli	c1067	64.5	5.9	1828	3	US-08-714-918-44	Sequence 44, Appl
C 995	65	5.9	2728	1	US-07-879-617A-7	Sequence 7, Appli	c1068	64.5	5.9	1996	3	US-09-265-315-44	Sequence 44, Appl
C 996	65	5.9	2728	1	US-08-753-985-7	Sequence 7, Appli	c1069	64.5	5.9	1996	3	US-09-266-417-44	Sequence 44, Appl
C 997	65	5.9	2880	2	US-08-987-289-1	Sequence 1, Appli	c1070	64.5	5.9	1996	3	US-09-528-709-44	Sequence 44, Appl
C 998	65	5.9	2934	4	US-09-949-016-5255	Sequence 5255, Ap	c1071	64.5	5.9	1996	4	US-09-527-745-44	Sequence 44, Appl
C 999	65	5.9	3069	4	US-09-514-907A-5	Sequence 5, Appli	c1072	64.5	5.9	1996	4	US-09-902-540-7526	Sequence 7, Appli
C 1000	65	5.9	3069	4	US-09-936-994-5	Sequence 5, Appli	c1073	64.5	5.9	2094	4	US-08-952-365-7	Sequence 84, Appl
C 1001	65	5.9	3157	1	US-08-336-343A-3	Sequence 3, Appli	c1074	64.5	5.9	2094	3	US-08-714-918-84	Sequence 84, Appl
C 1002	65	5.9	3157	1	US-08-336-343A-5	Sequence 5, Appli	c1075	64.5	5.9	2225	3	US-09-265-315-84	Sequence 84, Appl
C 1003	65	5.9	3361	4	US-10-101-464A-947	Sequence 947, App	c1076	64.5	5.9	2225	3	US-09-265-315-84	Sequence 84, Appl
C 1004	65	5.9	4114	4	US-09-710-279-3572	Sequence 3572, Ap	c1077	64.5	5.9	2225	3	US-09-266-417-84	Sequence 84, Appl
C 1005	65	5.9	4260	2	US-08-658-665-38	Sequence 38, Appl	c1078	64.5	5.9	2225	4	US-09-528-709-84	Sequence 84, Appl
C 1006	65	5.9	4260	3	US-08-796-101-2	Sequence 2, Appli	c1079	64.5	5.9	2225	4	US-09-817-180-3	Sequence 3, Appli
C 1007	65	5.9	4260	3	US-09-085-273-38	Sequence 38, Appl	c1080	64.5	5.9	2225	4	US-10-003-295-3	Sequence 3, Appli
C 1008	65	5.9	4260	3	US-09-916-963-38	Sequence 38, Appl	c1081	64.5	5.9	2225	4	US-09-054-272-50	Sequence 50, Appl
C 1009	65	5.9	4768	2	US-08-658-665-41	Sequence 41, Appl	c1082	64.5	5.9	2225	4	US-09-949-016-17363	Sequence 17363, A
C 1010	65	5.9	4768	3	US-08-796-101-5	Sequence 5, Appli	c1083	64.5	5.9	2225	4	US-09-949-016-17407	Sequence 17407, A
C 1011	65	5.9	4768	3	US-09-085-273-41	Sequence 41, Appl	c1084	64.5	5.9	2225	4	US-09-949-016-16848	Sequence 16848, A
C 1012	65	5.9	4768	4	US-09-916-963-41	Sequence 41, Appl	c1085	64.5	5.9	2225	4	US-09-949-016-13607	Sequence 12607, A
C 1013	65	5.9	5234	2	US-08-658-665-73	Sequence 73, Appl	c1086	64.5	5.9	2225	4	US-09-105-537-36	Sequence 36, Appl
C 1014	65	5.9	5234	3	US-08-796-101-37	Sequence 37, Appl	c1087	64.5	5.9	2225	4	US-09-949-016-5233	Sequence 5233, Ap
C 1015	65	5.9	5234	3	US-09-085-273-73	Sequence 73, Appl	c1088	64.5	5.9	2225	4	US-09-949-016-5295	Sequence 5295, Ap
C 1016	65	5.9	5234	3	US-09-916-963-73	Sequence 73, Appl	c1089	64.5	5.9	2225	4	US-09-949-016-732	Sequence 732, App
C 1017	65	5.9	7091	2	US-08-658-665-40	Sequence 40, Appl	c1090	64.5	5.9	2225	4	US-09-453-702B-213	Sequence 213, App
C 1018	65	5.9	7091	3	US-08-796-101-4	Sequence 4, Appli	c1091	64.5	5.9	2225	4	US-09-949-016-364	Sequence 364, App
C 1019	65	5.9	7091	3	US-09-085-273-40	Sequence 40, Appl	c1092	64.5	5.9	2225	4	US-08-956-171E-32	Sequence 32, Appl
C 1020	65	5.9	7091	3	US-09-916-963-40	Sequence 40, Appl	c1093	64.5	5.9	2225	4	US-08-781-986A-32	Sequence 32, Appl
C 1021	65	5.9	20099	4	US-09-949-016-13074	Sequence 13074, A	c1094	64.5	5.9	2225	4	US-09-949-016-15809	Sequence 15809, A
C 1022	65	5.9	21048	4	US-09-949-016-16091	Sequence 16091, A	c1095	64.5	5.9	2225	4	US-09-949-016-15558	Sequence 15558, A
C 1023	65	5.9	33248	4	US-09-596-002-24	Sequence 24, Appl	c1096	64.5	5.9	2225	4	US-09-817-180-3	Sequence 3, Appli
C 1024	65	5.9	42157	4	US-08-311-731A-126	Sequence 126, App	c1097	64.5	5.9	2225	4	US-10-003-295-3	Sequence 3, Appli
C 1025	65	5.9	51671	4	US-09-949-016-12668	Sequence 12668, A	c1098	64.5	5.9	2225	4	US-09-054-272-50	Sequence 50, Appl
C 1026	65	5.9	51671	4	US-09-949-016-15962	Sequence 15962, A	c1099	64.5	5.9	2225	4	US-09-949-016-17363	Sequence 17363, A
C 1027	65	5.9	56551	4	US-09-949-016-12030	Sequence 12030, A	c1100	64.5	5.9	2225	4	US-09-949-016-17407	Sequence 17407, A
C 1028	65	5.9	71879	4	US-09-949-016-17465	Sequence 17465, A	c1101	64.5	5.9	2225	4	US-09-949-016-16848	Sequence 16848, A
C 1029	65	5.9	80632	4	US-09-949-016-12951	Sequence 12951, A	c1102	64.5	5.9	2225	4	US-09-949-016-13607	Sequence 12607, A
C 1030	65	5.9	86439	4	US-09-949-016-11945	Sequence 11945, A	c1103	64.5	5.9	2225	4	US-09-105-537-5	Sequence 5, Appli
C 1031	65	5.9	86440	4	US-09-949-016-16990	Sequence 16990, A	c1104	64.5	5.9	2225	4	US-09-949-016-12294	Sequence 12294, A
C 1032	65	5.9	100567	4	US-09-949-016-16934	Sequence 16934, A	c1105	64.5	5.9	2225	4	US-09-949-016-15726	Sequence 15726, A
C 1033	65	5.9	119211	4	US-09-596-002-40	Sequence 40, Appl	c1106	64.5	5.9	2225	4	US-09-949-016-11840	Sequence 11840, A
C 1034	65	5.9	124884	4	US-09-661-596A-76	Sequence 76, Appl	c1107	64.5	5.9	2225	4	US-09-949-016-15969	Sequence 15969, A

c1108	64.5	5.9	48974	3	US-08-920-422-17	Sequence 17, Appl	c1181	64	5.8	3084	4	US-09-129-366-19	Sequence 19, Appl
c1109	64.5	5.9	55031	4	US-09-949-016-17389	Sequence 17389, A	1182	64	5.8	3385	4	US-09-949-016-1655	Sequence 1655, Ap
c1110	64.5	5.9	55703	4	US-09-949-016-12007	Sequence 12007, A	c1183	64	5.8	3466	3	US-09-027-166-10	Sequence 10, Appl
c1111	64.5	5.9	55703	4	US-09-949-016-16781	Sequence 16781, A	1184	64	5.8	3526	3	US-09-620-312D-182	Sequence 182, App
c1112	64.5	5.9	75674	4	US-09-949-016-17597	Sequence 17597, A	1185	64	5.8	3636	3	US-09-090-535-5	Sequence 5, Appli
c1113	64.5	5.9	77586	4	US-09-949-016-13220	Sequence 13220, A	1186	64	5.8	3636	3	US-09-090-535-6	Sequence 6, Appli
c1114	64.5	5.9	77586	4	US-09-949-016-13221	Sequence 13221, A	1187	64	5.8	3636	3	US-09-090-535-7	Sequence 7, Appli
c1115	64.5	5.9	78720	4	US-09-949-016-12710	Sequence 12710, A	1188	64	5.8	3636	3	US-09-090-535-8	Sequence 8, Appli
c1116	64.5	5.9	78720	4	US-09-949-016-17283	Sequence 17283, A	1189	64	5.8	5307	4	US-09-489-039A-4533	Sequence 4533, Ap
c1117	64.5	5.9	79595	4	US-09-949-016-15318	Sequence 15318, A	c1190	64	5.8	5496	1	US-08-181-629A-2	Sequence 2, Appli
c1118	64.5	5.9	92344	4	US-09-949-016-16802	Sequence 16802, A	1191	64	5.8	6158	4	US-09-919-497-6	Sequence 6, Appli
c1119	64.5	5.9	96109	4	US-09-596-002-35	Sequence 35, Appl	1192	64	5.8	6222	4	US-09-774-528-114	Sequence 114, App
c1120	64.5	5.9	105733	4	US-09-949-016-13080	Sequence 13080, A	1193	64	5.8	6439	3	US-09-837-863-26	Sequence 26, Appl
c1121	64.5	5.9	143248	4	US-09-949-016-16652	Sequence 16652, A	1194	64	5.8	6452	3	US-09-837-863-25	Sequence 25, Appl
c1122	64.5	5.9	148794	4	US-09-949-016-12751	Sequence 12751, A	1195	64	5.8	7076	3	US-09-837-863-20	Sequence 20, Appl
c1123	64.5	5.9	162465	4	US-09-949-016-14264	Sequence 14264, A	1196	64	5.8	7076	3	US-09-837-863-21	Sequence 21, Appl
c1124	64.5	5.9	186959	4	US-09-949-016-13125	Sequence 13125, A	1197	64	5.8	7092	3	US-09-837-863-19	Sequence 19, Appl
c1125	64.5	5.9	191433	4	US-09-949-016-16144	Sequence 16144, A	1198	64	5.8	7092	3	US-09-837-863-22	Sequence 22, Appl
c1126	64.5	5.9	194933	4	US-09-949-016-14172	Sequence 14172, A	1199	64	5.8	7573	3	US-09-837-863-27	Sequence 27, Appl
c1127	64.5	5.9	194937	4	US-09-949-016-17032	Sequence 17032, A	c1200	64	5.8	7609	4	US-09-949-016-16644	Sequence 16644, A
c1128	64.5	5.9	194937	4	US-09-949-016-17033	Sequence 17033, A	c1201	64	5.8	10660	2	US-08-267-803B-8	Sequence 8, Appli
c1129	64.5	5.9	237241	4	US-09-949-016-16101	Sequence 16101, A	c1202	64	5.8	10660	2	US-09-041-886-16	Sequence 16, Appl
c1130	64.5	5.9	264206	4	US-09-949-016-12731	Sequence 12731, A	1203	64	5.8	11460	4	US-09-336-910A-1	Sequence 1, Appli
c1131	64.5	5.9	264304	4	US-09-949-016-13249	Sequence 13249, A	1204	64	5.8	12658	4	US-08-956-171B-127	Sequence 127, App
c1132	64.5	5.9	340380	4	US-09-949-016-14179	Sequence 14179, A	1205	64	5.8	12658	4	US-08-781-986A-127	Sequence 127, App
c1133	64.5	5.9	363032	4	US-09-949-016-12415	Sequence 12415, A	c1206	64	5.8	17503	4	US-09-902-540-1114	Sequence 1114, Ap
c1134	64.5	5.9	363033	4	US-09-949-016-15754	Sequence 15754, A	c1207	64	5.8	23946	4	US-09-949-016-13381	Sequence 13381, A81
c1135	64.5	5.9	422592	4	US-09-949-016-14182	Sequence 14182, A	1208	64	5.8	31111	4	US-09-949-016-15628	Sequence 15628, A
c1136	64	5.8	432	5	PCT-US94-00545-11	Sequence 11, Appl	c1209	64	5.8	34266	4	US-09-949-016-13250	Sequence 13250, A
c1137	64	5.8	531	4	US-09-540-236-1119	Sequence 1119, Ap	1210	64	5.8	40085	4	US-08-311-731A-26	Sequence 26, Appl
c1138	64	5.8	572	4	US-09-535-315-26	Sequence 26, Appl	1211	64	5.8	43577	4	US-09-949-016-16094	Sequence 16094, A
c1139	64	5.8	600	4	US-09-902-540-2524	Sequence 2524, Ap	1212	64	5.8	52202	4	US-09-949-016-17006	Sequence 17006, A
c1140	64	5.8	601	4	US-09-949-016-50158	Sequence 50158, A	c1213	64	5.8	56523	4	US-09-949-016-14297	Sequence 14297, A
c1141	64	5.8	601	4	US-09-949-016-175433	Sequence 175433, A	1214	64	5.8	57002	4	US-09-949-016-13191	Sequence 13191, A
c1142	64	5.8	732	1	US-08-145-006C-21	Sequence 21, Appl	c1215	64	5.8	61042	4	US-09-949-016-13224	Sequence 13224, A
c1143	64	5.8	732	5	PCT-US94-00545-22	Sequence 22, Appl	c1216	64	5.8	61735	4	US-09-949-016-12084	Sequence 12084, A
c1144	64	5.8	753	4	US-09-252-991A-16456	Sequence 16456, A	1217	64	5.8	69709	4	US-09-949-016-15784	Sequence 15784, A
c1145	64	5.8	840	4	US-09-540-236-1197	Sequence 1197, Ap	c1218	64	5.8	72455	4	US-09-949-016-13793	Sequence 13793, A
c1146	64	5.8	840	4	US-09-540-236-1197	Sequence 2167, Ap	1219	64	5.8	76848	4	US-09-949-016-14201	Sequence 14201, A
c1147	64	5.8	1050	3	US-09-134-001C-1167	Sequence 1167, Ap	c1220	64	5.8	79835	4	US-09-949-016-12456	Sequence 12456, A
c1148	64	5.8	1059	4	US-09-252-991A-13997	Sequence 13997, A	c1221	64	5.8	79835	4	US-09-949-016-16121	Sequence 16121, A
c1149	64	5.8	1221	4	US-09-270-767-373	Sequence 373, App	1222	64	5.8	94156	4	US-09-949-016-12388	Sequence 12388, A
c1150	64	5.8	1221	4	US-09-270-767-15655	Sequence 15655, A	1223	64	5.8	102053	4	US-09-949-016-13053	Sequence 13053, A
c1151	64	5.8	1248	4	US-09-252-991A-14140	Sequence 14140, A	1224	64	5.8	102406	4	US-09-949-016-14673	Sequence 14673, A
c1152	64	5.8	1422	4	US-09-107-532A-2045	Sequence 2045, Ap	c1225	64	5.8	104475	4	US-09-949-016-12115	Sequence 12115, A
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c1154	64	5.8	1453	6	5194600-1	Patent No. 5194600	c1227	64	5.8	111282	3	US-09-754-250-3	Sequence 3, Appli
c1155	64	5.8	1461	4	US-09-252-991A-14083	Sequence 14083, A	1228	64	5.8	119762	4	US-09-949-016-17313	Sequence 17313, A
c1156	64	5.8	1545	4	US-09-540-236-1258	Sequence 1258, Ap	1229	64	5.8	133559	4	US-09-949-016-15845	Sequence 15845, A
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c1158	64	5.8	1689	3	US-08-335-844A-6	Sequence 6, Appli	1231	64	5.8	146039	4	US-09-949-016-12449	Sequence 12449, A
c1159	64	5.8	1689	4	US-09-139-366-6	Sequence 6, Appli	1232	64	5.8	150032	4	US-09-949-016-14321	Sequence 14321, A
c1160	64	5.8	1758	4	US-09-270-767-10804	Sequence 10804, A	1233	64	5.8	174170	4	US-09-949-016-14810	Sequence 14810, A
c1161	64	5.8	1779	3	US-09-323-427-1	Sequence 1, Appli	1234	64	5.8	174170	4	US-09-949-016-14811	Sequence 14811, A
c1162	64	5.8	1779	3	US-09-323-427-2	Sequence 2, Appli	1235	64	5.8	174318	4	US-09-949-016-11880	Sequence 11880, A
c1163	64	5.8	1779	3	US-09-812-642-1	Sequence 1, Appli	1236	64	5.8	174318	4	US-09-949-016-14812	Sequence 14812, A
c1164	64	5.8	1779	3	US-09-812-642-2	Sequence 2, Appli	1237	64	5.8	174318	4	US-09-949-016-14813	Sequence 14813, A
c1165	64	5.8	1779	4	US-10-054-562A-1	Sequence 1, Appli	1238	64	5.8	22750	4	US-09-949-016-17175	Sequence 17175, A
c1166	64	5.8	1779	4	US-10-054-562A-2	Sequence 2, Appli	c1239	64	5.8	256171	4	US-09-949-016-12822	Sequence 12822, A
c1167	64	5.8	1802	4	US-09-535-315-22	Sequence 22, Appl	c1240	64	5.8	256176	4	US-09-949-016-15534	Sequence 15534, A
c1168	64	5.8	1910	3	US-09-071-709-8	Sequence 8, Appli	1241	64	5.8	343352	4	US-09-949-016-13498	Sequence 13498, A
c1169	64	5.8	2019	3	US-09-160-494-3	Sequence 3, Appli	1242	64	5.8	389504	4	US-09-949-016-11774	Sequence 11774, A
c1170	64	5.8	2019	4	US-09-252-991A-16341	Sequence 16341, A	1243	63.5	5.8	405	4	US-09-640-211A-356	Sequence 356, App
c1171	64	5.8	2476	1	US-08-749-882A-1	Sequence 1, Appli	c1244	63.5	5.8	450	4	US-09-252-991A-3580	Sequence 3580, Ap
c1172	64	5.8	2476	2	US-08-539-134-1	Sequence 1, Appli	c1245	63.5	5.8	450	4	US-09-252-991A-12611	Sequence 12611, A
c1173	64	5.8	2476	5	PCT-US95-06816-1	Sequence 1, Appli	1246	63.5	5.8	483	4	US-09-270-767-6850	Sequence 6850, Ap
c1174	64	5.8	2724	2	US-08-658-665-37	Sequence 37, Appl	1247	63.5	5.8	483	4	US-09-270-767-22132	Sequence 22132, A
c1175	64	5.8	2724	3	US-08-796-101-1	Sequence 1, Appli	1248	63.5	5.8	601	4	US-09-949-016-20206	Sequence 20206, A
c1176	64	5.8	2724	3	US-09-085-273-37	Sequence 37, Appl	c1249	63.5	5.8	601	4	US-09-949-016-80919	Sequence 80919, A
c1177	64	5.8	2724	4	US-09-916-963-37	Sequence 37, Appl	c1250	63.5	5.8	601	4	US-09-949-016-90369	Sequence 90369, A
c1178	64	5.8	2818	4	US-09-751-687-10	Sequence 10, Appl	c1251	63.5	5.8	601	4	US-09-949-016-93779	Sequence 93779, A
c1179	64	5.8	3062	4	US-10-101-464A-866	Sequence 866, App	1252	63.5	5.8	601	4	US-09-949-016-165509	Sequence 165509, A
c1180	64	5.8	3084	3	US-08-335-844A-19	Sequence 19, Appl	1253	63.5	5.8	601	4	US-09-949-016-169969	Sequence 169969, A

1254	63.5	5.8	601	4	US-09-949-016-169970	Sequence 169970,	cl327	63.5	5.8	271134	4	US-09-949-016-13705	Sequence 12705, A
c1255	63.5	5.8	601	4	US-09-949-016-177087	Sequence 177087,	c1328	63.5	5.8	278866	4	US-09-949-016-13922	Sequence 13922, A
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c1258	63.5	5.8	617	4	US-09-043-506A-9	Sequence 9, Appl	c1331	63.5	5.8	278866	4	US-09-949-016-13925	Sequence 13925, A
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1260	63.5	5.8	762	4	US-09-543-681A-3870	Sequence 3870, Ap	c1333	63.5	5.8	278866	4	US-09-949-016-14699	Sequence 14699, A
1261	63.5	5.8	900	4	US-09-248-796A-6667	Sequence 6667, Ap	c1334	63.5	5.8	278866	4	US-09-949-016-14700	Sequence 14700, A
1262	63.5	5.8	954	4	US-09-543-681A-617	Sequence 617, App	c1335	63.5	5.8	278866	4	US-09-949-016-14701	Sequence 14701, A
1263	63.5	5.8	1086	4	US-08-914-372C-2	Sequence 2, Appl	c1336	63.5	5.8	278866	4	US-09-949-016-14702	Sequence 14702, A
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1265	63.5	5.8	1086	4	US-08-914-372C-35	Sequence 35, Appl	c1338	63.5	5.8	304533	4	US-09-949-016-15371	Sequence 15371, A
1266	63.5	5.8	1242	4	US-09-248-796A-4028	Sequence 4028, Ap	c1339	63.5	5.8	304533	4	US-09-949-016-15372	Sequence 15372, A
1267	63.5	5.8	1313	4	US-09-023-655-59	Sequence 59, Appl	c1340	63.5	5.8	305491	4	US-09-949-016-17550	Sequence 17550, A
1268	63.5	5.8	1458	3	US-09-105-537-9	Sequence 9, Appl	c1341	63.5	5.8	387902	4	US-09-949-016-14543	Sequence 14543, A
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1271	63.5	5.8	1565	4	US-09-141-908-22	Sequence 22, Appl	c1344	63	5.7	345	2	US-08-284-391B-36	Sequence 36, Appl
1272	63.5	5.8	1565	4	US-09-657-440-24	Sequence 24, Appl	c1345	63	5.7	345	3	US-09-218-950-36	Sequence 36, Appl
1273	63.5	5.8	1802	4	US-09-508-370A-10	Sequence 10, Appl	c1346	63	5.7	400	4	US-08-394-388A-36	Sequence 36, Appl
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1276	63.5	5.8	1875	5	PCT-US96-10618-1	Sequence 1, Appl	1349	63	5.7	414	4	US-09-647-468-63	Sequence 63, Appl
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c1280	63.5	5.8	2046	4	US-09-543-681A-1281	Sequence 1281, Ap	c1351	63	5.7	461	4	US-09-736-457-792	Sequence 792, App
1279	63.5	5.8	2082	4	US-09-248-796A-345	Sequence 345, App	c1352	63	5.7	461	4	US-09-614-124B-792	Sequence 792, App
c1281	63.5	5.8	2166	4	US-09-134-000C-2061	Sequence 2061, Ap	c1353	63	5.7	461	4	US-09-671-325-792	Sequence 792, App
c1282	63.5	5.8	2284	4	US-09-866-028-82	Sequence 82, Appl	c1354	63	5.7	461	4	US-09-589-184-792	Sequence 792, App
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c1286	63.5	5.8	2638	3	US-09-221-017B-232	Sequence 232, App	c1358	63	5.7	479	4	US-09-614-124B-70	Sequence 70, Appl
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1289	63.5	5.8	3695	2	US-08-822-238-1	Sequence 1, Appl	c1361	63	5.7	479	4	US-09-658-824-70	Sequence 70, Appl
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c1291	63.5	5.8	5181	1	US-08-257-073-10	Sequence 10, Appl	c1363	63	5.7	513	4	US-09-248-796A-3508	Sequence 3508, Ap
1292	63.5	5.8	5255	4	US-09-949-016-16351	Sequence 16351, A	1364	63	5.7	514	4	US-09-495-050A-203	Sequence 203, App
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1306	63.5	5.8	54707	4	US-09-949-016-13120	Sequence 13120, A	1378	63	5.7	906	4	US-09-489-039A-1893	Sequence 1893, Ap
c1307	63.5	5.8	54711	4	US-09-949-016-17489	Sequence 17489, A	1379	63	5.7	909	4	US-09-107-532A-1981	Sequence 1981, Ap
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c1319	63.5	5.8	152486	4	US-09-949-016-12869	Sequence 12869, A	c1391	63	5.7	1368	3	US-08-464-000-79	Sequence 79, Appl
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1324	63.5	5.8	246230	4	US-09-949-016-17021	Sequence 17021, A	1396	63	5.7	1452	4	US-09-949-016-5251	Sequence 5251, Ap
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1412	63	5.7	2022	4	US-09-583-110-199	Sequence 199, App	c1485	63	5.7	232024	4	US-09-949-016-13477	Sequence 13477, A
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c1468	63	5.7	96327	4	US-09-949-016-16541	Sequence 16541, A							
1469	63	5.7	97989	4	US-09-949-016-13208	Sequence 13208, A							
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1471	63	5.7	119981	4	US-09-949-016-11844	Sequence 11844, A							
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## ALIGNMENTS

RESULT 1  
US-08-905-223-27  
; Sequence 27, Application US/08905223  
; Patent No. 6222029  
; GENERAL INFORMATION:  
; APPLICANT: Edwards, Jean-Baptiste D.  
; APPLICANT: Duelt, Aymeric  
; APPLICANT: Lacroix, Bruno  
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS  
; NUMBER OF SEQUENCES: 503  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Knobbe, Martens, Olson & Bear  
; STREET: 501 West Broadway  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92101-3505  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy Disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: Win95  
; SOFTWARE: Word  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/905,223  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Israelsen, Ned A.  
; REGISTRATION NUMBER: 29,655  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 235-8550  
; TELEFAX: (619) 235-0176  
; INFORMATION FOR SEQ ID NO: 27:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 848 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: DOUBLE  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: CDNA  
; ORIGINAL SOURCE:



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; ORGANISM: Homo Sapiens
; DEVELOPMENTAL STAGE: Fetal
; TISSUE TYPE: kidney
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 10.7
; OTHER INFORMATION: seq LMLFLPLVTAIHA/EL
US-08-905-223-27

Alignment Scores:
Pred. No.: 3..7e-131 Length: 848
Score: 1064.00 Matches: 208
Percent Similarity: 97.65% Conservatives: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
DB: 3 Gaps: 0

US-09-989-724-387 (1-212) x US-08-905-223-27 (1-848)
QY 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 32 ATGTTGGTCTCTCTTTTCTGGTGAAGTCCCATTCATGCTGAACCTCTGTCAACCAAGT 91
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 151
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 152 GCCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAA 211
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 212 GTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAG 271
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 272 GTATCATTCTGGTTGTGGTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 151
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 332 GTGCAATCAGCCATAGAATGAACAAGACCGGATCAACAATGCCCTTCTTCTTAATGAC 391
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 392 CAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGGACCCCATCTGTG 451
QY 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu 160
Db 452 CCCATCTGGATTATATATTGTGGTGATATTTTGCATCATCATATGTTGCAATTGCACATA 511
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 512 CTGATTTTATCAGGATCTGGCAACCTADAAARAAGAACCAACCACTGAAGTGGAT 571
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 572 GACGCTGAARATAAATGTGAAACATGATCACAATTGAAATGGCATCCCTCTGTATCCC 631
QY 201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212
Db 632 CTGGACATGAAGGAGGCGCATATTAATGATGCTTCA 668

RESULT 2
US-09-247-155-27
; Sequence 27, Application US/09247155A
; Patent No. 6312922
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
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; TITLE OF INVENTION: Complementary DNAs
; FILE REFERENCE: GENSET.021A
; CURRENT APPLICATION NUMBER: US/09/247,155A
; CURRENT FILING DATE: 1999-02-09
; EARLIER APPLICATION NUMBER: 60/074,121
; EARLIER FILING DATE: 1998-02-09
; EARLIER APPLICATION NUMBER: 60/081,563
; EARLIER FILING DATE: 1998-04-13
; EARLIER APPLICATION NUMBER: 60/096,116
; EARLIER FILING DATE: 1998-08-10
; EARLIER APPLICATION NUMBER: 60/099,273
; EARLIER FILING DATE: 1998-10-04
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-247-155-27

Alignment Scores:
Pred. No.: 3..7e-131 Length: 848
Score: 1064.00 Matches: 208
Percent Similarity: 97.65% Conservatives: 0
Best Local Similarity: 97.65% Mismatches: 4
Query Match: 96.55% Indels: 1
DB: 3 Gaps: 0

US-09-989-724-387 (1-212) x US-09-247-155-27 (1-848)
QY 1 MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20
Db 32 ATGTTGGTCTCTCTTTTCTGGTGAAGTCCCATTCATGCTGAACCTCTGTCAACCAAGT 91
QY 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40
Db 92 GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 151
QY 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60
Db 152 GCCTGGGATACCAATGAAGATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAA 211
QY 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80
Db 212 GTTCCCAACAGAGAAGCAACAGAAAATTTCCCATGTCTACTTTGCAATGTAACCCAGAG 271
QY 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100
Db 272 GTATCATTCTGGTTGTGGTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAGCATAT 151
QY 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120
Db 332 GTGCAATCAGCCATAGAATGAACAAGACCGGATCAACAATGCCCTTCTTCTTAATGAC 391
QY 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db 392 CAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGCACACCCATGGACCCCATCTGTG 451
QY 141 ProIleTrpIleIlePheGlyValIlePheCysIleIleValAlaIleAlaLeu 160
Db 452 CCCATCTGGATTATATATTGTGGTGATATTTTGCATCATCATATGTTGCAATTGCACATA 511
QY 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180
Db 512 CTGATTTTATCAGGATCTGGCAACCTADAAARAAGAACCAACCACTGAAGTGGAT 571
QY 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200
Db 572 GACGCTGAARATAAATGTGAAACATGATCACAATTGAAATGGCATCCCTCTGTATCCC 631
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Qy	201	Leu	Asp	Met	Lys	Gly	-Gly	Ile	Leu	Met	Met	Pro	Ser	212
Db	632	CTG	GAC	CAT	GAA	GGG	AGG	GCG	ATT	TAT	TAT	GAT	GCTTCA	668

### RESULT 3

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US-09-663-600A-27
; Sequence 27, Application US/09663600A
; Patent No. 6573068
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, Jean-Baptiste
; APPLICANT: Duclert, Aymeric
; APPLICANT: Bougueleret, Lydie
; TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
; FILE REFERENCE: 31.US3.CIP
; CURRENT APPLICATION NUMBER: US/09/663.600A
; CURRENT FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/191,997
; PRIOR FILING DATE: 1998-11-13
; PRIOR APPLICATION NUMBER: 60/066,677
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/069,957
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/074,121
; PRIOR FILING DATE: 1998-02-09
; PRIOR APPLICATION NUMBER: 60/081,563
; PRIOR FILING DATE: 1998-04-13
; PRIOR APPLICATION NUMBER: 60/096,116
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: 60/099,273
; PRIOR FILING DATE: 1998-09-04
; NUMBER OF SEQ ID NOS: 229
; SOFTWARE: Patent.pm
; SEQ ID NO 27
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-663-600A-27

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Alignment Scores:		
Pred. No.:	3.7e-131	Length:
Score:	1064.00	Matches:
Percent Similarity:	97.65%	Conservative:
Best Local Similarity:	97.65%	Mismatches:
Query Match:	96.55%	Indels:
DB:	4	Gaps:
		848
		208
		0
		4
		1
		0

US-09-989-724-387 (1-212) x US-09-663-600A-27 (1-848)

Qy	1	MetLeuTrpLeuLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly	20
Db	32	ATGTGTGGCTGCTCTTTTTCGTGGTACTGCCATTATGCTGAACCTCTGTCAACAGGT	91
Qy	21	AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr	40
Db	92	GCAGAAAATGCTTTTAAAGTGAGACTTAGTATCAGACAGCTCTGGGAGATAAAGCATAT	151
Qy	41	AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys	60
Db	152	GCGTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAA	211
Qy	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80
Db	212	GTTCCCAACAGAGAGCAACAAATTTCCCATGTCTTACTTTCGAATGTAAACCCAGGG	271
Qy	81	ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu	100
Db	272	GTAATCATCTCGTTTGTGGTTATCAGACCCCTTCAAAAAATCAACCCCTCTCGTGTGTAG	331

Qy	101	ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp	120
Db	332	GTGCAATCAGCCATAAGAATGAACAAGAACCGAGTCAACAATGCCTTCTTTCTTAATGAC	391
Qy	121	GlnThrLeuGluPheLeuLeuIleProSerThrLeuAlaProProMetAspProSerVal	140
Db	392	CAAACTCTGGAAATTTTAAAAATCCCTTCCACACTTGACACCCATGGACCCATCTGTG	451
Qy	141	ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu	160
Db	452	CCCATCTGGATTATATATTTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACATA	511
Qy	161	LeuIleLeuSerGlyIleTrpGlnArgArgLysAsnLysGluProSerGluValAsp	180
Db	512	CTGATTTTATCAGGATCTGGCAACGTAADAAAAAGAACAAAGAACCATCTCGAAGTGGAT	571
Qy	181	AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro	200
Db	572	GACCTGAARATAAKTGTGAANAACATGATACAAATGAAATGGCATCCCCCTCTGATCCC	631
Qy	201	LeuAspMetLysGly-GlyIleLeuMetMetProSer	212
Db	632	CTGACATGAAGGAGGAGGCATTAATGATGCCTTCA	668

## RESULT 4

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US-09-621-976-5
; Sequence 5, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 32..697
; NAME/KEY: sig_peptide
; LOCATION: 32..73
; OTHER INFORMATION: Von Heijne matrix
US-09-621-976-5

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Alignment Scores:		
Pred. No.:	3,7e-131	Length:
Score:	1064.00	Matches:
Percent Similarity:	97.65%	Conservative:
Best Local Similarity:	97.65%	Mismatches:
Query Match:	96.55%	Indels:
DB:	4	Gaps:
		848

US-09-989-724-387 (1-212) x US-09-621-976-5 (1-848)

Qy	1	MetLeuTrpLeuPhePheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly	20
Db	32	ATGTTGGGCTGCTCTTTTCTGGTGACTGCATTCATGCTGAACCTCTGTCAACAGGT	91
Qy	21	AlaGluAsnAlaPheIysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaIleTyr	40
Db	92	GCAGAAAAATGCTTTTAAAGTGAGACTTAGTATCAGAACAGCTCTGGGAGATAAAGCATAT	151
Qy	41	AlaTrpAspThrAsnGluGluIleTyrLeuPheIysAlaMetValAlaPheSerMetArgLys	60
Db	152	GCTCGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTCTCCATGAGAAA	211
Qy	61	ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg	80



Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200  
 Db 572 GACGCTGAARATAAATGTGAACCATGATCAATGAAATGGCATCCCTCTGATGCC 631

Qy 201 LeuAspMetLysGly-GlyIleLeuMetMetProSer 212  
 Db 632 CTGGACATGAAGGAGGAGGCATATTAAATGATGCCTTCA 668

RESULT 6  
 US-09-471-276-5  
 ; Sequence 5, Application US/09471276  
 ; Patent No. 6822072  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Duclert A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; Patent No. 6822072  
 ; FILE REFERENCE: GENSET.025CPI  
 ; CURRENT APPLICATION NUMBER: US/09/471.276  
 ; CURRENT FILING DATE: 1999-12-21  
 ; EARLIER APPLICATION NUMBER: 09/057,719  
 ; EARLIER FILING DATE: 1998-04-09  
 ; EARLIER APPLICATION NUMBER: 09/069,047  
 ; EARLIER FILING DATE: 1998-04-28  
 ; EARLIER APPLICATION NUMBER: PCT/IB99/00712  
 ; EARLIER FILING DATE: 1999-04-09  
 ; NUMBER OF SEQ ID NOS: 1622  
 ; SOFTWARE: Patent.pm  
 ; SEQ ID NO 5  
 ; LENGTH: 848  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 32...697  
 ; NAME/KEY: sig\_peptide  
 ; LOCATION: 32...73  
 ; OTHER INFORMATION: Von Heijne matrix

US-09-471-276-5  
 Alignment Scores:  
 Pred. No.: 3.7e-131 Length: 848  
 Score: 1064.00 Matches: 208  
 Percent Similarity: 97.65% Conservative: 0  
 Best Local Similarity: 97.65% Mismatches: 4  
 Query Match: 96.55% Indels: 1  
 DB: 4 Gaps: 0

US-09-989-724-387 (1-212) x US-09-471-276-5 (1-848)  
 Qy 1 MetLeuTrpLeuLeuPheLeuValThrAlaIleHisAlaGluLeuCysGlnProGly 20  
 Db 32 ATGTTGTGGCTGCTCTTTTCTGGTACTCCCATTCATGCTGAACCTGTGCAACCAAGGT 91  
 Qy 21 AlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLysAlaTyr 40  
 Db 92 GCAGAAATGCTTTTAAAGTGAGACTTAGTATCAGACAGCTCTGGAGATAAGCATAT 151  
 Qy 41 AlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMetArgLys 60  
 Db 152 GCCTGGGATACCAATGAAGATACCTCTTCAAGCGATGGTAGCTTTCTCCATGAGAAA 211  
 Qy 61 ValProAsnArgGluAlaThrGluIleSerHisValLeuLeuCysAsnValThrGlnArg 80  
 Db 212 GTTCCCCAACAGAGAAGCAACAGAAATTTCCCATGTCTTCAATGTAAACCCAGAG 271  
 Qy 81 ValSerPheTrpPheValValThrAspProSerLysAsnHisThrLeuProAlaValGlu 100  
 Db 272 GTATCATCTGGTTGGTTACAGACCTTCAAAAATATCACACCTTCTCGCTGTTGAG 331  
 Qy 101 ValGlnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAsp 120

Db 332 GTGCAATCACCCATAAGAAATGAACACGGGATCAACATGCTTCTTTCTAAATGAC 391  
 Qy 121 GlnThrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140  
 Db 392 CAAACTCTGGAATTTTAAATAATCCCTTCCACACTTGACACCCATGGACCCATCTGTG 451  
 Qy 141 ProIleTrpIleIleIlePheGlyValIlePheCysIleIleIleValAlaIleAlaLeu 160  
 Db 452 CCCATCTGGATTAATATATTGTTGTCATATTTTGCATCATCATAGTTGCAATTGCACCTA 511  
 Qy 161 LeuIleLeuSerGlyIleTrpGlnArgArgArgLysAsnLysGluProSerGluValAsp 180  
 Db 512 CTGATTTTATCAGGGATCTGGCAACGTAADAAAGAACCAAGAACCATCTGGAAGTGGAT 571  
 Qy 181 AspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGlyIleProSerAspPro 200  
 Db 572 GACGCTGAARATAAATGTGAACCATGATCAATGAAATGGCATCCCTCTGATGCC 631

RESULT 7  
 US-08-989-299-3  
 ; Sequence 3, Application US/08989299  
 ; Patent No. 6194556  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Acton, Susan L.  
 ; APPLICANT: Robinson, Keith E.  
 ; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOGY  
 ; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
 ; STREET: One Post Office Square  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: USA  
 ; ZIP: 02109-2170  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/989,299  
 ; FILING DATE: 11-DEC-1997  
 ; CLASSIFICATION: 514  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Arnold E., Beth  
 ; REGISTRATION NUMBER: 35,430  
 ; REFERENCE/DOCKET NUMBER: MIA-025.01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617-832-1000  
 ; TELEFAX: 617-832-7000  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2415 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-989-299-3

Alignment Scores:  
 Pred. No.: 3.45e-39 Length: 2415  
 Score: 376.00 Matches: 79  
 Percent Similarity: 67.27% Conservative: 32  
 Best Local Similarity: 47.88% Mismatches: 48  
 Query Match: 34.12% Indels: 6  
 DB: 3 Gaps: 3

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US-09-989-724-387 (1-212) x US-08-989-299-3 (1-2415)
QY 19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
Db 1834 CCATATGCAGACCAAGCATCAAGATGAGGATAAGCCTAAATCAGCTCTTGGAGATAAA 1893
QY 39 AlaTyrAlaTrpAspThrAsnGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
Db 1894 GCATATGAATGGAACGACCAATGAAATGTACCTGTTCGGATCATCTGTTCATATGCTATG 1953
QY 59 Arg-----LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
Db 1954 AGGCAGTACTTTTTTAAAGATAAAATCAGATGATTCTTTTGGGAGGAGGATGTGCGA 2013
QY 74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
Db 2014 GTGGCTAAATTTGAAACCAAGATCTCCTTTAATTTCTTGTCTCAGTCACCTAAAAATGTG 2073
QY 93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
Db 2074 TCTGATATCATTTCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCCCGGAGCCGTATC 2133
QY 113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
Db 2134 AATGATGCTTTTCGTCTGAATGACACAGCCTAGAGTTTCTGGGATACAGCCACACTT 2193
QY 133 AlaProPheMetAspProSerValProIleTrpIleIlePheGlyValIlePheCys 152
Db 2194 GGACCTCTTAACAGCCCCCTGTTCCATATGGCTATGTTTGGAGTTGTGATGGGA 2253
QY 153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgLys 172
Db 2254 GTGATAGTGTGGCATTGTCATCTCTGATCTTCACTGGGATCAGAGATCGGAAGAGAAA 2313
QY 173 AsnLysGluProSer 177
Db 2314 AATAAGCAAGAAGT 2328
RESULT 9
US-09-949-016-5413
; Sequence 5413, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5413
; LENGTH: 3388
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5413
Alignment Scores:
Pred. No.: 5,89e-39 Length: 3388
Score: 376.00 Matches: 79
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
DB: 4 Gaps: 3
US-09-989-724-387 (1-212) x US-09-949-016-5413 (1-3388)
QY 19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
Db 1937 CCATATGCAGACCAAGCATCAAGATGAGGATAAGCCTAAATCAGCTCTTGGAGATAAA 1996
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Qy 39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
Dy 1997 GCATATGAATGGAACGACAAATGAAATGACCTGTTCCGATCATCTGTTGCATATGCTATG 2056
Qy 59 Arg-----LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
Dy 2057 AGGCAGTACTTTTAAAGTAAATAAATCAGATGATCTTTTGGGAGGAGGATGTCGGA 2116
Qy 74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
Dy 2117 GTGGCTAATTGGAACCAAGATCTCTTAAATTTCTTTGTCATGTCACCTAAATAATGTG 2176
Qy 93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
Dy 2177 TCTGATATCATCTCTAGAACTGAAAGTTGAAAGGCCATCAGATGTCCTCGGAGCGGTATC 2236
Qy 113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
Dy 2237 AATGATGCTTTCCGCTCTGAATGAAACAGCCTAGAGTTTCTGGGGATACAGCCACACTT 2296
Qy 133 AlaProProMetAspProSerValProIleIleIlePheGlyValIlePheCys 152
Dy 2297 GGACTCTCTAACACGCCCCCTGTTCCATATGGCTGATGTTTGGAGTTGTGATGGA 2356
Qy 153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgLys 172
Dy 2357 GTGATAGTGGTTGGCTATGTCATCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAA 2416
Qy 173 AsnLysGluProSer 177
Dy 2417 AATAAGCAAGAAGT 2431
RESULT 10
US-09-989-299-1
; Sequence 1, Application US/08989299
; Patent No. 6194556
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robinson, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG
; TITLE OF INVENTION: AND THERAPEUTIC AND DIAGNOSTIC USES THEREFOR.
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109-2170
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/989,299
; FILING DATE: 11-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold E., Beth
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MTA-025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-832-1000
; TELEFAX: 617-832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3396 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: 82..2496
US-08-989-299-1
Alignment Scores: 5.91e-39 Length: 3396
Pred. No.: 376.00 Matches: 79
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
DB: 3 Gaps: 3
US-09-989-724-387 (1-212) x US-08-989-299-1 (1-3396)
Qy 19 ProGlyValAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
Dy 1915 CCATATGCAGACCAAGCATCAAGTGAGGATGAAGCTAAATCAGCTCTTTGGAGATAAA 1974
Qy 39 AlaTyrAlaTrpAspThrAsnGluGluTyrLeuPheLysAlaMetValAlaPheSerMet 58
Dy 1975 GCATATGAATGGAACGACAAATGAAATGACCTGTTCCGATCATCTGTTGCATATGCTATG 2034
Qy 59 Arg-----LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
Dy 2035 AGGCAGTACTTTTAAAGTAAATAAATCAGATGATCTTTTGGGAGGAGGATGTCGGA 2094
Qy 74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
Dy 2095 GTGGCTAATTGGAACCAAGATCTCTTAAATTTCTTTGTCATGCACCTAAATAATGTG 2154
Qy 93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
Dy 2155 TCTGATATCATCTCTAGAACTGAAAGTTGAAAGGCCATCAGGATGTCCTCGGAGCGGTATC 2214
Qy 113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
Dy 2215 AATGATGCTTTCCGCTCTGAATGAAACAGCCTAGAGTTTCTGGGGATACAGCCACACTT 2274
Qy 133 AlaProProMetAspProSerValProIleIleIlePheGlyValIlePheCys 152
Dy 2275 GGACTCTCTAACACGCCCCCTGTTCCATATGGCTGATGTTTGGAGTTGTGATGGA 2334
Qy 153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgLys 172
Dy 2335 GTGATAGTGGTTGGCTATGTCATCTGATCTTCACTGGGATCAGAGATCGGAAGAAGAAA 2394
Qy 173 AsnLysGluProSer 177
Dy 2395 AATAAGCAAGAAGT 2409
RESULT 11
US-10-158-847-141
; Sequence 141, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PE557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 141
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-158-847-141
Alignment Scores: 5.91e-39 Length: 3396
Pred. No.: 376.00 Matches: 79
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
DB: 3 Gaps: 3
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Score: 376.00 Matches: 79
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
DB: 4 Gaps: 3

US-09-989-724-387 (1-212) x US-10-158-847-141 (1-3396)

QY 19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
Db 1915 CCATATGCAGACCAAGCAAGTCAAAAGTGAGGATAAGCTAAAAATCAGCTCTTTGGAGATAA 1974
QY 39 AlaTyAlaTrpAspThrAsnGluTyLeuPheLysAlaMetValAlaPheSerMet 58
Db 1975 GCATATGAATGGAAACGACAAATGATACCTGTTCCGATCATCTGTTGCATATGCTATG 2034
QY 59 Arg-----LysValProAsnArgGluAlaThr-----GluIleSerHisValLeu 73
Db 2035 AGGCAGTACTTTTAAAGTAAAAAATCAGATGATCTTTTGGGAGGAGGATGTGCGA 2094
QY 74 LeuCyAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
Db 2095 GTGGCTAAATTTGAAACCAAGATCTCTTAAATTTCTTTGTCACTGCACCTAAAAATGTG 2154
QY 93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
Db 2155 TCTGATATCATCTTAGAACTGAAGTTGAAAGGCCATCAGGATGTCCCGAGCCGTATC 2214
QY 113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
Db 2215 AATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGATACAGCCACACTT 2274
QY 133 AlaProProMetAspProSerValProIleTrpIleIlePheGlyValIlePheCys 152
Db 2275 GGACCTCTCAACACAGCCCCCTGTTCCATATGGCTGATTGTTTGGAGTTGTGATGGGA 2334
QY 153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgLys 172
Db 2335 GTGATAGTGGTGGCAATGTCATCTTCATGATCTTCATGGGATCAGAGATCGAAGAGAAA 2394
QY 173 AsnLysGluProSer 177
Db 2395 AATAAAGCAAGAAGT 2409

RESULT 12
US-09-407-427-1
; Sequence 1, Application US/09407427
; Patent No. 6610497
; GENERAL INFORMATION:
; APPLICANT: Acton, Susan L.
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
; FILE OF INVENTION: AND DIAGNOSTIC USES THEREFOR
; FILE REFERENCE: MNI-132CP2
; CURRENT APPLICATION NUMBER: US/09/407,427
; CURRENT FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/163,648
; PRIOR FILING DATE: 1998-09-30
; PRIOR APPLICATION NUMBER: 08/989,299
; PRIOR FILING DATE: 1997-12-11
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (82)..(2496)
US-09-407-427-1
Alignment Scores:
Pred. No.: 5.91e-39 Length: 3396

Score: 376.00 Matches: 79
Percent Similarity: 67.27% Conservative: 32
Best Local Similarity: 47.88% Mismatches: 48
Query Match: 34.12% Indels: 6
DB: 4 Gaps: 3

US-09-989-724-387 (1-212) x US-09-407-427-1 (1-3396)

QY 19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
Db 1915 CCATATGCAGACCAAGCAAGTCAAAAGTGAGGATAAGCTAAAAATCAGCTCTTTGGAGATAA 1974
QY 39 AlaTyAlaTrpAspThrAsnGluTyLeuPheLysAlaMetValAlaPheSerMet 58
Db 1975 GCATATGAATGGAAACGACAAATGATACCTGTTCCGATCATCTGTTGCATATGCTATG 2034
QY 59 Arg-----LysValProAsnArgGluAlaThr-----GluIleSerHisValLeu 73
Db 2035 AGGCAGTACTTTTAAAGTAAAAAATCAGATGATCTTTTGGGAGGAGGATGTGCGA 2094
QY 74 LeuCyAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
Db 2095 GTGGCTAAATTTGAAACCAAGATCTCTTAAATTTCTTTGTCACTGCACCTAAAAATGTG 2154
QY 93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
Db 2155 TCTGATATCATCTTAGAACTGAAGTTGAAAGGCCATCAGGATGTCCCGAGCCGTATC 2214
QY 113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
Db 2215 AATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGGATACAGCCACACTT 2274
QY 133 AlaProProMetAspProSerValProIleTrpIleIlePheGlyValIlePheCys 152
Db 2275 GGACCTCTCAACACAGCCCCCTGTTCCATATGGCTGATTGTTTGGAGTTGTGATGGGA 2334
QY 153 IleIleIleValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgLys 172
Db 2335 GTGATAGTGGTGGCAATGTCATCTTCATGATCTTCATGGGATCAGAGATCGAAGAGAAA 2394
QY 173 AsnLysGluProSer 177
Db 2395 AATAAAGCAAGAAGT 2409

RESULT 13
US-10-158-847-137
; Sequence 137, Application US/10158847
; Patent No. 6592865
; GENERAL INFORMATION:
; APPLICANT: Tom Parry et al.
; TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
; FILE REFERENCE: PF557
; CURRENT APPLICATION NUMBER: US/10/158,847
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: 60/295,004
; PRIOR FILING DATE: 2001-06-04
; NUMBER OF SEQ ID NOS: 158
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 137
; LENGTH: 2920
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1707)..(1707)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (2702)..(2702)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (2749)..(2749)
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; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2757)..(2757)
; OTHER INFORMATION: n equals any amino acid
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; NAME/KEY: misc feature
; LOCATION: (2788)..(2789)
; OTHER INFORMATION: n equals any amino acid
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; NAME/KEY: misc feature
; LOCATION: (2819)..(2819)
; OTHER INFORMATION: n equals any amino acid
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2835)..(2835)
; OTHER INFORMATION: n equals any amino acid
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; NAME/KEY: misc feature
; LOCATION: (2856)..(2856)
; OTHER INFORMATION: n equals any amino acid
; US-10-158-847-137

Alignment Scores:
Pred. No.:      8.37e-37      Length:      2920
Score:          359.00      Matches:      75
Percent Similarity: 67.30%      Conservative: 32
Best Local Similarity: 47.17%      Mismatches: 46
Query Match:     32.58%      Indels:      6
DB:              4          Gaps:      3

US-09-989-724-387 (1-212) x US-10-158-847-137 (1-2920)

Qy 19 ProGlyAlaGluAsnAlaPheLysValArgLeuSerIleArgThrAlaLeuGlyAspLys 38
Db 1863 CCATATGACGACCAAGCATCAAGTGGAGTAAAGCTTAAATCAGCTCTTGGAGATAA 1922

Qy 39 AlaTyrAlaTrpAspThrAsnGluGlyTrpLeuPheLysAlaMetValAlaPheSerMet 58
Db 1923 GCATATGAATGGAACGACAAATGAAATGTACCTGTTCCGATCATCTGTTGCATATGCTATG 1982

Qy 59 Arg-----LysValProAsnArgGluAlaThr---GluIleSerHisValLeu 73
Db 1983 AGCGAGTACTTTTAAAGTAAATAAATCAGATGATCTTTTGGGGAGGAGGATGCGGA 2042

Qy 74 LeuCysAsnValThrGlnArgValSerPheTrpPheValValThrAspProSerLys--- 92
Db 2043 GTGGCTAATTGAAACCAAGAAATCTCCTTTAATTTCTTGTCACTGCACCTAAATAATGTG 2102

Qy 93 AsnHisThrLeuProAlaValGluValGlnSerAlaIleArgMetAsnLysAsnArgIle 112
Db 2103 TCTGATATCAATCTAGAACTGAAGTTGAAAAGGCCATCAGGATGTCGCGAGCGGTATC 2162

Qy 113 AsnAsnAlaPhePheLeuAsnAspGlnThrLeuGluPheLeuLysIleProSerThrLeu 132
Db 2163 AATGATGTTTCCGCTGCAATGACGACAGCCCTAGAGTTTCTGGGGATACAGCCAACTT 2222

Qy 133 AlaProMetAspProSerValProIleTrpIleIlePheGlyValIlePheCys 152
Db 2223 GGACCTCTCAACGAGCCCCCTGTTTCCATATGGCTGATGTTTGGAGTGTGATGGGA 2282

Qy 153 IleIleIleValAlaIleAlaLeuLeuLeuSerGlyIleTrpGlnArgArg 171
Db 2283 GTGATAGTGGTGGCATGTCATCTTCATCTTCATGGGATCAGAGATCGGAGAAG 2339

RESULT 14
US-09-289-349-6
; Sequence 6, Application US/09289349
; Patent No. 6277574
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Klinger, Tod, M.
```

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; APPLICANT: Azimzai, Valda
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: GENES ASSOCIATED WITH DISEASES OF THE KIDNEY
; FILE REFERENCE: PB-0010 US
; CURRENT APPLICATION NUMBER: US/09/289,349
; CURRENT FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 862
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 2580580CT1
; US-09-289-349-6

Alignment Scores:
Pred. No.:      2.71e-27      Length:      862
Score:          281.00      Matches:      57
Percent Similarity: 98.28%      Conservative: 0
Best Local Similarity: 98.28%      Mismatches: 0
Query Match:     25.50%      Indels:      1
DB:              3          Gaps:      0

US-09-989-724-387 (1-212) x US-09-289-349-6 (1-862)

Qy 156 ValAlaIleAlaLeuLeuIleLeuSerGlyIleTrpGlnArgArgGlyAsnLysGlu 175
Db 1 GTTGCAATTGCACCTACTGATTTTATCAGGGATCTGGCAAGCTAGAACAGAACAAAGAA 60

Qy 176 ProSerGluValAspAspAlaGluAspLysCysGluAsnMetIleThrIleGluAsnGly 195
Db 61 CCATCTCAAGTGGATCAGCTGAAGATAAGTGTGAAACATGATCATCAATTTGAAATGCG 120

Qy 196 IleProSerAspProLeuAspMetLysGly-GlyIleLeuMetMetProSer 212
Db 121 ATCCCTCTGATCCCTGGACATGAAGGGGCGCATATTATGATGCTTCA 172

RESULT 15
US-09-280-116-40/c
; Sequence 40, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
; FILE REFERENCE: 5800-24, 035800/176965
; CURRENT APPLICATION NUMBER: US/09/280,116A
; CURRENT FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40
; LENGTH: 2350
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: angiotensin-converting enzyme
; US-09-280-116-40

Alignment Scores:
Pred. No.:      2.63e-20      Length:      2350
Score:          233.50      Matches:      61
Percent Similarity: 62.86%      Conservative: 27
Best Local Similarity: 43.57%      Mismatches: 37
Query Match:     21.19%      Indels:      16
DB:              3          Gaps:      4

US-09-989-724-387 (1-212) x US-09-280-116-40 (1-2350)

Qy 10 ThrAlaIleHisAlaGluLeuCysGlnProGlyAlaGluAsnAlaPheLysValArgLeu 29
Db 435 ACTGGAGTCCATATGCAG-----ACCAAGCATCAAGTGAGAGATA 394

Qy 30 -SerIleArgThrAlaLeuGlyAspLysAlaTyrAlaTrpAspThrAsnGluGlyLe 49
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Db      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 334
QY      393 AACCTAAATCAGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCT 334
Db      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 65
QY      49 uPheLysAlaMetValAlaPheSerMetArg-----LysValProAsnArgGl 65
Db      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 274
QY      333 GTTCCGATCATCTGTTCATATGCTATGAGCGAGTACTTTTAAAGTAAAAAATCAGCA 274
QY      65 uAlaThrGluIleSerHis-----ValLeuLeuCysAsnValThrGlnArgValSerPh 83
Db      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 215
QY      273 TGATTCCTT--TTGGGAGGAGGATGCGAGTGGCTAATTGAAACCAAGAAATCTCCTT 215
QY      83 eTrpPhe-ValValThrAspProSerLys---AsnHisThrLeuProAlaValGluValG 102
Db      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 155
QY      214 TAATTTCTTTGGTCACTGCCCTTAAATGTGTCTGATATCATTCTAGAACTGAAGTTG 155
QY      102 lnSerAlaIleArgMetAsnLysAsnArgIleAsnAsnAlaPhePheLeuAsnAspGlnT 122
Db      ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 95
QY      154 AAAAGGCCATCAGGATGTCGCGAGCGGTATCAATGATGCTTCCGCTCTGAATGACAACA 95
QY      122 hrLeuGluPheLeuLysIleProSerThrLeuAlaProProMetAspProSerVal 140
Db      ::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 39
QY      94 GCCTAGAGTTTCTGGGGATACAGCCAACTTGGACCTCTTAACCAAGCCCCCTGT 39
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Job time : 233 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: September 4, 2005, 10:10:34 ; Search time 612 Seconds  
(without alignments)  
2268.577 Million cell updates/sec

Perfect score: 1102  
Sequence: 1 MLWLLFLYTAHAEICQPG.....ENCIPSDPLDMKGGILMPS 212

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7338684 seqs, 3274456166 residues

Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries

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-TRANS=human40.cdi -LIST=1500 -DOCALLIGN=200 -THR SCORE=pcr -THR MAX=100  
-THR\_MIN=0 -ALIGN=0 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZES=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US0989724 @CIGN 1 1 723 @runat\_02092005\_161422\_19574  
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12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
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14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
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19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
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23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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518	1102	100.0	1346	21	US-10-931-886-481	Sequence 481, App
520	1102	100.0	1346	22	US-10-955-952-481	Sequence 481, App
521	1102	100.0	1346	22	US-10-950-374-386	Sequence 386, App
522	1089	98.8	1312	16	US-10-133-013-205	Sequence 205, App
523	1089	98.8	1322	14	US-10-097-065-17	Sequence 17, Appl
524	1089	98.8	1432	17	US-10-372-876-17	Sequence 17, Appl
525	1082	98.2	1447	10	US-09-892-877-22	Sequence 22, Appl
526	1082	98.2	1447	10	US-09-948-783-22	Sequence 22, Appl
527	1064	96.6	848	10	US-09-903-190-27	Sequence 27, Appl
528	1064	96.6	848	15	US-10-319-763-27	Sequence 27, Appl
529	1064	96.6	848	21	US-10-926-683-5	Sequence 5, Appl
530	1064	96.6	848	21	US-10-930-331-27	Sequence 27, Appl
531	1062	96.4	1356	14	US-10-097-065-122	Sequence 122, App
532	1062	96.4	1356	17	US-10-372-876-122	Sequence 122, App
533	924	83.8	1181	18	US-10-152-319A-1744	Sequence 1744, Ap
534	597	54.2	532	9	US-09-728-445-570	Sequence 570, App
535	597	54.2	532	22	US-10-964-549-570	Sequence 570, App
536	463	42.0	355	9	US-09-867-701-1636	Sequence 1636, Ap
537	376	34.1	2415	24	US-11-059-218-3	Sequence 3, Appl
538	376	34.1	3324	14	US-10-116-802-172	Sequence 172, App
539	376	34.1	3325	13	US-10-114-893-85	Sequence 85, Appl
540	376	34.1	3334	9	US-09-978-385-1	Sequence 1, Appl
541	376	34.1	3396	11	US-09-999-781-1	Sequence 1, Appl
542	376	34.1	3396	14	US-10-158-847-141	Sequence 141, App
543	376	34.1	3396	15	US-10-158-825-141	Sequence 141, App
544	376	34.1	3396	15	US-10-158-825-141	Sequence 141, App
545	376	34.1	3396	24	US-11-059-218-1	Sequence 1, Appl
546	376	34.1	3405	15	US-10-005-956-569	Sequence 569, App
547	376	34.1	3405	15	US-10-005-956-842	Sequence 842, App
548	376	34.1	3405	21	US-10-956-157-2371	Sequence 2371, Ap
549	376	34.1	3405	22	US-10-756-149-2496	Sequence 2496, Ap
996	369	33.5	3732	21	US-10-931-886-71	Sequence 71, Appl
998	369	33.5	3732	22	US-10-955-952-71	Sequence 71, Appl
999	361	32.8	2638	9	US-09-978-385-5	Sequence 5, Appl
1000	361	32.8	2638	9	US-09-978-385-8	Sequence 8, Appl
1001	359	32.6	2911	9	US-09-969-384-12	Sequence 12, Appl
1002	359	32.6	2920	9	US-09-969-384-2	Sequence 2, Appl
1003	359	32.6	2920	14	US-10-158-847-137	Sequence 137, App
1004	359	32.6	2920	15	US-10-158-825-137	Sequence 137, App
1005	359	32.6	2920	19	US-10-158-825-137	Sequence 137, App
1006	335	30.4	213	9	US-09-864-761-23160	Sequence 23160, A
1007	324	29.4	464	9	US-09-864-761-6445	Sequence 6445, Ap
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1010	261.5	23.7	561	11	US-09-969-034-1556	Sequence 1556, Ap
1011	259	23.5	2415	9	US-09-978-385-7	Sequence 7, Appl
1012	243	22.1	620	13	US-10-027-632-228334	Sequence 228334, A
1013	243	22.1	620	17	US-10-027-632-228334	Sequence 228334, A
1014	238	21.6	3474	21	US-10-204-921-37	Sequence 37, Appl
1015	232	21.1	1013	21	US-10-651-237-64	Sequence 64, Appl
1016	232	21.1	1013	21	US-10-782-413-64	Sequence 64, Appl
1017	106.5	9.7	3666	19	US-10-466-531-28	Sequence 28, Appl
1018	102	9.3	60	10	US-09-908-975-8765	Sequence 8765, Ap
1019	98	8.9	531	10	US-09-814-353-18996	Sequence 18996, A
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1024	91.5	8.3	3134	14	US-10-152-661-478	Sequence 478, App
1025	91.5	8.3	3380	10	US-09-866-050A-514	Sequence 514, App
1026	91.5	8.3	3380	14	US-10-152-661-514	Sequence 514, App
1027	91	8.3	2421	17	US-10-282-122A-27318	Sequence 27318, A
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1029	91	8.3	38459	10	US-09-960-858-3	Sequence 3, Appl
1030	91	8.3	38459	18	US-10-251-668-3	Sequence 3, Appl

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1032	89.5	8.1	2545	15	US-10-678-160A-18	Sequence 18, Appl	1105	82	7.4	4986	21	US-10-956-157-1788	Sequence 1788, Ap
1033	89.5	8.1	3146	20	US-10-037-270-277	Sequence 277, App	1106	82	7.4	4995	10	US-09-984-120-17	Sequence 17, Appl
1034	89.5	8.1	3146	17	US-10-117-722-277	Sequence 277, App	1107	82	7.4	4995	10	US-09-836-353A-17	Sequence 17, Appl
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1036	89.5	8.1	3150	9	US-09-969-708-453	Sequence 453, App	1109	82	7.4	6314	17	US-10-366-547-48	Sequence 48, Appl
1037	89.5	8.1	3150	9	US-09-954-456-1234	Sequence 1234, Ap	1110	81.5	7.4	910	22	US-10-032-214-258	Sequence 258, App
1038	89.5	8.1	3150	21	US-10-843-641A-2790	Sequence 2790, Ap	1111	81.5	7.4	910	22	US-10-479-901-258	Sequence 258, App
1039	89.5	8.1	3150	21	US-10-843-641A-4251	Sequence 4251, Ap	1112	81.5	7.4	3147	19	US-10-384-339C-12	Sequence 12, Appl
1040	89.5	8.1	3150	21	US-10-843-641A-4251	Sequence 4251, Ap	1113	81.5	7.4	3147	20	US-10-769-565-8	Sequence 8, Appli
1041	89.5	8.1	3617	17	US-10-161-493-65	Sequence 65, Appl	1114	81.5	7.4	3269	9	US-09-969-347-167	Sequence 167, App
1042	88.5	8.0	3617	22	US-10-161-493-63	Sequence 63, Appl	1115	81.5	7.4	3269	21	US-10-843-641A-8296	Sequence 8296, Ap
1043	88	8.0	1177	22	US-10-024-607-24	Sequence 24, Appl	1116	81.5	7.4	3269	22	US-10-756-149-2141	Sequence 2141, Ap
1044	87	7.9	1089	22	US-10-024-607-25	Sequence 25, Appl	1117	81.5	7.4	5717	18	US-10-211-462-188	Sequence 188, App
1045	87	7.9	4631	10	US-09-984-130-25	Sequence 25, Appl	1118	81.5	7.4	5717	18	US-10-641-643-1333	Sequence 1333, Ap
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1047	86	7.8	2747	9	US-09-917-800A-1588	Sequence 1588, Ap	1120	81.5	7.4	6952	20	US-10-357-930-25820	Sequence 25820, A
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1051	85.5	7.8	3447	9	US-09-884-441-456	Sequence 456, App	1124	80.5	7.3	903	19	US-10-437-963-85740	Sequence 85740, A
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1055	85.5	7.8	3447	21	US-10-860-790-456	Sequence 456, App	1128	80.5	7.3	1636	10	US-09-907-969-467	Sequence 467, App
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1057	85.5	7.8	3557	9	US-09-884-441-463	Sequence 463, App	1130	80.5	7.3	1636	21	US-10-860-790-467	Sequence 467, App
1058	85.5	7.8	3557	10	US-09-907-969-457	Sequence 457, App	1131	80.5	7.3	1704	17	US-10-333-900-11	Sequence 11, Appl
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1060	85.5	7.8	3557	10	US-09-827-271-457	Sequence 457, App	1133	80.5	7.3	2166	15	US-10-101-510-326	Sequence 326, App
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1075	84.5	7.7	529	19	US-10-430-201-1558	Sequence 1558, Ap	1148	79.5	7.2	9023608	15	US-10-156-761-1	Sequence 1, Appli
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1077	84.5	7.7	3967	17	US-10-291-265-574	Sequence 574, App	1150	79	7.2	1512	9	US-09-974-300-2191	Sequence 2191, Ap
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1080	84.5	7.7	38306	19	US-10-708-763-5	Sequence 5, Appli	1153	79	7.2	5205	15	US-10-288-232-29	Sequence 29, Appl
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1083	83.5	7.6	5117	15	US-10-390-501-1	Sequence 1, Appli	1156	79	7.2	254087	13	US-10-087-132-223	Sequence 223, App
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1085	83.5	7.6	5117	19	US-10-723-606-1	Sequence 1, Appli	1158	79	7.2	3011208	17	US-10-398-221-2058	Sequence 2058, Ap
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1088	83	7.5	5588	9	US-09-917-800A-1565	Sequence 1565, Ap	1161	78.5	7.1	781	17	US-10-027-632-172011	Sequence 172011,
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1090	83	7.5	1830121	17	US-10-329-670-1	Sequence 1, Appli	1163	78.5	7.1	1060	10	US-09-907-969-387	Sequence 387, App
1091	83	7.5	1830121	17	US-10-158-865-1	Sequence 1, Appli	1164	78.5	7.1	1060	10	US-09-907-969-387	Sequence 387, App
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c1096	82.5	7.5	560	20	US-10-425-115-92183	Sequence 92183, A	1168	78.5	7.1	1761	9	US-09-884-441-387	Sequence 387, App
c1097	82.5	7.5	13884	9	US-09-070-927A-341	Sequence 341, App	1169	78.5	7.1	1761	10	US-09-907-969-387	Sequence 387, App
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1101	82	7.4	1929	15	US-10-106-698-805	Sequence 805, App	1173	78.5	7.1	1845	19	US-10-437-963-63705	Sequence 63705, A
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1103	82	7.4	4986	16	US-10-096-534-20	Sequence 20, Appl	1175	78.5	7.1	2100	14	US-10-152-661-479	Sequence 479, App
							1176	78.5	7.1	2608	9	US-09-884-441-386	Sequence 386, App

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1178	78.5	71.1	2608	10	US-09-827-271-386	Sequence 386, App	1251	76.5	6.9	5793	14	US-10-097-340-213	Sequence 213, App
1179	78.5	71.1	2608	15	US-10-198-053-386	Sequence 386, App	1252	76.5	6.9	5796	18	US-10-302-172-48	Sequence 48, Appl
1180	78.5	71.1	2608	21	US-10-860-790-386	Sequence 386, App	1253	76.5	6.9	36535	19	US-10-739-096-9	Sequence 9, Appli
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1182	78.5	71.1	2608	9	US-09-910-689-205	Sequence 205, App	1255	76	6.9	657	13	US-10-027-632-145096	Sequence 145096,
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1184	78.5	71.1	2608	9	US-09-884-441-462	Sequence 462, App	1257	76	6.9	730	15	US-10-029-517-20	Sequence 20, Appl
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1187	78.5	71.1	2608	13	US-09-827-771-311	Sequence 311, App	1260	76	6.9	981	15	US-10-029-517-16	Sequence 16, Appl
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1193	78.5	71.1	2608	21	US-10-860-790-311	Sequence 311, App	1266	75.5	6.9	520	19	US-10-021-323-9630	Sequence 9630, Ap
1194	78.5	71.1	2608	21	US-10-860-790-462	Sequence 462, App	1267	75.5	6.9	570	9	US-09-864-761-18556	Sequence 18556, A
1195	78.5	71.1	6384	19	US-10-437-963-96102	Sequence 96102, A	1268	75.5	6.9	768	19	US-10-775-920-94	Sequence 94, Appl
1196	78.5	71.1	10622	10	US-09-907-969-569	Sequence 569, App	1269	75.5	6.9	805	19	US-10-775-920-78	Sequence 78, Appl
1197	78.5	71.1	10622	15	US-10-198-053-569	Sequence 569, App	1270	75.5	6.9	806	18	US-10-424-599-56356	Sequence 56356, A
1198	78.5	71.1	10622	21	US-10-860-790-569	Sequence 569, App	1271	75.5	6.9	859	15	US-10-029-517-103	Sequence 103, App
1199	78.5	71.1	11288	9	US-09-947-9258-4	Sequence 4, Appli	1272	75.5	6.9	859	17	US-10-439-703-49	Sequence 49, Appl
1200	78.5	71.1	11288	9	US-09-822-634-1	Sequence 1, Appli	1273	75.5	6.9	859	19	US-10-775-920-79	Sequence 79, Appl
1201	78.5	71.1	15056	9	US-09-322-822-4	Sequence 4, Appli	1274	75.5	6.9	900	15	US-10-032-214-2	Sequence 2, Appli
1202	78.5	71.1	15056	10	US-09-814-357-14	Sequence 14, Appl	1275	75.5	6.9	900	22	US-10-479-901-2	Sequence 2, Appli
1203	78.5	71.1	15056	14	US-09-814-351-14	Sequence 14, Appl	1276	75.5	6.9	909	15	US-10-032-214-15	Sequence 15, Appl
1204	78.5	71.1	15056	14	US-10-045-116-25	Sequence 25, Appl	1277	75.5	6.9	909	15	US-10-032-214-101	Sequence 101, App
1205	78.5	71.1	15056	15	US-10-226-820-10	Sequence 10, Appl	1278	75.5	6.9	909	15	US-10-032-214-124	Sequence 124, App
1206	78.5	71.1	15056	22	US-10-691-045-14	Sequence 14, Appl	1279	75.5	6.9	909	15	US-10-032-214-134	Sequence 134, App
1207	78.5	71.1	15056	22	US-10-938-227-3	Sequence 3, Appli	1280	75.5	6.9	909	22	US-10-479-901-15	Sequence 15, Appl
1208	78.5	71.1	177380	21	US-10-484-577-693	Sequence 683, App	1281	75.5	6.9	909	22	US-10-479-901-101	Sequence 101, App
1209	78	71.1	903	22	US-10-032-214-117	Sequence 117, App	1282	75.5	6.9	909	22	US-10-479-901-124	Sequence 124, App
1210	78	71.1	903	22	US-10-479-901-117	Sequence 117, App	1283	75.5	6.9	909	22	US-10-479-901-134	Sequence 134, App
1211	78	71.1	1621	19	US-10-115-635-99	Sequence 99, Appl	1284	75.5	6.9	910	15	US-10-032-214-116	Sequence 116, App
1212	78	71.1	2012	20	US-10-723-860-4949	Sequence 4949, Ap	1285	75.5	6.9	910	15	US-10-032-214-140	Sequence 140, App
1213	78	71.1	2664	16	US-10-132-350-19	Sequence 19, Appl	1286	75.5	6.9	910	22	US-10-479-901-116	Sequence 116, App
1214	78	71.1	2664	24	US-11-071-833-19	Sequence 19, Appl	1287	75.5	6.9	910	22	US-10-479-901-116	Sequence 116, App
1215	78	71.1	3003	18	US-10-425-114-34535	Sequence 34535, A	1288	75.5	6.9	912	15	US-10-032-214-125	Sequence 125, App
1216	78	71.1	3080	24	US-10-132-350-17	Sequence 17, Appl	1289	75.5	6.9	912	15	US-10-032-214-132	Sequence 132, App
1217	78	71.1	3080	24	US-11-071-833-17	Sequence 17, Appl	1290	75.5	6.9	912	22	US-10-479-901-125	Sequence 125, App
1218	78	71.1	70019	19	US-10-322-281-823	Sequence 823, App	1291	75.5	6.9	912	22	US-10-479-901-132	Sequence 132, App
1219	78	71.1	82121	17	US-10-085-117-136	Sequence 136, App	1292	75.5	6.9	962	9	US-09-864-761-1805	Sequence 1805, Ap
1220	78	71.1	134481	13	US-10-087-192-295	Sequence 295, App	1293	75.5	6.9	962	17	US-10-282-122A-8082	Sequence 8082, Ap
1221	78	71.1	367378	16	US-10-312-841-1	Sequence 1, Appli	1294	75.5	6.9	1296	19	US-10-775-920-82	Sequence 82, Appl
1222	77.5	7.0	583	17	US-10-374-780A-572	Sequence 572, App	1295	75.5	6.9	1296	19	US-10-775-920-83	Sequence 83, Appl
1223	77.5	7.0	583	18	US-10-412-699B-1064	Sequence 1064, Ap	1296	75.5	6.9	1355	9	US-09-925-301-19	Sequence 19, Appl
1224	77.5	7.0	642	21	US-10-794-514A-445	Sequence 445, App	1297	75.5	6.9	1428	17	US-10-447-839A-20	Sequence 20, Appl
1225	77.5	7.0	945	16	US-10-032-585-6686	Sequence 6686, Ap	1298	75.5	6.9	1428	21	US-10-778-859-20	Sequence 20, Appl
1226	77.5	7.0	1480	21	US-10-495-148-80	Sequence 80, Appl	1299	75.5	6.9	1572	24	US-11-055-119-1	Sequence 1, Appli
1227	77.5	7.0	2309	18	US-10-424-599-107910	Sequence 107910,	1300	75.5	6.9	1650	17	US-10-282-122A-6619	Sequence 6619, Ap
1228	77.5	7.0	2313	9	US-09-789-919-19	Sequence 19, Appl	1301	75.5	6.9	1721	9	US-09-864-864-280	Sequence 280, App
1229	77.5	7.0	3857	9	US-09-789-919-65	Sequence 65, Appl	1302	75.5	6.9	1721	9	US-09-967-768A-224	Sequence 224, App
1230	77.5	7.0	36462	19	US-10-739-096-1	Sequence 1, Appli	1303	75.5	6.9	1721	14	US-10-097-340-211	Sequence 211, App
1231	77.5	7.0	36462	22	US-10-494-364-1	Sequence 1, Appli	1304	75.5	6.9	1721	14	US-10-171-311-155	Sequence 155, App
1232	77.5	7.0	188169	22	US-10-981-277-45	Sequence 45, Appl	1305	75.5	6.9	1721	15	US-10-007-926A-19	Sequence 58, Appl
1233	77	7.0	916	18	US-10-424-599-84484	Sequence 84484, A	1306	75.5	6.9	1721	15	US-10-029-517-3	Sequence 3, Appli
1234	77	7.0	2433	19	US-10-437-963-80528	Sequence 80528, A	1307	75.5	6.9	1721	17	US-10-173-118-775	Sequence 775, App
1235	77	7.0	2907	21	US-10-887-553A-983	Sequence 983, App	1308	75.5	6.9	1721	18	US-10-342-887-775	Sequence 775, App
1236	77	7.0	2979	16	US-10-181-804A-1	Sequence 1, Appli	1309	75.5	6.9	1721	21	US-10-775-920-88	Sequence 88, Appl
1237	77	7.0	165539	22	US-10-981-277-32	Sequence 32, Appl	1310	75.5	6.9	1721	21	US-10-843-641A-6369	Sequence 6369, Ap
1238	77	7.0	211257	13	US-10-087-192-529	Sequence 529, App	1311	75.5	6.9	1799	17	US-10-477-839A-19	Sequence 19, Appl
1239	77	7.0	225646	19	US-10-470-565-1	Sequence 1, Appli	1312	75.5	6.9	1799	21	US-10-778-859-19	Sequence 19, Appl
1240	77	7.0	225646	19	US-10-470-565-1	Sequence 1, Appli	1313	75.5	6.9	1804	9	US-09-964-824A-573	Sequence 573, App
1241	76.5	6.9	826	18	US-10-424-599-135108	Sequence 135108,	1314	75.5	6.9	1804	15	US-10-029-517-17	Sequence 17, Appl
1242	76.5	6.9	912	15	US-10-032-214-12	Sequence 12, Appl	1315	75.5	6.9	1804	15	US-10-717-597-30	Sequence 30, Appl
1243	76.5	6.9	912	22	US-10-479-901-12	Sequence 12, Appl	1316	75.5	6.9	1804	19	US-10-775-920-84	Sequence 84, Appl
1244	76.5	6.9	1437	20	US-10-425-115-116718	Sequence 116718,	1317	75.5	6.9	1804	21	US-10-843-641A-5876	Sequence 5876, Ap
1245	76.5	6.9	1644	14	US-10-161-572-5	Sequence 5, Appli	1318	75.5	6.9	1804	22	US-10-756-149-1275	Sequence 1275, Ap
1246	76.5	6.9	1650	10	US-09-972-268-3	Sequence 3, Appli	1319	75.5	6.9	1823	15	US-10-101-510-339	Sequence 339, App
1247	76.5	6.9	1650	10	US-09-972-268-3	Sequence 3, Appli	1320	75.5	6.9	2026	14	US-10-198-846-12589	Sequence 12589, A
1248	76.5	6.9	1650	14	US-10-161-572-4	Sequence 4, Appli	1321	75.5	6.9	2032	18	US-10-425-114-30364	Sequence 30364, A
1249	76.5	6.9	2388	20	US-10-425-115-22693	Sequence 22693, A	1322	75.5	6.9	2221	18	US-10-425-114-583	Sequence 583, App

1323	75.5	6.9	2502	20	US-10-425-115-145912	Sequence 145912,	1396	74.5	6.8	1711	18	US-10-152-319A-1765	Sequence 1765, Ap
1324	75.5	6.9	2678	16	US-10-252-157-103	Sequence 103, App	1397	74.5	6.8	1725	19	US-10-363-829-117	Sequence 117, App
1325	75.5	6.9	2678	16	US-10-252-157-103	Sequence 103, App	1398	74.5	6.8	1727	9	US-09-822-830A-41	Sequence 41, Appl
1326	75.5	6.9	4139	9	US-09-964-824A-105	Sequence 105, App	1399	74.5	6.8	2149	18	US-10-641-643-765	Sequence 765, App
1327	75.5	6.9	4139	9	US-09-964-824A-578	Sequence 578, App	1400	74.5	6.8	2297	17	US-10-406-317-41	Sequence 41, Appl
1328	75.5	6.9	4139	9	US-09-864-864-334	Sequence 334, App	1401	74.5	6.8	2472	18	US-10-424-599-17581	Sequence 17581, A
1329	75.5	6.9	4139	9	US-09-880-107-2121	Sequence 2121, Ap	1402	74.5	6.8	17758	17	US-10-264-237-2833	Sequence 2833, Ap
1330	75.5	6.9	4139	11	US-09-968-007A-751	Sequence 751, App	1403	74.5	6.8	36312	19	US-10-322-281-205	Sequence 205, App
1331	75.5	6.9	4139	14	US-10-171-311-157	Sequence 157, App	1404	74.5	6.8	38521	19	US-10-477-527-33	Sequence 33, Appl
1332	75.5	6.9	4139	15	US-10-177-293-310	Sequence 310, App	1405	74.5	6.8	402850	10	US-09-844-653-5	Sequence 9, Appl1
1333	75.5	6.9	4139	17	US-10-440-464-155	Sequence 155, App	1406	74	6.7	797	21	US-10-677-662-9	Sequence 9, Appl1
1334	75.5	6.9	4139	19	US-10-734-564-53	Sequence 53, Appl	1407	74	6.7	807	19	US-10-437-963-67457	Sequence 67457, A
1335	75.5	6.9	4139	19	US-10-775-920-80	Sequence 80, Appl	1408	74	6.7	1122	19	US-10-706-763-1	Sequence 1, Appl1
1336	75.5	6.9	4139	19	US-10-775-920-85	Sequence 85, Appl	1409	74	6.7	1287	17	US-10-369-493-26045	Sequence 26045, A
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1338	75.5	6.9	4139	21	US-10-843-641A-5881	Sequence 5881, Ap	1411	74	6.7	1770	17	US-10-369-493-47001	Sequence 47001, A
1339	75.5	6.9	4139	21	US-10-843-641A-7221	Sequence 7221, Ap	1412	74	6.7	1861	20	US-10-739-930-476	Sequence 476, App
1340	75.5	6.9	5037	20	US-10-723-860-5585	Sequence 5585, Ap	1413	74	6.7	1919	17	US-10-333-227-4	Sequence 4, Appl1
1341	75.5	6.9	5167	14	US-10-270-333-176	Sequence 176, App	1414	74	6.7	1919	17	US-10-333-227-15	Sequence 15, Appl
1342	75.5	6.9	7646	8	US-08-781-986A-121	Sequence 121, App	1415	74	6.7	1919	19	US-10-755-889-349	Sequence 349, App
1343	75.5	6.9	7646	18	US-10-323-624-121	Sequence 121, App	1416	74	6.7	2163	18	US-10-425-114-22715	Sequence 32715, A
1344	75.5	6.9	9461	13	US-10-194-163-513	Sequence 513, App	1417	74	6.7	2163	20	US-10-425-115-66386	Sequence 66386, A
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1346	75.5	6.9	102980	13	US-10-087-192-1330	Sequence 1330, Ap	1419	74	6.7	2651	18	US-10-424-599-83946	Sequence 83946, A
1347	75.5	6.9	160810	22	US-10-981-277-28	Sequence 28, Appl	1420	74	6.7	2693	21	US-10-956-157-4716	Sequence 4716, Ap
1348	75.5	6.9	179887	22	US-10-981-277-29	Sequence 29, Appl	1421	74	6.7	2862	9	US-09-354-453-35	Sequence 35, Appl
1349	75.5	6.9	3186778	13	US-10-027-632-174961	Sequence 174961, App	1422	74	6.7	2862	14	US-10-267-718-35	Sequence 35, Appl
1350	75.5	6.9	3186778	17	US-10-027-632-174961	Sequence 174961, App	1423	74	6.7	2954	9	US-09-354-453-34	Sequence 34, Appl
1351	75	6.8	667	13	US-10-027-632-239890	Sequence 239890,	1424	74	6.7	2954	14	US-10-267-718-34	Sequence 34, Appl
1352	75	6.8	667	17	US-10-027-632-239890	Sequence 239890,	1425	74	6.7	4398	20	US-10-425-115-119186	Sequence 119186,
1353	75	6.8	867	9	US-09-815-243-6588	Sequence 6588, Ap	1426	74	6.7	6760	14	US-09-354-453-33	Sequence 33, Appl
1354	75	6.8	1158	20	US-10-425-115-75349	Sequence 75349, A	1427	74	6.7	6760	14	US-10-267-718-33	Sequence 33, Appl
1355	75	6.8	1324	15	US-10-017-161-1785	Sequence 1785, Ap	1428	74	6.7	39003	18	US-10-672-787-21	Sequence 21, Appl
1356	75	6.8	1324	17	US-10-292-798-1441	Sequence 1441, Ap	1429	74	6.7	45152	13	US-10-087-192-1387	Sequence 1387, Ap
1357	75	6.8	1647	22	US-10-724-972A-3716	Sequence 3716, Ap	1430	74	6.7	113486	20	US-10-417-375-18	Sequence 18, Appl
1358	75	6.8	1861	16	US-10-424-599-42805	Sequence 42805, A	1431	74	6.7	142318	13	US-10-087-192-1504	Sequence 1504, Ap
1359	75	6.8	1986	16	US-10-168-651-37	Sequence 37, Appl	1432	73.5	6.7	375	22	US-10-724-972A-1148	Sequence 1148, Ap
1360	75	6.8	2443	18	US-10-424-599-88558	Sequence 88558, A	1433	73.5	6.7	422	17	US-10-242-535A-48373	Sequence 48373, A
1361	75	6.8	3462	18	US-10-336-603A-41	Sequence 41, Appl	1434	73.5	6.7	422	17	US-10-085-783A-48373	Sequence 48373, A
1362	75	6.8	4140	17	US-10-369-493-39217	Sequence 39217, A	1435	73.5	6.7	453	10	US-10-918-995-29228	Sequence 29228, A
1363	75	6.8	4140	17	US-10-369-493-39588	Sequence 39588, A	1436	73.5	6.7	804	9	US-09-738-626-1734	Sequence 1734, Ap
1364	75	6.8	4140	17	US-10-369-493-39960	Sequence 39960, A	1437	73.5	6.7	825	17	US-10-369-493-25356	Sequence 25356, A
1365	75	6.8	4780	21	US-10-461-862-145	Sequence 145, App	1438	73.5	6.7	900	15	US-10-032-214-3	Sequence 3, Appl1
1366	75	6.8	5361	14	US-10-160-354-1	Sequence 1, Appl1	1439	73.5	6.7	900	22	US-10-479-901-3	Sequence 3, Appl1
1367	75	6.8	5361	17	US-10-295-027-1069	Sequence 1069, Ap	1440	73.5	6.7	912	15	US-10-032-214-109	Sequence 109, App
1368	75	6.8	5361	18	US-10-211-462-186	Sequence 186, App	1441	73.5	6.7	912	15	US-10-032-214-122	Sequence 122, App
1369	75	6.8	5361	19	US-10-783-528-19	Sequence 19, Appl	1442	73.5	6.7	912	22	US-10-479-901-109	Sequence 109, App
1370	75	6.8	5361	21	US-10-928-465-90	Sequence 90, Appl	1443	73.5	6.7	912	22	US-10-479-901-122	Sequence 122, App
1371	75	6.8	5361	22	US-10-491-545A-33	Sequence 33, Appl	1444	73.5	6.7	913	15	US-10-032-214-121	Sequence 121, App
1372	75	6.8	5361	22	US-10-764-425-43	Sequence 43, Appl	1445	73.5	6.7	913	22	US-10-479-901-121	Sequence 121, App
1373	75	6.8	5373	18	US-10-641-643-1318	Sequence 1318, Ap	1446	73.5	6.7	915	22	US-10-724-972A-832	Sequence 832, App
1374	75	6.8	5701	16	US-10-240-965-34	Sequence 34, Appl	1447	73.5	6.7	934	21	US-10-494-672-327	Sequence 327, App
1375	75	6.8	7886	21	US-10-461-862-147	Sequence 147, App	1448	73.5	6.7	939	21	US-10-774-355A-1246	Sequence 1246, Ap
1376	75	6.8	8827	9	US-09-893-238-1	Sequence 1, Appl1	1449	73.5	6.7	1034	18	US-10-236-392-205	Sequence 205, App
1377	75	6.8	12571	9	US-09-965-553-20	Sequence 20, Appl	1450	73.5	6.7	1270	9	US-09-764-853-294	Sequence 294, App
1378	75	6.8	12571	17	US-10-615-005-20	Sequence 20, Appl	1451	73.5	6.7	1272	17	US-10-282-122A-17357	Sequence 17357, A
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1380	75	6.8	12571	19	US-10-799-870-20	Sequence 20, Appl	1453	73.5	6.7	1488	17	US-10-282-122A-41754	Sequence 41754, A
1381	75	6.8	73900	17	US-10-085-117-295	Sequence 295, App	1454	73.5	6.7	1494	17	US-10-369-493-32706	Sequence 32706, A
1382	75	6.8	153740	19	US-10-322-696-85	Sequence 85, Appl	1455	73.5	6.7	1621	18	US-10-424-599-100296	Sequence 100296,
1383	74.5	6.8	600	22	US-10-972-079-53258	Sequence 53258, A	1456	73.5	6.7	1631	10	US-09-882-227-115	Sequence 115, App
1384	74.5	6.8	600	22	US-10-972-079-53259	Sequence 53259, A	1457	73.5	6.7	1638	19	US-10-437-963-45599	Sequence 45599, A
1385	74.5	6.8	600	22	US-10-972-079-53260	Sequence 53260, A	1458	73.5	6.7	1644	9	US-09-860-232A-6	Sequence 6, Appl1
1386	74.5	6.8	924	9	US-09-825-882-17	Sequence 17, Appl	1459	73.5	6.7	1681	17	US-10-093-463-19	Sequence 19, Appl
1387	74.5	6.8	924	18	US-10-343-650A-679	Sequence 679, App	1460	73.5	6.7	1822	9	US-09-776-705-1	Sequence 1, Appl1
1388	74.5	6.8	924	20	US-10-724-208-17	Sequence 17, Appl	1461	73.5	6.7	1822	20	US-10-851-185-1	Sequence 1, Appl1
1389	74.5	6.8	924	20	US-10-770-127-188	Sequence 188, App	1462	73.5	6.7	1949	9	US-09-742-582-7	Sequence 7, Appl1
1390	74.5	6.8	924	20	US-10-724-209-17	Sequence 17, Appl	1463	73.5	6.7	1949	10	US-09-742-580-7	Sequence 7, Appl1
1391	74.5	6.8	924	21	US-10-986-871-17	Sequence 17, Appl	1464	73.5	6.7	1949	10	US-09-742-581-7	Sequence 7, Appl1
1392	74.5	6.8	1239	9	US-09-823-245A-467	Sequence 467, App	1465	73.5	6.7	2247	15	US-10-437-963-13272	Sequence 13272, A
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1394	74.5	6.8	1286	17	US-10-027-632-122566	Sequence 122566,	1467	73.5	6.7	2625	16	US-10-269-909-6	Sequence 6, Appl1
1395	74.5	6.8	1561	17	US-10-220-381-42	Sequence 42, Appl	1468	73.5	6.7	2625	17	US-10-172-118-670	Sequence 670, App

1469	73.5	6.7	2625	17	US-10-457-257-1	Sequence 1, Appli
1470	73.5	6.7	2625	18	US-10-342-887-670	Sequence 670, App
1471	73.5	6.7	2625	20	US-10-678-160A-19	Sequence 19, Appl
1472	73.5	6.7	2625	21	US-10-941-442-1	Sequence 1, Appli
1473	73.5	6.7	2625	22	US-10-712-892A-1	Sequence 1, Appli
1474	73.5	6.7	2828	14	US-10-198-846-12465	Sequence 12465, A
1475	73.5	6.7	2828	20	US-10-357-930-23223	Sequence 23223, A
1476	73.5	6.7	2828	20	US-10-357-930-29095	Sequence 29095, A
1477	73.5	6.7	3403	13	US-10-044-090-597	Sequence 597, App
1478	73.5	6.7	3403	15	US-10-084-817-136	Sequence 136, App
1479	73.5	6.7	3654	21	US-10-956-157-698	Sequence 698, App
1480	73.5	6.7	3661	17	US-10-440-464-151	Sequence 151, App
1481	73.5	6.7	3661	18	US-10-240-425-1210	Sequence 1210, Ap
1482	73.5	6.7	3768	9	US-09-860-232A-4	Sequence 4, Appli
1483	73.5	6.7	3925	14	US-10-198-846-12213	Sequence 12213, A
1484	73.5	6.7	6534	15	US-10-231-778-5	Sequence 5, Appli
1485	73.5	6.7	7015	9	US-09-071-838-6	Sequence 6, Appli
1486	73.5	6.7	7015	15	US-10-213-512-6	Sequence 6, Appli
1487	73.5	6.7	65464	9	US-09-859-888-3	Sequence 3, Appli
1488	73.5	6.7	65464	20	US-10-476-543-3	Sequence 3, Appli
1489	73.5	6.7	108845	19	US-10-367-094-7	Sequence 7, Appli
1490	73.5	6.7	164875	17	US-10-085-117-322	Sequence 322, App
1491	73.5	6.7	414295	20	US-10-719-993-6876	Sequence 6876, Ap
1492	73.5	6.7	3309400	9	US-09-738-626-1	Sequence 1, Appli
1493	73	6.6	413	19	US-10-674-124A-2159	Sequence 2159, Ap
1494	73	6.6	452	10	US-09-918-995-19717	Sequence 19717, A
1495	73	6.6	553	18	US-10-424-599-102056	Sequence 102056,
1496	73	6.6	618	13	US-10-081-218-2	Sequence 2, Appli
1497	73	6.6	794	19	US-10-767-795-34	Sequence 34, Appl
1498	73	6.6	813	15	US-10-106-698-771	Sequence 771, App
1499	73	6.6	850	20	US-10-425-113-176609	Sequence 176609,
1500	73	6.6	864	17	US-10-282-122A-21045	Sequence 21045, A

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